	MPSrch_nn n.a n.a. date Copyright (c) 1993 Distribution Copyright (c) 1993 Distribution Tabular output not generated Title: Description (1-1891) from Perfect Score: 1891 Tapular output not generated Title: N.A. Sequence: 1891 TTTTT N.A. Sequence: 1891 TTTTT N.A. Sequence: 1891 TTTTT N.A. Sequence: 1891 TTTTT Description (1-1891) from Perfect Score: 1891 TTTTT N.A. Sequence: 1891 TTTTT Description (1-1891) from Perfect Score: 1891 TTTTT N.A. Sequence: 1891 TTTTT Description (1-1891) from Perfect Score: 1891 Description (1-1891) from Perfect Score: 1891 TTTTT Description (1-1891) from Perfect Score: 1891 TTTTT Description (1-1892) TTTTT TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
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Variance 5.068; scale 2.252

Mean 11.454;

Statistics:

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LYIDALDVTAHPMTGATGVAALQVQSEFQKAYERGIHKSKYMEPTYDDSMNLIAQVP
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841 GAAATGCATGAACTTCTTATGAGGCTCTATGTAACAATACACAGTGATCATGAAGGTGGT
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1861 TTTGCTAATTCTTATTTGATGATATTATGAA 1891

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VOELIPEQQDERKRIKEDMKGSIGNITVDMVLGGMRGWTGLLWRPHYLDPDEGIFFFG
LSIPECQKVLPAAKPGGEPLEBGLLWLLLTGRVPSKEDVNSIVSGIAESGIISLIIMY
TIDALPVTAHPMTOFATGWALQVOSEFGKAFSKGIHKKKWEPTEDSMNLTAQVP
LVAAVYYRRWYKNGOTIFKDESLDYGANFAHLGFSSEBHELLMRLYVTHEDHEGG
NVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEEGGENISKE
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LLFLQNLAKLKPWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALG
LPLERPKSVTMEWLENQCKKA"
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                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
Asteridae; Solananae; Solanales; Solanaceae; Solanum; Potatoe;
section Petota
                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (20-SEP-1993) V. Landschuetze, Inst. fuer Genbiologische
Forschung, Berlin GmbH, Ihnestr. 63, 14195 Berlin, FRG
2 (bases 1 to 1891)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Landschutze, V., Mulier-Rober, B. and Willmitzer, L.
Mitochondrial citrate synthase from potato: predominant expression
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Pred. No. 0.00e+00;
                                       S.tuberosum mRNA for mitochondrial citrate-synthase. X75082
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/protein_id="CAA52976.1"
/db_xref="PID:9483510"
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Planta 196 (4), 756-764 (1995)
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/clone="5-25-10"
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                                                                                                              X75082.1 GI:483509
mitochondrial citrate synthase
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Solanum tuberosum
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Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
Asteridae; Solananae; Solanales; Solanaceae; Nicotiana.
(bases 1 to 1747)
Mueller-Roeber, B., Landschuetze, V. and La.C. U
PROCESSES FOR INHIBITING AND FOR INDUCING FLOWER FORMATION IN
                                                                                  1381 CTTGGCATTTGCTCTCAGCTAATTTGGGACCGAGCTCTTGGATTGCCGCTAGAGAGGCCA 1440
                                                                                                                                                                                                                                                                                                                                                                                                                                         1621 ACTGAATTTGTGTGAATTGTATGGTTTCTCGAGACTTGTCCTGAATTTTGAACTTAGTCT 1680
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                                         1321 AACTATTATGGTTTAACTGAAGCAAGATATTATACGGTCCTCTTTGGCGTATCAASAGCT 1380
                                                                                                                                                                                                                                                                                                        1501 CTCGCGAGCATAAAACACAATGTATAATCTCTATGAATAATTGCTTGACAAGCACTCCT 1550
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TIDALPVTAHPMTQFATGWALQVQSEFGKAYEKGIHKSKLWEPTYEDSMSLIAOVPL
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KDYAMWTLKSGKVVDGFGHGVLKKTDPRYTCQREFALKHLPEDPLFGLVAKLYFEVLL
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LERPKSVTMEWLENHCKKA"
                                                                                                      /translation="MVFYRGVSLLSKLRSRAVQQTNLSNSVRWLQVQTSSGLDLRSEL
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Eukaryota; Viridiplantae; Streptophyta; Embr;ophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; Asteridae; Solanales; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 1747)
La Cognata, U., Landschuetze, V., Willmitzer, L. and Mueller-Roeber, B.
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876 AATACACAGIGAICAIGAAGGIGGIAAIGICAGIGCICACACAGGGICACIIGGIIGCIAG 935
                                                                                                                                                        927 IGCITIGICAGACCCTIACCTCTCCTTCGCTGCTGCTTTGAATGGTTTAGCTGGACCACT 986
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Submitted (23-JAN-1995) U. La Cognata, Institute fuer
Genbiologische Forschung, Berlin GmbH, Innestrasse 63, 14195
                                                                                                                                                                                                    936 IGCTITGICIGAICCITACCICTCCCTITGCIGCIGCITTGAAIGGITTAGCCGGACCACI
                                                                                                                                                                                                                                             987 ICATGGTTTAGCCAATCAGGAAGTTTTGCTATGGATCAAATCTGTTGTAGAGGAGTGTGG
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                                                                  867 GATACACAGTGATCATGAAGGTGGTAACGTCAGTGCTCACACAGGTCACTTGGTTGCTAG
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La Cognata, U.
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SAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWI KSVVEECGENI SKEQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 CTGTCAAAGCTCCGCTCTCGAGCGGTCCAACAGTCAAATGTTAGCAATTCTGTGCGCTGG 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 CCAGAACAACAGGATCGCCTAAAGAAGCTCAAGTCAGAGCATGGAAAGGTTCAATTGGGA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 AACAICACAGIIGAIAIGGIICIIGGIGGAAIGAGGAAIGACAGGAIIACIGIGGGAA 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 65.5%; Score 1238; DB 27; Length 1747; Best Local Similarity 92.8%; Pred. No. 0.00e+00; Matches 1439; Conservative 0; Mismatches 93; Indels 18;
                                                     /organism="Nicotiana tabacum"
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                                                                                                                                                                                                                                                                                      /product="citrate synthase"
/protein_id="CAA59008.1"
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                                                                                                                                                                          750 GTACAAGAAGGCAACACTATACCTAAGGATGACTCACTGGATTATGGTGCAAATTTTGC 809
                                                                                                                                                                                                                                                                             810 TCACATGCTTGGTTTCAGTAGCTCTGACATGCATGAGCTT---ATGAAGCTCTATGTCAC 865
                                                                                                                                                                                                                                                                                                                                                                                                                                   936 IGCTITGTCTGATCCTTACCTCTCCTTTGCTGCTGCTTTGAATGGTTTAGCCGGACCACT 995
                        636 ATTTCAAAAGGCATACGAGAAAGGGATTCACAAATCAAAGTATTGGGAACCAACATATGA 695
                                                                        690 GGATTCCATGAGTTTGATTGCTCAAGTTGCACTTGTTGCTGCTTATGTTTATCGCAGGAT 749
                                                                                                                          696 GGATTCCATGAATCTGATTGCTCAAGTTCCACTTGTTGCTGCTTATGTTTATCGCAGGAT 755
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VVAAYIYRRMYKNGQSISTDDSLDYGANFAHMLGYDSPSMQELMRLYVTIHTDHEGGN
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LKELIPEQQERIKKLKAEHGKVQLGNITVDMVLGGMRGMTGLLWETSLLDPEEGIRFF
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LKDYIWKTLNSGKVVPGYGHGVLRNTDPRYICQREFALKHLPDDPLF0I,VSNLFEVVP
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LPLERPKSVTMEWLENHCKKSS"
                  Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; euphyllophytes: Spermatophyta; Magnoliophyta; eudicotyledons; Asteridae; Araliales: Applaceae; Dancus 1 (bases 1 to 1859)
Takte.E., Koyama, H., Shirano, Y., Shibata, D. and Hara, T. Direct Submission
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                                                                                                                                                           Submitted (26-AUG.1998) to the DDBJ/EMBL/GenBank databases. Eiji Takita, Gifu University, Laboratory of Plant Cell Technology, Faculty of Agriculture: Yanaqido 1-1, Gifu, Gifu, 501-1193, Japan (E-mailtakitadec.qifu-u.ac.jp, Tel:+81-58-293-2911, Eax:+81-58-293-2911, bases 1 to 1859)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 GAGAAATGGTGTTTTTGGAGTGTTTGGCTGCTTAACAAGCTSGGGTGTGGSGGTGTT
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/protein_id-"BAA32557.1"
/db_xref-"PID:d1033521"
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                                                                                                                                                                                                                                                                                                      TG-TATACAAAACCATCGATGCGTTACCTGTTACAGCTCATCCAATGACTCAATTGCAA 688
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452 TTCGCTTTAGGGGGTTGTCCATACCTGAATGTCAGAAGCTATTACCAGGAGCGAAGCCCG 511
                                                                                                                                                                                                                                                   485 AAGAGCAAGTGAATTCAATTGTCTCAGGAATTGCAGAGTCGGGCATCATATCCCTGATCA 544
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                                             365 ITCGCTTCCGGGGGTTGTCTATACCTGAATGCCAAAAGGTATTACCTGCAGCAAAGCCTG
                                                                                                                            425 GGGGTGACCCTTGCCTGAAGGTCTTCTCTGGCTTTTAACAGGAAAGGTGCCATCAA
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Canel,C., Bailey-Serres,J. and Roose,M. Physiological and molecular genetic studies of acid accumulation in
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SHYCHLVASALSDPYLSFLAALNGLAGPLHGLANQEVLUTIKSVVDECGENVYTEQL
KDYVMKTLNSGKVVPGFGHQVLKKTDPRYTCQREFALKHLPDDPLFQLVSKLYEVVPP
ILTKLGKVKNPWPNVDAHSGYLLNHFGLAEARYYTVLFGVSKSLGICSQLIWDRALGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thesis (1994) Botany & Plant Sciences, University of California at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (04-JAN-1995) Camilo Canel, University of California at Riverside, Botany & Plant Sciences, Riverside, CA 92521-0124, USA Location/Qualifiers
                                                                                                                       CMU19481 1733 bp mRNA PLN 04-DEC-1995 Citrus maxima citrate synthase (cit) mRNA, nuclear gene encoding mitochondrial protein, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"There is a single copy of the cit gene in the citrus genome. A single transcript with an estimated length of 1,850 nucleotides can be detected in juice cells"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function="synthesis of citrate from oxaloacetate and
                          1442 AGAGTGTCACAATGGAGTGGCTTGAGAACCAGTGCAAGAAAGCATGAATTGTTTGAAA 1499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    function="targets the protein to the mitochondrial
                                                                                                                                                                                                                                                                                                                                             Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Magnoliopsida; Rutanae; Sapindales; Rutaceae; Citrus.
1 (bases I to 1733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="Slamese sweet (pummelo 2240)"
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/protein_id="AAA82743.1"
/db_xref="PID:9624676"
/db_xref="taxon:37334"
/sex="hermaphrodite"
/cell_type="juice cell"
/tissue_type="juice tissue"
/dev_stage="immature"
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                                                                                                                                                                                                                                             68 GAGCAATGGTGTTCTACCGTAGCGTTTCGTTGCTGTCAAAGCTCCGCTCTCGAGCGGTCC 127
                                                                                                                                                                                                                                                                                                                                                                                             172 ACCTICATICICAGCIC---A-AGGAAATGATTCCAGAACAACAGGGGGGCGCTGAAGAAG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                               188 ATCTGCGTTCTGAGCTGGTACAAGAATTGATTCCTGAACAACAGGATCGCCTGAAAAAGA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 GGATGAGAGGAATGACTGGCTTACTTTGGGAAACCTCATTAC-TTGACCCTGATGAGGGA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 GAATGAGAGGAATGACAGGATTACTGTGG-AAACCTCATTACCTTGACCCTGATGAGGGA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348 ATTCGCTTTCGGGGTCTGTCTATTCCTGAGTGCCAGAAGTTGTTACCTGCCGCTAAGCCA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           364 ATTCGCTTCCGGGGTTGTCTATACCTGAATGCCAAAAGGTATTACCTGCAGCAAAGCCT 423
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/db_xref="PID:92300710"
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                       1024 CTATGGATAAAATCTGTTGTAGAAGAATGTGGGGGAGAACATTTCCAAAGAGCAGTTGAAA 1083
                                                                                   1062 GATTATGTCTGGAAAACATTGAATAGTGGCAAGGTTGTCCCTGGATTTGGTCATGGTGTT 1121
                                                                                                                                      1084 GACTATGTTTGGAAAACATTGAACAGTGGCAAGGTTGTCCCTGGTTTTGGACATGGAGTT 1143
                                                                                                                                                                                               1122 TTGCGTAAAACTGATCCGAGATACACTTGTCAGAGGGAGTTTGCCTTGAAGCATTTGCCT 1181
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Mueller-Roeber, B., Landschuetze, V. and La, C.U.
PROCESSES FOR INHIBITING AND FOR INDUCING FLOWER FORMATION IN
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1422 AAAAGTGTAACTTTAGATTGGATTGAGAAAATTGCAAGAAAGCA 1466
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/strain="ZUCHTLINIE 5S 0026"
/db_xref="taxon:3555"
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HOECHST SCHERING AGREVO GMBH (DE)
Other publication DE 4438821 960425
Other publication DE 4435366 960328
Other publication AU 2067995 950925
Other publication DE 4408629 950914.
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A46546
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DSPQMLELMRLYVTHSDHEGGNVSAHTGHLVGSPLSDPYLSFAAALNGLAGFLHGLA
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                                                                                                                                                                                                                                                 0; Mismatches 261; Indels 12; Gaps
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DSPOMLELMRLYVIIHSDHEGGNVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLA
NQEVLLMIKSVVDECGENISTEQLKDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQRE
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1 (bases 1 to 1551)
1 (bases 1 to 1551)
1 a Cognata,U., Landschuetze,V., Willmitzer,L. and Mueller-Roeber,B. Plant Cell Physiol. In press
2 (bases 1 to 1551)
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                                             1103 TGAACAGTGGCAAGGTTGTCCCTGGTTTTTGGACATGGAGTTCTGCGAAAGACTGTACCAA 1162
                                                                                               983 GATACACATGCCAAAGAGAATTTGCGTTGAAGCACTTGCCTGATGACCCATTTTTTCAAT 1042
Submitted (23.JAN-1995) U. La Cognata, Institute fuer
Genbiologische Forschung, Berlin GmbH, Ihnestrasse 63, 14195
                                                                                                                                                                                                                                                                                                                                                                                                    1163 AAGCAAGATACTATACGGTTTTGTTTGGGGTATCAAGGAGTCTTGGAATATGCTCACAGC
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                                                                                                                                                                                                                                                                                                                                     89 GTTTCCAGCTGGGGAATATCAATGTTGACATGGTATTGGGCGGAATGAGAGGAATGACTG 148
                                                                                                                                                                                                                                                                                                                                                                                          265 GGTTCAAT-TGGG-AACATCACAGTTGATATGGTTCTTGGTGGAATGAGAGGAATGACAG 322
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TVLFGVSRSLGIGSQLIWDRALGLPLEPPKSVTMEWLEKFCKRRA"
258 c 370 g 458 t
                                                                                                                                                               0; Mismatches 261; Indels 12;
                                                                                                          Length 1551;
                                                                                                       Score 664; DB 27;
Pred. No. 0.00e+00;
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Similarity 78.5%;
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QLKEYVWKTLNSGKVIPGYGHGVLRNTDPRYVCQPEFALKHHPDDPLFGGCKLMKLAS
CLTELESEEBPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRELLLA
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PVVAAYVYRRMYKNGDSIPSDKSLDYGANFSHMLGFDDERLKELMRLTSPSTVMHEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta: euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 317; Indels 34; Gaps 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolation of a cDNA encoding mitochondrial citrate synthase from Arabidopsis thaliana
                                                                                                                                                                                                                   TTATATGGGACCGAGCTCTTGGCTTGCCGCTAGAGGGCCCAAAGAGTGTCACTATGGAAT 1282
                         1163 GATATACATSCCAGAGAGAGTTCGCTATGAAGCATTTGCCTGAAGATCCACTGTTTCAAC 1222
                                                                           1043 TGGTGTCAAAGTTGTATGAAGTGGTGCCTCCTATTCTATTAGAGGTTGGAAAGGTAAAGA 1102
                                                                                                                             1223 TGGTTTCAAAACTCTACGAAGTTTT-CCTCCTGTTCTTACAGAACTTGGCAAAGTTAA-A 1280
                                                                                                                                                                                     1103 ATCCATGGCCTAATGTTGATGCTCATAGTGGAGTTTTGCTGAACCACTATGGTTTGACAG 1162
                                                                                                                                                                                                                                                                                         1163 AAGCAAGATACTATACGGTTTTGTTTGGGGTATCAAGGAGTCTTGGAATATGCTCACAGC 1222
                                                                                                                                                                                                                                                                                                                                           1340 AAGCAAGATATTATACGGICCTCTTTGGCGTATCAAGAGCTCTTGGCATTTGCTCTCAGC 1399
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1400 TAATTTGGGACCGAGCTCTTGGATTGCCGCTAGAGGGCCAAAGAGTGTCACAATGGAGT 1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION Armbidopsis thallana mRNA for mitochondrial citrate synthetase. ACCESSION X17528
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Unger, E. A., Hand, J.M., Cashmore, A. R. and Vasconcelos, A. C.
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1 (bases 1 to 1680)
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/db_xref="taxon:3702"
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Pred. No. 0.00e+00;
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/protefalid-"c7AA35570.1"
/db_xref-"PID:e1188578"
/db_xref-"PID:92652924"
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943 ICATITGCAGCIGCATTAAATGGITTAGCIGGGCCACTCCATGGTTIGGCIAATCAGGAA 1002
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                                                                                      480 AICA-AAAGAGCAAGIGAAIICAAIIGICICAGGAAIIGCAGAGICGGGCAICAIAICCC 538
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72 AATGGTGTTCTACCGTAGCGTTTCGTTGCTGTCAAAGCTCCGGCTCTCGAG--C-GGTCCA 128
                                                 117 ACAATCTTCACTCAGCAATTCTGTCAGATGGATTCAGATGCAGAGCTCTACCGACCTGGA 175
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/translation="MPTKEQVGALSKELRDRALVHDYVFKAIDALPVTAHPMTQFATG
VMALQVQSEFQKAYEKGIHKSKYWEPTYEDSLSLIARVPIVASYIYRRIYKDGKVIPM
NDSLVIGGNFSHMLGFDSPEMQELMRLYVTNHSDHEGGNVSAHTGHLVASALSDPYLS
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HGVLRKTVPRYTCQREFALKHLPDDPLFQLVSKLYEVVPPVLIQLGKVKNPWPNVDAH
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1 (bases 1 to 1378)
La Cognata, U, LandSchuetze, V., Willmitzer, L and Myeller-Poeber, B. Plant Cell Physiol. In press

2 (bases 1 to 1378)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          citi gene; citrate synthase.

Populus balsamifera subsp. trichocarpa X Populus deltoides.

Populus balsamifera subsp. trichocarpa X Populus deltoides.

Bukaryota, Viridiplantae; Streptophyta: Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta: Magnoliophyta; eudicotyledons;
                                                                                                                                                                                                                                                                                                       1183 CATCCTGACGACCCTCT-TTTCCAGTG-TTGCAAG-CT-TATGAAGTTGGGGTGTTGT-C 1237
                                           1198 ITGCCTGAAGATCCACTGTTTCAACTGGTTTCAAAACTCTAGGAAGTTTTGCTGTTG 1257
                                                                                                 1238 TCACTGAGCTTGAAAGTGA-AGAACCCTGGCCAAATGTTGATGCTCACAGTGGGGTCTTG 1296
                                                                                                                                                  1258 TTACAGAACTIGGCAAAGTTAAAACCTIGGCCAAAIGTIGAIGCCCACAGIGGIGIGIIG 1317
                                                                                                                                                                                                   1297 CIGAACCACTAIGGICIAACCGAAGCAAGGIACTACACCGIGCICTIIGGIGIIICAAGG 1356
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Genbiologische Forschung, Berlin GmbH, Ihnestrasse 63,
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/transl_except=(pos:16. .18,aa:Met)
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/protein.id="CaA59009.1"
/db_xref="PID:e276838"
/db_xref="PID:91648926"
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DB 27; Length 1378

29.8%; Score 564;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1013 AGGAAGTTTTGCTATGGATAAAATCTGTTGTAGAAGAATGTGGGGGAGAACATTTCCAAAG 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1193 AGCATTTGCCTGAAGATCCACTGTTTCAACTGGTTTCAAAACTCTACGAAGTTTT-CCTC 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1252 CTGTTCTTACAGAACTTGGCAAAGTTAAAA--CCTTGGCCAAATGTTGATGCCCACAGTG 1309
                                                                                                                                                                                                                                                                                                                                   191 AAAAAGGGATTCATAAATCAAAGTACTGGGAGCCAACATATGAGGATTCTCTTAGTCTGA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     833 GTAGCTCTGAAATGCATGAACTTCTTATGAGGCTCTATGTAACAATACACAGTGATCATG 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                608 AACAACTTAAAGACTATGTTTGGAAAACATTAAATAGCGGAAAGGTTGTTCCTGGATTTG 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       668 GTCATGGAGTTCTACGCAAAACTGTACCAAGATATACATGTCAAAGGGAGTTTGCATTGA 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                728 AGCATTTACCTGATGATCCATTGTTCCAGCTGGTCTCTAAGCTATATGAAGTTGTACCTC 787
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                                                                                                                                                                                         72 GGTTCATGATTATG-TCTTTAAGGCCATTGATGCCTTACCTGTCACTGCTCATGA 130
                                                                                                                                                                                                                                                                                                   131 CTCAGTTTGGAACTGGTGTTATGGCCCTACAGGTTCAGAGTGAATTTCAAAAGCCTATG 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 TTGCTCGTGTGCCAATAGTAGCTTCATATATTTATCGAAGGTTTACAAAGATGGGAAAG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        713 TIGCICAAGIICCACIIGIIGCIGCIIAIGIIIAICGCAGGAIGIAACAAAGAAIGGIGACA 772
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                                                                                                                                   473 AGGTGCCATCAAAAGAGCAAGTGAATTCAATTGTCTCAGGAATTGCAGAGTGGGGCATCA 532
                                                                                                                                                                                                                                                533 TATCCCTGATCATCATGTATACAACTATTGATGCCTTACCAGTCACAGCTCATCAATGA 592
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                                                                                14 AGGIACCAACCAAAGAAGAGGGGGGGGGGTTTATGGAAGGAATIGGGTGACGGIGC-TCT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   548 AGGAAGTTCTCCTTTGGATCAAATCCGTGGTAGAAGAGTGTGGAGAGAATATAACCACAG
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                            Mismatches 194; Indels
Best Local Similarity 80.0%; Fred. No. 0.00e+00;
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RESULT

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/translation-"MALLTAAARLLGTKNASCLVLAARHASASSTNLKDILADLIPKE
QARIKTFRQQHGKTVVGQTTVDMMYGGMPGMKGLVYETSVLDPNEGIPFPGFSIPEYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLHPMSQLSAAVTALNSESNFAQAYARGISRTKYWELIYEDSVDLIAKLPCVAAKIYR
NLYWEGSGIGAIDSNLDWSHNFTNMLGYTDHQFTELMRLYLTIHSDHEGGNVSAHTSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVGSALSDPYLSFAAAMNGLAGPLHGLANOEVLVWLTOLOKEVGKDVSDEKLRDY IWN TALNSGRVPGOTGHAVLEKTDPRYTCOREFALKHLPNDPMFKLVAOLYK IVPNVLLEOG KAKNPWPNVDAHSOYLLQYYGMTEMNYYTVLEGVSRALGVLAOLIWSRALGFPLERPK SMSTEGLMKFVDSKSG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLLPKAKGGEEPLPEGLFWLLVTGCIPTEEQVSWLSKEWAKRAALPSHVVTMLDNFPT
                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (06-FEB-1998) Molecular Cardiology Institute, 75 Raritan Avenue, Highland Park, NJ 08904, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 ATCACTGTGGACATGATGTATGGTGGCATGAGAGCCATGAAGGGATTGGTGTATGAAACA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 ATCACAGTIGATATGGTTCTTGGTGGAATGAGAGGAATGACAGGATTACTGTG-GAAACC 338
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                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1401)
  05-JUL-1998
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                                                                                                                                                                                                                                                                                          Cloning and sequence analysis of human citrate synthase Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 16;
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                         Homo sapiens citrate synthase mRNA, complete cds.
AF047042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="heart"
/note="isolated from a 22-year old"
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Pred. No. 2.77e-187;
U; Mismatches 41U;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-"citrate synthase"
/protein_id-"AAC25560.1"
/db_xref-"PID:g3288815"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606'
/sex="male"
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Local Similarity 63.7%;
les 746; Conservative
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Direct Submission
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Artlodactyla; Suiformes; Suina; Suidae; Sus. 1 (bases 1 to 1455)
Evans, C.T., Owens, D.D., Sumegi, B., Kispal, G. and Srere, P.A. Isolation, nucleotide sequence, and expression of a cDNA encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1175 AGAGAGACTICGCTAIGAAGCAITIGCCIGAAGAICCACIGIIICAACTGGIIICAAAAC 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1139 IGTACAAGATIGIGCCCAAIGTCCTCTTAGAGCAGGGTAAAGCCAAGAATCCTTGGCCCA 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1235 ICTACGAAGITITCCTCC-TGITCITACAGAACITGGCAAAGITAA-AA-CCTTGGCCAA 1291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1199 ATGIAGATGCTCACAGTGGGGTGCTGCTCCAGTATTATGGCATGACGGAGATGAATTACT 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1292 ATGTTGATGCCCACAGTGGTGTTGTTGAACTATTATGGTTTAACTGAAGCAAGATATT 1351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1352 ATACGGTCCTCTTTGGCGTATCAAGAGCTCTTGGCATTTGCTCTCAGCTAATTTGGGACC 1411
                                                                        603 ITCTGTGGGATCTAATAGCAAAGCTACCTTGTGTTGCAGCAAAGATCTACCGAAATCTCTA 662
                                                                                                                                                                                                                             759 CAAGAATGGTGACACTATACCTAAGGATGAATC---CCTGGATTATGGTGCAAATTTTGC 815
                                                                                                                                                                                                                                                                                723 CAACATGTTAGGCTATACT-GATCATCAGTTCACTGAGCTC--ATGCGCCTGTACCTCAC 779
                                                                                                                                                                                                                                                                                                                                                                                    780 CATCCACAGTGACCATGAGGGTGGCAATGTAAGTGCCCATACCAGCCACTTGGTGGGGCAG 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        840 IGCCCTTTCCGACCCTTACCTGTCCTTTGCAGCCATGAACGGGCTGGCAGGGCCTCT 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            900 CCAIGGACTGGCAAATCAGGAAGTGCTTGTCTGGCTAACA-CAGCTGCAGAAGGAAGTTG 958
                                                                                                                            699 TICCATGAAICTGATIGCTCAAGTICCACTIGTIGCTGCTTATGTTIAICGCAGGAIGTA 758
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663 CIGGGAAGGCAGCGGTAITGGGGCCAITGACICIAACCIGGACIGGICICACAAITICAC
                                                                                                                                                                                                                                                                                                                                 816 TCACATGCTTGGTTTCAGTAGCTCTGAAATGCATGAACTTCTTATGAGGCTCTATGTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                  876 AATACACAGTGATCATGAAGGTGGTAATGTCAGTGCTCACACGGTCACTTGGTTGCTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIGCITSYN 1455 bp mRNA MAM Porcine citrate synthase mRNA, complete cds. M21197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         citrate synthase.
Porcine kidney, cDNA to mRNA, clone PCS4.
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1319 GAGCCTTAGGCTTCCCTCTAGAAAGGCCCAAG 1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1412 GAGCTCTTGGATTGCCGCTAGAGGCCCAAAG 1443
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Biochemistry 27, 4680-4686 (1988)
89000665
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/translation-*MALLTAAARLFGAKNASCLVLAARHASASSTNLKDILADLIPKE
QARIKTFRQOHGNTVVGQITVDAMYGGMRGMKGLVYETSVLDPDEGIRFRGYSIPECQ
KMLPKAKGGEEPLPEGLFWLLVTGQIPTEEQVSWLSKEWAKRAALPSHVVTMLDNFPT
                                                                                                                                                                                                                                                                                                                                                                                                NLHPMSQLSAAITALNSESNFARAYAEGIHRTKYWELIYEDCMDLIAKLPCVAAKIYR
NLYREGSSIGAIDSKLDWSHNFTNMLGYTDAQFTELMRLYLTIHSDHEGGNVSAHTSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVGSALSDPYLSFAAAMGLAGPLHGLANQEVLVWLTQLQKEVGKDVSDEKLRDY IWN
TLNSGRVVPGYGHAVLRKTDPRYTCQREFALKHLPHDPMFKLVAQLYK IVPNVLLEQG
KAKNPWPNVDAHSGVLLQYYGMTEMNYYTVLFGVSRALGVLAQLIWSRALGFPLERPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 241; DB 23; Length 1455;
Pred. No. 3.19e-188;
0; Mismatches 416; Indels 14; Gaps 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           817 CACATGCTTGGTTTCAGTAGCTCTGAAATGCATGAACTTCTTATGAGGCTCTATGTAACA 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 ATCACTGTGGACATGATGTATGGTGGCATGAGAGGCATGAAGGGATTGGTGTATGAAACA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 ATCACAGITGAIAIGGITCIIGGIGGAAIGAGGAAIGACAGGAIIACIGIGGAAACCI 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 TCGGTTCTTGATCCTGATGAGGCCATCCGTTTCCGAGGCTACAGTATCCCTGAATGCCAG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                340 CATTACCTTGACCCTGATGAGGGAATTCGCTTCCGGGGGTTGTCTATACCTGAATGCCAA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313 AAAATGCTGCCCAAGGCTAAGGGTGGGGAAGAACCGCTGCCAGAGGGCTTATTTTGGCTG 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               400 AAGGTATTACCTGCAGCAAAGCCTGGGGGTGAGCCCTTGCCTGAAGGTCTTCTCTGGCTT 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             373 CTGGTAACTGGACAGATCCCAACAGAGGAGCAGGTGTCTTGGCTC-TCAAAAGAGTGGGC 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      432 AAAGAGGGCAGC-TCTGCCCTTCCCATGTGGTC-ACCATGCTGGACAACTTTCCCACGAAT 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 520 GAGTCGGGCATCATATCCCTGATCATCATGTATACAACTATTGATGCCTTACCAGTCACA 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  640 CAAAAGGCATACGAGAAAGGGATTCACAAATCAAAGTATTGGGAACCAACATATGAGGAT 699
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759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             787 ATCCACAGIGACCAIGAAGGIGGCAAIGIAAGIGCICAIACCAGCCAIIIGGIGGGCAGI 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     460 cititaacaggaaaggigccaicaaaagagcaagigaaticaatigicicaggaatigca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  490 CTACACCCCATGTCTCAGCTCAGTGCAGCCATTACAGCCCTCAACAGTGAAAGTAACTTT
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                                                                                                                                                     /note="citrate synthase precursor (EC 4.1.3.7)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="citrate synthase signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333 t
                                                                                                                                                                                                          /protein_id="AAA31017.1"
/db_xref="PID:9164419"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="citrate synthase"
                                                          /organism="Sus scrofa"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                           /db_xref-"GI:164419"
Location/Qualifiers
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Best Local Similarity 63.3%;
Matches 741; Conservative
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Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 1481)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1026 GGTTGTCCCAGGCTAFGGCCACGCAGTACTAAGGAAGACTGATCCACGATATACCTGTCA 1085
                                                                                                                                                                                                                                                                                                                      1086 AAGAGGTTTGCTCTGAAACACCTGCCTCATGACGCCCATGTTTAAGCTGGTTGCTCAGCT 1145
                                                                                                                                                                                                                                                                                                                                                                                                      1146 GTACAAGATTGTGCCCCAATGTCCTCCTGGAACAGGGCAAGGCTAAGAATCCTTGGCCCAA 1205
                                                                                                                                                                                                                                                                                                                                                                                                                                            1236 CTACGAAGITITCCTCC-TGTTCTTACAGAACITGGCAAAGITAA-AA-CCTTGGCCAAA 1292
                                                                                                                    997 CATGGTTTAGCCAATCAGGAAGTTTTGCTATGGATAAAATCTGTTGTAGAAGAATGTGGG 1056
                                                                                                                                                              966 CAAAGATGTGTGAGATGAGAAGTTACGAGACTACATGTGGAATACACTCAACTCAGGACG 1025
                                                                                                                                                                                                1057 GAGA-ACATITCCAAAGAGCAGTIGAAAGACTATGTITGGAAAACATIGAACAGTGGCAA 1115
                                                                                                                                                                                                                                                                 1176 GAGAGAGTIUGUTATGAAGUATTIGUCTGAAGATCCACTGTTTCAACTGGTTTGAAAACT 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1206 TGTGGATGCTCACAGTGGGGTGCTGCTCCAGTACTATGGCATGACGGAGATGAACTACTA 1265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1266 CACAGTCCTGTTCGGGGTATCACGGGCACTGGGTGTATTAGCACAGCTCATCTGGAGCCG 1325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1353 TACGGTCCTCTTTGGCGTATCAAGAGCTCTTGGCATTTGCTCTCAGCTAATTTGGGACCG 1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S.cerevisiae mitochondrial citrate synthase gene, complete CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fifteen other mitochondrial proteins by a new screening method EMRD J. 3 (A), 1773-1781 (1984)
                   847 GCCCTTTCAGACCCCTACTTGTCCTTTGCAGCCATGAATGGGCTGGCAGGGCCCCTA 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolation of the nuclear yeast genes for citrate synthase and
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Lindner,P. and Plueckthun,A.
The effect of point mutations in the hinge of yeast citrate
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Submitted (05-JUL-1993) Peter Lindner, Protein Engineering,
                                                                                907 CATGGGCTGGCAAATCAGGAAGTGCTTGTTTGGCTGACA-CAGCTGCAGGAAGTCGG
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Suissa, M., Suda, K. and Schatz, G.
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EGGNVSAHTTHLVGSALSSPYLSLAAGLNGLAGPLHGRANOEVLEWLFKLREEVKGDY
SKETIEKYLMDTLNAGRVHOYGGHAVLKTDPRYTAOREFALKHFPDYELFKLVSTIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MSAILSTTSKSFLSRGSTRQCONMQKALFALLNARHYSSASEOT
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IRFRGRTIPEIQRELPKAEGSTEPLPEALFWLLLTGEIPTDAOVKALSADLAAKSEIP
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/product-"the processing site has been determined by
direct N-terminal protein sequencing"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref-"SGD:L0000341"
/product-"mitochondrial citrate synthase"
/protein.id="CAA80781.1"
/db_xref-"PID:9313750"
/organism="Saccharomyces cerevisiae"
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Local Similarity 61.2%; Pred. No. 1.82e-143;
les 703; Conservative 0; Mismatches 432;
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                            /strain="D273-10B
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Saccharomyces cerevisiae
Eukaryota; Fungi, Ascomycota; Hemiascomycetes; Saccharomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1078 TTGAAAGACTATGTTTGGAAAACATTGAACAGTGGCAAGGTTGTCCCTGGTTTTGGACAT 1137
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                                                 599 IIGCTACTGGAGTCATGGCTCTTCAGGTTCAAAGTGAATTTCAAAAGGCATACGAGAAAG 658
                                                                                                                                                 659 GGATICACAAAICAAAGIAIIGGGAACCAACAIAIGAGGAIICCAIGAAICIGAIIGCIC 718
                                                                                                                                                                                               659 AATTACCTGTTATTGCTTCCAAAATTTATCGTAATGTGTTCAAGGATGGTAAAATTACTT 718
                                                                                                                                                                                                                                                 719 AAGTICCACTIGIIGCIGCIIATGIIIAICGCAGGAIGIACAAGAAIGGIGACACIAIAC 778
                                                                                                                                                                                                                                                                                                  719 CAACCGATCCTAATGCTGACTATGGTAAAAATTTGGCCCAACTTTTGGGCTACGAAAACA 778
                                                                                                                                                                                                                                                                                                                                              779 CTAAGGATGAATCCCTGGATTATGGTGCAAATTTTGCTCACATGCTTGGTTTCAGTAGCT 838
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539 ITICIATIGCCGIGACTGCTTIAGAAAGCGAGTCTAAGTTIGCCAAAGCATAIGCTCAAG 598
                                                                                                  599 GIGTATCCAAGAAAGAATATIGGAGCTATACATTIGAAGATICGTIAGATCTGCIGGGTA 658
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Saccharomycetaceae; Saccharomyces.

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LGKLPVIASKIYRNVFKDGKITSTDPNADYGKNLAQLLGYENKDFIDLMRLYLTIHSD
HEGGNVSAHTTHLVGSALSSPYLSLAAGLNCLACPLHGRANQEVLEWLFKLREEVKGD
YSKETIEKYLWDTLNAGRVVPGYGHAVLRKTDPRYTAQREFALKHFPDYELFKLVSTI
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DRAVGAPIERPKSFSTEKYKELVKKIESKN"
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/translation-"mSalLSTTSKSFLSRGSTRQCQNMQKaLFALLNARHYSSASEQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIRFRGRIIPEIQRELPKAEGSTEPLPEALFWLLLTGEIPTDAOVKALSADLAARSEI
PEHVIQLLDSLPKDLHPMAQFSIAVTALESESKFAKAYAQGVSKKEYWSYTFEDSLDL
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l (bases 1 to 2427)
Suissa.M., Suda.K. and Schatz,G.
Isolation of the nuclear yeast genes for citrate synthase and fifteen other mitochondrial proteins by a new screening method BMBO J. 3 (8), 1773-1781 (1984)
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                                                                                                                                                                                       Data kindly reviewed (09-MAY-1985) by G. Schatz.
                                                                                                                                                                                                                                                                        /organism="Saccharomyces cerevisiae"
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Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                    959 CCTTTGCTGCTGCTTTGAATGGTTTAGCCGGACCACTTCATGGTTTAGCCAATCAGGAAG 1018
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                                             899 GTAATGTCAGTGGTCACTGGTTGGTTGGTTGTTTGTCTTGTCTTACCTCT 958
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Aert, R , Verhasselt, P., Voet, M. and Volckaert, G.
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EVARGVLTKHGKTRWEWPRVDSHSGVLLQYYGLTEASFYTVLFGVARAIGVLPOLITD
RAVGAPIERPKSFSTEKYKELVKKIESKN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(3230. .3301)
/gene="tP(AGG)NR - systematic name"
/note="anticodon gene: AGG; tRNA-Pro2
complement(3230. .3301)
/gene="tP(AGG)NR - systematic name"
complement(3382. .3497)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  //octe-fanticodon gene: GTT; tRNA-Asn
3983. 4056
/gene=fkn(GTT)NR - systematic name"
803 c 784 g 1392 t
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                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SWISS-PROT:P00890"
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                                                                                                                                           complement(1006. .2445)
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complement(3503, .3873)
/note="solo-tau"
                                                                                                                           /db_xref-"SGD:L0000341"
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1603 AACGTTACCACCTTCATGATCAGATGAATAGATTAAATATAGTCTCATTA--AGTCAATA 1660
1483 ITCTAAAACTICTIGAITGGCACGACCAIGTAATGGGCCAGCTAAACCAITCAAACCAGC 1542
                                                                                                                                                                                                                                                                 1661 AAAICCTIGTTICGTAGCCCAAAAGI-TGGGCCAAATITITACCAIAGTCAGCATTAGG 1719
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                                                                                      1543 GGCCAAAGATAAGTATGGCGAAGATAAGGCAGAACCCACTAAATGTGTAGTATGGGCAGA 1602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        606 AGTAGCAAACTGGGTCATTGGATGAGCTGTGACTGGTAAGGCATC-AATAGTTGTATACA 548
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                                                                                                                                                                                                                                                                                                             846 CATITICAGAGCIACIGAAACCAAGCAIGIGAGCAAAAITIGCACCAIAATCCAGGGAITC 787
                                                                                                                                                                                                                                                                                                                                                                                 547 IGAIGAICAGGATATGAIGCCCGACICIGCAATICCIGAGACAATIGAATICACTIGCI 488
                                                                                                                              966 AGCAAAGGAGAGGTAAGGATCAGACAAAGCACTAGCAACCAAGTGACCGGTGTGAGCACT 907
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Search completed: Sat Oct 23 15:30:05 1999 Job time : 3443 secs.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Pred. No.	ha 0.00e+00			_	` '	_	, ,		_
	Description	Potato citrate syntha	Potato citrate syntha	Tobacco citrate synth	Sugar beet citrate sy	Base substituted E.co	Base substituted E.co	Oligonucleotide probe	Oligonucleotide pro	Generic DNA sequence
SUMMARIES	ID	T03410	T04199	T04201	T04200	N81164	N81164	051746	051746	070468
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æ	Query Match	100.0	100.0	65.5	35.1	2.3	(1 (1	2.1	2.1	1.7
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ivity the DNA sequences can also be used to identify similar unchess in the genomes of other plants and in the production of nsgenic plants with altered CS activity uence 1891 BP; 512 A; 370 C; 425 G; 584 T;	tch 100.0%; Score 1891; DB 17; Length 1891; 2al Similarity 100.0%; Pred. No. 0.00e+00; 1891; Conservative 0; Mismatches 0; Indels 0; Ga	l ttttcgttccatcagcctacttgagatgtattcccactggtaaaagttaattttttga 	ltttcgcgagcaatggtgttctaccgtagcgtttcgttgctgtcaaagctccgctctcgaiiiiiiiiii	gcggtccaacagtcaaatgttagcaattctgtgcgctggcttcaagtccaaacctcttcc 	ggtcttgatctgcgttctgagctggtacaagaattgattcctgaacaacaggatcgctg	l aaaaagatcaagtcagatatgaaaggttcaattgggaacatcacagttgatatggttctt 	ggtggaatgagaatgacaggattactgtggaaacctcattaccttgaccctgatgag 	ggaattcgcttccgggggttgtctatacctgaatgccaaaaggtattacctgcagcaaag	cctgggggtgagccttgcctgaaggtcttctctggcttcttttaacaggaaaggtgcca 	1 tcaaaagagcaagtgaattcaattgtctcaggaattgcagagtcgggcatcatatccctg 	atcatcatgtatacaactattgatgccttaccagtcacagctcatccaatgacccagttt	gctactggagtcatggctcttcaggttcaaagtgaatttcaaagggcatacgagaaaggg 	1 attcacaaatcaaagtattgggaaccaacatatgaggattccatgaatctgattgctcaa 	gttccacttgttgctgctatgtttatcgcaggatgtacaagaatggtgacactatacct	aaggatgaatccctggattatggtgcaaatttgctcacatgcttggtttcagtagctct 	gaaatgcatgaacttcttatgaggctctatgtaacaatacacagtgatcatgaaggtggt 	aatgtcagtgctcacaccggtcacttggttgctagtgctttgtctgatccttacctctcc
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Citrate synthase; flower formation; tuber storage; ss.
Solanum tuberosum.
Exequences
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                                                                                                                                                                                                                                                                                                        To identify a cDNN from potato which codes for citrate synthase, a cDNA fragment of citrate synthase from Arabidopsis thaliana was firstly amplified using A.thaliana cDNA and oligos T04202 and T04203 which are complementary to the 5' or 3' end of the coding region of A. thaliana CDNA for citrate synthase. The oligos additionally introduce BamHI cleavage sites at both ends of the amplified cDNA fragment. a cDNA library was prepd. from potato leaves and screened with A. thaliana citrate synthase CDNA. Positive clones were benufied and sequenced Then the sequence is given in T04199. Sequence 1891 BP; 512 A; 770 C; 425 G; 584 T;
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22-SEP-1994; DE-435366.
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07-MAR-1995; E00859.
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P-PSDB; R82838.
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601 GCTACTGGAGTCATGGCTCTTCAGGTTCAAAGTGAATTTCAAAAGGCATACGAGAAAGGG 660
                                                                             661 attcacaaatcaaagtattgggaaccaacatatgaggattccatgaatctgattgctcaa 720
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DNA encoding plant citrate synthase - used to regulate flower formation, to improve storage of tubers, etc. and to reduce sprouting Claim 7: Page 60-63: 8Tpp: English.

Claim 7: Page 60-63: 8Tpp: English.

Claim 7: Page 60-63: 8Tpp: English.

Synthase, a cDNA from tobacco which codes for citrate synthase, a cDNA bank of leaf tissue from tobacco was prepd. Plaques of this cDNA bank were screened using a radioactive DNA probe which comprises Solanum tuberosum citrate synthase cDNA (104199). One of the clones was sequenced. The nt. sequence is given in T04201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.00e+00;
0; Mismatches 93; Indels 18; Gaps 14;
                   1801 gctggaaagttagtaatcggctgattcacgcaataaactgcaattgtgtagtttcttaaa 1860
1741 ataggicaaigciaitaaicgcgilictiggilgccailtagacilgigaaigacilccili 1800
                                                                                                                         1801 GCTGGAAAGTTAGTAATCGGCTGATTCACGCAATAAACTGCAATTGTGTAGTTTCTTAAA 1860
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                                                                                                                                                                                                                                                                                                                                                       Tobacco citrate synthase cDNA.
Citrate synthase; flower formation; ss.
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Matches 1439; Conservative
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                                                                                              456 GCTTCTTTTAACAGGAAAGGTGCCATCAAAAGAGCAAGTGAATTCAATTGTCTCAGGAAT
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/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding plant citrate synthase - used to regulate flower formation, to improve storage of tubers, etc. and to reduce sprouting Claim 6: Page 57-60: 87pp. English.

To identify a cDNA from sugar beet which codes for citrate synthase, a cDNA bank of leaf tissue from sugar beet was prepd. Plaques of this cDNA bank were screened using radioactive DNA probes which comprise a mixture of Solamum tuberosum citrate synthase cDNA (104199) and Nicotian tabacum citrate synthase cDNA (see T04201). One of the clones was sequenced. The nt. sequence is
                   1476 CAAGAAAGCATGAATTGTITIGAAATCTC-GCGAGCATAAAA-CACAATGTATAATGTT 1533
1467 caagaaagcatgatttgtttgaaatctctgcgagcataaaagcacaatgtaaaatcttta 1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 gittecagetggggaatateaatgitgaeatggtattgggeggaatgagggaatgaetg 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265 GGTTCAAT-TGGG-AACATCACAGTTGATATGGTTCTTGGTGGAATGAGAGGAATGACAG 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 gittacitigggagacitccitacicgacccagaagagggtaiccggitcaagggitti 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209 ctatacctgaatgccagaaacttttacccgctgcaagtgctggtgcagagccattgcctg 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 aaggtettetttggettetttaaceggaaaggtteetageaaagageaagtagatgete 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 443 AAGGICTICICIGCIICITIIAACAGGAAAGGIGCCAICAAAAGAGCAAGIGAATICAA 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tatcagcag-atttacgaaaacgtgcttc-tatcccagaccatg-tgtacaaaacaattg 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   503 TIGICICAGGAATIGCAGAGTCGGGCAICATATCCCTGATCATCATGTATACAACTATIG 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 563 ATGCCTTACCAGTCACAGCTCATCCAATGACCCAGTTTGCTACTGGAGTCATGGCTCTTC 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206 TACAAGAATTGATTCCTGAACAACAGGATCGCCTGAAAAAGATCAAGTCAGA-TATGAAA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   323 GATTACTGTGGAAACCTCATTACCTTGACCCTGATGAGGGAATTCGCTTCCGGGGGTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                 Landschutze V, Muller-rober B, Landschuetze V;
                                                                               1527 tgaataattgcttgagaaagcagttttttttttggagc-caaggtaggtcg 1575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 35.1%; Score 664; DB 16; Length 1551; Best Local Similarity 78.5%; Pred. No. 0.00e+00; Matches 997; Conservative 0; Mismatches 261; Indels 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                458 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370 G;
                                                                                                                                                                                         25-JAN-1996 (first entry)
Sugar beet citrate synthase CDNA.
Citrate synthase; flower formation; ss.
Beta vulgaris strain Zuchtlinie 5S 0026
Key
Location/Qualifiers
cds
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                                                                                                                                                               T04200 standard; cDNA to mRNA; 1551 BP
                                                                                                                                                                                                                                                                                                                                                               09-MAR-1994; DE-408629.
22-SEP-1994; DE-43586.
19-CCT-1994; DE-438821.
(AGPE ) HOECHST-SCHEPING ASPEVO GMBH.
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Sequence 1551 BP; 455 A;
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07-MAR-1995; E00859.
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1043 TAGAAGAATGTGGGGAGAACATTTCCAAAGAGCAGTTGAAAGACTATGTTTGGAAAACAT 1102
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                                                                                              623 AGGTTCAAAGTGAATTTCAAAAGGCATACGAGAAAGGGGATTCACAAATCAAAGTATTGGG 682
                                                                                                                                                                                                                                                                                                 683 AACCAACAIAIGAGGAIICCAIGAAICIGAIIGCICAAGIIICCACIIGIIGCIGCIIAIG 742
                                                                                                                                                                                                                                                                                                                                                                                                    566 tttatoggaggatgtataagaatggacaagtaataccgctggatgactcccttgattatg 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gtggaaatttcgcacacatgttgggatttgatagccctcagatgcttgagctg---atgc 682
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                                                                                                                                                                                                       506 agccaacatatgaggactgccttagtttgattgctcaagttcctgttgttgcagcttatg 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   743 TITATCGCAGGATGTACAAGAAIGGTGACACTATACCTAAGGAIGAATCCCTGGATTATG
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446 agactegaagegaattteagaaggeatatgagaaagggateeataagteaagttttggg
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Base substituced E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            757 TACAAGAATGGTGACACTATATGCTAAGGATGAATCCCTGGATTATGGTGCAAATTTTGCT 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Introducing random point mutations into nucleic acods - by prepn of single stranded template, annealing a primer, elongation, misincorporation, completion of molecules and screening.
                                                                                                                                                         WPI; 88-279927/40.
Introducing random point mutations into nucleic acods -
los prepn of single stranded template, annealing a primer, elongation, misincorporation, completion of molecules and screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Gaps
                                                                                                                                                                                                                                                                               E.coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the
                                                                                                                                                                                                                                                                                                                                                                                                       transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which occurred singularly in any given mutant.
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Random point mutations were introduced into the alpha fragment of E.coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to lit to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system.
                                                                                                                                                                                                                                           Disclosure; p; English.
Random point mutations were introduced into the alpha fragment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E.coli beta galactosidase alpĥa-fragment; base substitutions; ss.
Escherichia coli.
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                                                                                              03-APR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 2.3%; Score 44; DB 1; Length 204; Local Similarity 6.5%; Pred. No. 3.92e-12; nes 6; Conservative 55; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Base substituted E.coli beta-galactosidase alpha-fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function=multiple cloning site 187..204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 ccbnnhvchnvhbnnhrnwayvrhdarrddvh 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         817 CACATGCTTGGTTTCAGTAGCTCTGAAATGCA 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N81164 standard; DNA; 204 BP. N81164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-NOV-1990 (first entry)
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187..204
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                     /*tag=
                                                         05-MAY-1988.
30-MAR-1988; 105163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-1988; 105163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        See also P80575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
primer_bind
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                                                                                                                                                                                                    1149 TCGCAGAACTCCATGTCCAAAACCAGGGACAACCTTGCCACTGTTCAATGTTTTCCAAAC 1090
                                                                                                                                                                                                                                                                      1089 ATAGTCTITCAAC-TGCTCTTTGGAAATGTTCTCCCCCACATTCTTCTACAACAGATTTTA 1031
                                                                                                                                                                                                                                       85 gymrttthhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvyn 144
                                                                                                                                                                  25 yyrcayrccbgcaggycgacbcyrraggnyccccggggywccgagcycgaayycdchvgcc 84
                                                                                                                               Gaps
The sequence covers all 176 difft base substitutions, most of which occurred singularly in any given mutant. See also P80575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide probe MX14-A consists of nucleotides 5-95 or MX14 (Q51735). It hybridized to all spp. of mycobacteria tested, but cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59. Sequence 91 BP, 5 A, 17 C, 15 G, 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New oligo:nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New oligo:nucleotide probes specific for Mycobacteria - used for
                                                           108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 566 CCTTACCAGTCACAGCTCATCCAATGACCCAGTTTGCTACTGGAGTCATGGCTC 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 yvvhvvshhhsvhhvvhhvhvsvvvvhhvvhvvhhvhyhvyvsvctcaagcctc 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide probe MKÍ4-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                            Score 42; DB 1; Length 204; Pred. No. 6.81e-11; 71; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 91;
                                                                                                                                                                                                                                                                                                                                  1030 TCCATAGCAAAACTICCTGATIGGCTAAACCAIGAAGTGGTCCG 987
                                                                                                                                                                                                                                                                                                          145 vhnhnncncccbnnhvchnvhbnnhrnwayvrhdarrddvhccv 188
                                                           11 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 9; L4
Pred. No. 1.14e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40; Mismatches
                                                           47 C; 17 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 14; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               Q51746 standard; cDNA; 91 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  051746 standard; cDNA; 91 BP
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Shank DD, Spears PA;
WPI; 93-378844/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BECT ) BECTON DICKINSON CO.
                                                                                            Match 2.2%;
Local Similarity 16.5%;
les 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           // Match 2.1%;
Local Similarity 13.0%;
                                                         21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAY-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Conservative
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26-MAY-1992; US-889651.
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26-MAY-1992; US-889651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spears PA;
                                                           204 BP;
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EP-571911-A.
01-DEC-1993.
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01-DEC-1993.
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                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                              8 gcgssvhsyyvvhvvshhhsvhhvvhhvhhvhvvhhvvhhvhhyhvyvsvctcaa 65
                                                                                                                                                                                                                                                                                                            114 GCGGAGCTTTGACAGCAACGAAGGTACGGTAGAACACCCATGCTCGCGAAAATCAA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/note= "this sequence_represents'z'; Z can be
                                                    Oligonuclectide probe MK14.A consists of nucleotides 5-95 of (051735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also (051735-45 and 051747-59.

Sequence 91 BP: 5 A; 17 C; 15 G; 4 T;
detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                        9; Indels
                                                                                                                                                                                                     Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence of 6, 9 or 12 nucleotides (see
                                                                                                                                                                                                   Score 40; DB 9; L
Pred. No. 1.14e-09;
                                                                                                                                                                                                                                        42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                       Claim 3; Page 14; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  Q70468 standard; DNA; 114 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                              Query Match 2.1%;
Best Local Similarity 12.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                       Q70468;
05-APR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comments)"
                                                                                                                                                                                                                                        7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fowlkes DM, Kay BP
WPI; 94-279739/34.
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01-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09418318-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                       samples
                                                                                                                                                                                                                                      Matches
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Translight of process of peptide(s) which bind a lighalor by screening a recombinant vector library expressing fusion proteins Disclosure; Page 35, 25pp; English.

Comprising a binding domain and an effector domain proteins Disclosure; Page 35, 25pp; English.

Comprising a binding domain and an effector domain proteins of 270465 is a generic DNA sequence used to generate random TSAR (Totally Comprised as follows: X(NNB) [GGC] (NNB) 12 (NNB) 14 (TGC] (NNB) 37. X and Y are flanking restriction sites (X is not the same as Y) that are not specific peptides generated by these generic sequences are shown in Comprising at least two functional regions - a binding domain with a ffinity for a ligand and a second effector peptide portion that is chanically or biologically active. They may further comprise a linker of peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues societ that the expressed peptide contains 2 or 4 cysteine residues societ comprises or comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eq. metal ion, a radioisotope, peptide, toxin or enzyme, to the specific target or on the composition. They can also replace the function of macromoleules, eq. metal ion, and complex methods of hybridoma formation or in vivo antibody concluding direct and rapid detection in a screening process. Sequence 114 BP; 0 A; 2 C; 2 C; 2 T;
                                            ö
                                                                                                                                                                             943 ICIGATCCTTACCTCTCCTCTTGCTGCTGCTTTGAATGGTTTAGCCGGACCACTTCATGGT 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 GTTTCGTTGCTGTCAAAGCTCCGCTCTCGAGCGGTCCAACAGTCAAATGTTAGCAATTCT 150
                                                                                                          3 banbanbanbanbanbanbanbanbanbanbtgenabanbanbanbanbanbannan 62
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                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/note= "this sequence represents '2'; 2 can be
sequence of 6, 9 or 12 nucleotides (see
                                            ;
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                                                                                                                                                                                                                                                                                                              1003 ITAGCCAATCAGGAAGITITGCTATGGATAAAATCTGTTGTAGAAGAATGTG 1054
                                                                                                                                                                                                                                               63 banbanbanbanbanbanbtgcanbanbanbanbanbanbanbanbanbanb 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 114;
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       Pred. No. 5.88e-05;
31; Mismatches 76; Indels
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Pred. No. 7.75e-04;
30; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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30-DEC-1993; US-105500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWLKES DM, KAY BK;
WPI: 94-279739/34.
P-PSDB; R65150 and R65151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q70465 standard; DNA; 114 BP.
Q70465;
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llarity 4.5%;
Conservative
Best Local Similarity 4.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Best Local Similarity
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Length 114;

DB 12;

Score 32;

1.78;

Query Match

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Tribular Notations or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comparising a binding domain and an effector domain proteins by binding domain and an effector domain proteins of binding domain and an effector domain proteins of bisclosure; page 35; 255pp; English.

20 070467 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagen's) peptides. This generic formala can also be represented as follows: X(NNB)16(TGC)(NNB)16(TGC)(NNB)18. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68. Other specified further other generated by these generic sequences are shown in R5151-54. TSARs are concatenated heterotunctional proteins or peptides, comprising at least two functional regions - a binding domain with R5151-54. TSARs are concatenated heterotunctional proteins or peptides, comprising at least two functional regions - a binding domain with a finity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking a TBARS binding domain residues. There residues confer some degree of conformational rigidity to the peptides. The TSARS and allows and protein and be used in vivo to deliver a chomically or biologically active in a manner of the compans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    deliver a chemically or biologically active moiety, eg. metal ion, radiolostope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       922 GACCGGTGTGAGCACTGACATTACCACCTTCATGATCACTGTGTATTGTTACATAGAGCC 863
                                                                                                                                                                                                                         Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "this sequence represents 'Z'; Z can be a sequence of 6, 9 or 12 nucleotides (see comments)"
                                               151 GIGCGCTGGCTTCAAGTCCAAACCTCTTCCGGTCTTGATCTGCGTTCTGAGC 202
  1.6%; Score 31; DB 12; Length 114; 3.7%; Pred. No. 2.15e-04; attive 31; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       862 TCATAAGAAGTTCATGCATTTCAGAGCTACTGAAACCAAGCATGTGAGC 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           direct and rapid detection in a screening process. Sequence 114\ BP; 0\ A; 2\ C; 2\ C; 2\ T;
                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                 Q70467 standard; DNA; 114 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 3.7%;
Matches 4; Conservative
                                                                                                                                                                                                 05-APR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-013416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-176500.
                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-189331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fowlkes DM, Kay BK;
WPI; 94-279739/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U00977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; R65153
                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1993;
30-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9418318-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-AUG-1994
                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                            070467;
Dp
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LT 12 Q70465 standard; DNA; 114

RESULT

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or compans. Comparising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eq. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eq. monoclonal or polyclonal antibodies and therefore circumvent the need
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 CTGTCATTCCTCTATTCCACCAAGAACCATATCAACTGTGATGTTCCCCAATTGAACCTT 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR peptide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain:
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
                              Generic DNA sequence to generate a random TSAR petide library. TSAR: totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening, treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 banbanbanbanbanbtgcanbanbanbanbanbanbanbanbanbanbanbananna 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                         Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain bisclosure; Page 35: 255pp; English.
                                                                                                                                              /*tag- a
/note- "this sequence represents 'Z'; Z can be a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 114,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68; Indels
                                                                                                                                                                              sequence of 6, 9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 bnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnb 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 TCATATCTGACTTGATCTTTTTCAGGCGATCCTGTTGTTC 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 1.6%; Score 30, DB 12; I Local Similarity 2.0%; Pred. No. 7.75e-04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30;
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                                                                                                                                                                                                                                                                                          31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
                 (first entry)
                                                                                                                                                                                              comments)"
                                                                                                                                                                                                                                                                                                                                                            P-PSDB; R65150 and R65151
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                                                                                                                                                                                                                                                                             30-DEC-1993; US-176500.
                                                                                                                                                                                                                                                            US-013416.
                                                                                                                                                                                                                                                                                                                         Kay BK;
                                                                                                                                                                                                                                              U00977
                                                                                                                                                                                                                                                                                                                                           94-279739/34
                 05-APR-1995
                                                                                                                              misc_feature
                                                                                                                                                                                                                                                               01-FEB-1993;
                                                                                                                                                                                                            WO9418318-A
                                                                                                                                                                                                                                                                                                                           Fowlkes DM,
                                                                                                 Synthetic.
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070465:
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WHY: 94-279/3434.

Identifying proteins or peptide(s) which bind a ligand - by
Identifying proteins or peptide(s) which bind a ligand - by
Identifying proteins or peptide(s) which bind a ligand - by
Ischeming a recombinant vector library expressing fusion proteins
Disclosure; Page 35; 255pp; English.

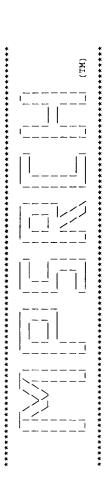
CC 07469 is a generic DNA Sequence used to generate random TSAR peptide
This generic formula can be represented as follows: X(TSC)(NNB)10-
CC (TGC)(NNB)2(TGC)(NNB)14(TGC)Y. A and Y are flanking restriction
sites (X is not the same as Y) that are not specified further. This sequence generates peptides that are cloverleaf in structure. Other
CC (TGC)(NNB)2(NNB)2(TGC)(NNB)14(TGC)Y. A and Y are flanking restriction
sites (X is not the same as Y) that are not specified further. This sequence generic sequences are shown in Q70465-68. Other specifies peptides
CC generic sequences are shown in Q70465-68. Other specifies proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains.
CC contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues positioned in, or flanking, the conformational rigidity to the peptides. The TSARs or compone conformation in rigidity to the peptides. The TSARs or compone conformation or mostly active moiety, es, metal ion, radioisotope, peptide, toxin to a TSAR binding domain can be used in vivo to deliver a chemically or biologically and therefore circumvent the need for complex methods of hybridoma or in vivo antibody production. The TSARs are easily conformed and have designed activity allowing direct and rapid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-007-1998 (first entry)
Mammalian DNA replication origin consensus sequence, uniorsconsensus.
DNA replication origin; human; mammal; alphaconsensus; uniorsconsensus; anti-gene; DNA replication inhibitor; shuttle vector construct creation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321 IGTCATTCCTCTCATTCCACCAAGAACCATATCAACTGTGATGTTCCCAATTGAACCTTT 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 tgcnnbnnbnnbnnbnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnbn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                        /note- "this sequence represents 'Z'; Z can be a sequence of 6,9 or 12 nucleotides (see comments)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 CATATCTGACTTGATCTTTTTCAGGCGATCCTGTTGTTGAGGATCAATTCT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
1.6%; Score 30; DB 12; Length 114;
Best Local Similarity 5.4%; Pred. No. 7.75e-04;
Matches 6; Conservative 30; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cossons NH, Nielsen TO, Price GB, Zannis-Hadjopoulos M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 G;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detection in a screening process.
Sequence 114 BP; 0 A; 4 C;
                                                                                                                                                                                                                                                                  (UYNC-) UNIV NORTH CAROLINA. Fowlkes DM, Kay BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V44650 standard; DNA; 91 BP.
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12-DEC-1997; CA0972.
21-MAY-1997; US-047322.
16-DEC-1996; US-033374.
(UYMC-) UNIV MCGILL.
                                                                                                                                                                                                  01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
                     55..60
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                                                                                                                                                                                                                                                                                            Kay BK;
                                                                                                                                                                               . 77600U
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                misc_feature
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This sequence represents a human or mammalian DNA replication origin consensus sequences of the invention, designated uniorsconsensus.

Administration of the consensus sequence or an anti-gene (comprising a double stranded copy of the consensus) is used to inhibit DNA replication in vivo or in vitro. The consensus sequences can also be inserted into an expression vector, used subsequently for in vitro transfection of mammalian cells, to control initiation of DNA replication. They can also be used used to maintain circular plasmids that are capable of semi-conservative replication in proliferating mammalian cells, or inserted into amammalian or human artificial chromosome vectors for gene therapy. Particularly, they are used to create shuttle vector constructs for defining the essential mammalian elements required for maintenance of chromosomal function. The consensus sequence can be combined with cloned human relomeres and large centromeric blocks for assembly of human artificial chromosomes and maintained as bacterial plasmids, circular or linear, large or small yeast artificial chromosomes (YACS) or as episomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a human or mammalian DNA replication origin consensus sequence of the invention, designated uniorsconsensus. Administration of the consensus sequence or an anti-gene (comprising a daministration of the consensus sequence or an anti-gene (comprising a double stranded copy of the consensus) is used to inhibit DNA replication in vivo or in vitro. The consensus sequences can also be inserted into an mammalian cells, to control initiation of DNA replication. They can also be used to maintain circular plasmids that are capable of semi-conservative replication in proliferating mammalian cells, or linserted into mammalian or human artificial chromosome vectors for gene therapy. Particularly, they are used to create shuttle vector constructs for defining the essential mammalian elements required for maintenance of chromosomal function. The consensus sequence can be combined with cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA replication origin; human; mammal; alphaconsensus; uniorsconsensus; anti-gene; DNA replication inhibitor; shuttle vector construct creation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-ocr-1998 (first entry)
Mammalian DNA replication origin consensus sequence, unjorsconsensus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 mtwaakrawrwwkkdavwwgakrwwkwvwhrassacmdwkaaktwkggwtwarrywkgrk 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 1.5%; Score 28; DB 46; Length 91;
Best Local Similarity 15.3%; Pred. No. 9.56e-03;
Matches 13; Conservative 46; Mismatches 25; Indels 1; Gaps
WPI; 98-362770/31.
Human or mammalian origin of replication consensus sequences - for
inhibiting DNA replication, for controlling initiation of
replication, maintaining circular plasmids and in assembly of human
artificial chromosomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human or mammalian origin of replication consensus sequences - for inhibiting DNA replication, for controlling initiation of replication, maintaining circular plasmids and in assembly of human artificial chromsomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cossons NH, Nielsen TO, Price GB, Zannis-Hadjopoulos M; WPI; 98-362770/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 G;
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                                                                                                                              Claim 1; Page 42; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V44650 standard; DNA; 91 BP.
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12-DEC-1997; CA0972.
21-MAY-1997; US-047322.
16-DEC-1996; US-033374.
(UIMC-) UNIV MCGILL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                elements.
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CC human telomeres and large centromeric blocks for assembly of human control of artificial chromosomes and maintained as bacterial plasmids, circular or continear, large or small yeast artificial chromosomes (YACs) or as episomal contemporary large or small yeast artificial chromosomes (YACs) or as episomal contemporary large or small yeast artificial chromosomes (YACs) or as episomal contemporary large or small yeast artificial chromosomes (YACs) or as episomal contemporary large or sepisomal contemporary large or sepisomal large large large or lar
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Search completed: Sat Oct 23 16:31:37 1999 Job time: 429 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_nn n.a. n.a. database search, using Smith-Waterman algorithm

Sat Oct 23 16:31:55 1999; MasPar time 136.79 Seconds 1195.578 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-702-718-1 (1-1891) from US08702718.seq 1891 Description: Perfect Score: Title:

1 TITITCGTICCATCAGCCIA........1TATITGATGATATTATGAA 1891 AAAAAGCAAGGTAGTGGGAT.......AATAAACTACTATAATACTI N.A. Sequence: Comp:

TABLE default Gap 6 Scoring table:

165359 seqs, 43243793 bases x 2 Searched:

Dbase 0; Query 0

Nmatch STD

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

n-issued 1:5A\_COMB 2:5B\_COMB 3:5C\_COMB 4:PCT9\_COMB 5:backfiles1

Mean 9.032; Variance 4.369; scale 2.067 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	t . Score	Query Match	Length	DB	ID	Description	Pred. No.
ט	1 45	4.5	7218	(1	US-08-232-	Sequence 14, Applicati	4.04e-16
	2 42	ci ci	7218	~	US-08-232-	14,	5.99e-14
	3 34	1.8	965	٣	US-08-388-	Sequence 22, Applicati	2.31e-08
-	4 31	1.6	215	7	US-08-238-	'n	2.30e-06
0	5 31	1.6	215	Н	US-08-238-	Sequence 5, Applicatio	2.30e-06
0	6 28	1.5	965	m	-886-80-SD	Sequence 22, Applicati	1.95e-04
	7 28	1.5	1302	m	US-08-529-	Sequence 3, Applicatio	1.95e-04
- 0	8 26	1.4	74	4	PCT-US95-1	Sequence 100, Applicat	3.40e-03
0	9 26	1.4	81	4	PCT-US95-1	98, A	3.40e-03
Н	0 24	1.3	75	4	PCT-US95-1	99,	5.36e-02
٦	1 24	1.3	81	4	PCT-US95-1	92,	5.36e-02
H	2 24	1.3	82	4	PCT-US95-1	97,	5.35e-02
Н	3 24	1.3	92	m	US-08-353-	16,	5.36e-02
<del>-</del> i	4 24	1.3	105	Н	US-07-865-	Sequence 13, Applicati	5.36e-02
H	5 25	1.3	1958	m	US-08-137-	Sequence 7, Applicatio	1.37e-02
i c	6 23	1.2	65	Н	US-08-471-	145	2.04e-01
0		1.2	68	H	US-08-471-	143,	2.04e-01
H	8 22	1.2	74	4	PCT-US95-1	94, A	7.54e-01
c 1	9 22	1.2	75	4	PCT-US95-1	66	7.54e-01
Ci	0 22	; ;	C3 80	4	PCT-US95-1	Sequence 97, Applicati	7.54e-01

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                     527 CCCGACTCTGCAATTCCTGAGAGTAGTTGAGTTCACTTGCTCTTTGATGGCACCTTTCCT 468
                                                                                                                                                                                 457 GITAAAARAAAGGGAGAGAAGAGCITGAGGGAAGGGGICACGCCCAGGCITIGCIGCAGGI 408
                                                                                                                                                                                                                      407 AATACCITTTGGCATTCAGGTATAGACCAACCCCAAGCGAATTCCCTCATCAGGTCCA 348
                                                                                                                                                                                                                                                               347 AGGTAATGAGGTTTCCACAGTAATCGTGTCATTCCTCTCTTTCCACCACGAGACCATATCA 288
                                                                                                                                                                                                                                                                                                     287 ACTGIGATGTICCCAATIGAACCITICATATCTGACTIGATCITITICAGGCGAICCTGT 228
                                                                                                   Gaps
                                                                                                  0
                                              CLONE: pT29pt-Fls
SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
                                                                              DB 2; Length 7218;
                                                                            2.4%; Score 45; DB 2; Length 7218 Similarity 1.8%; Pred. No. 4.04e-16; 6; Conservative 179; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: SCHEFILINGER, F. APPLICANT: APPLICANT: FALKNER, F. G. TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: FOLEY & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                         JT 2
US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSEE: Foley & Lardner
T: 1800 Diagonal Road, Suite 500
Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: EP 91 114 300.6 FILLING DATE: 26-40G-1991 ATTORNEY AGENT INFORMATION: NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                         1416 YYYYYYYYYYYYYYYYYYYYYY 1440
                                                                                                                                                                                                                                                                                                                                            227 IGTICAGGAATCAATTCTTGTACCA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
7218 base pairs
         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PPIOP APPLICATION DATA:
                             linear
                                     IMMEDIATE SOURCE:
                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                             TOPOLOGY:
 LENGIH:
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                                                                               Query Match
                                                                                                  Matches
8000000
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121 GCGGTCCAACAGTCAAATGTTAGCAATTGTGTGCGCTGGCTTCAAGTTCCAAAGCTTTTGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TITITGGITCCATCAGCCTACTIGAGAIGIATICCCACIGGIAAAAGTTAATTTTTGA 60
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TITTCGCGAGCAATGGFSTTCTACCGTAGGGTTTCGTTGGTGTCAAAGCTCCGGTTCTGA
                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                  TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pT28pt-F1s
SEQUENCE 7218 PP: 1944 A, 1491 C, 148G G, 1929 T, 368 OTHER.
                                                                                                                                                                                                                                                                                                                                       2.2%; Score 42, DB 2, Length 7218; Similarity 1.9%; Pred. No. 5.99e-14; 4; Conservative 121; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Carr, Frank J.
APPLICANT: Old, Lloyd J.
APPLICANT: Welt, Sydney
APPLICANT: Welt, Sydney
TITLE OF INVENTION: Recombinant Human Anti-Lewis B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
RECISTRATION NUMBER: 29,768
REPERBNIE/DOCKT NUMBER: 30472/114 IMMU
TELECOMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)833-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-388-672A-22 STANDARD, DNA, UNC; 965 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: US/08/388,672A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1411 YYYYYYYYYYYYYYYYYYYYYYYYYYY 1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GGTCTTGATCTGCGTTCTGAGCTGGTAC 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22, Application US/08388672A Sequence 22, Application US/08388672A Patent No. 5795961 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ö,
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NAME: Hanson, No. 5795961man
REGISTRATION NUMBER: 30,946
                                                                                     TELETAR: 1899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wallace, T. Paul
Harris, William J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Felfe and Lynch
805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                single
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: U.S.A.
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                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
Patent No. 5569830
GENERAL INFORMATION
APPLICANT: BENNETT, Alan
APPLICANT: BARVITCH, John M.
APPLICANT: POWELL, Ann
APPLICANT: STOTZ, Henrik
TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEA
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                            129 SRNRTGKTANNAVDSRNMGDASVGSDKNTKKHAKNSADGKVGSKNNGDRNNRYGTGTKSN 188
                                                                                                                                                                                               69 GGNNVGAAKTHYYTHTNVSGADSKTVTDSYNASGTSSSNGGTDGNRSGADSYGSSKTAMT 128
                                                                                                                                       9 SSVVSRTASCNDKAKKDGNTTSSWTTDCCNRTWGVCDTDTTYRVNNDSGHNKYSSANYNY 68
                                                                                                           1; Gaps
                  /standard_name= "Deduced amino acid
                                                                          Score 31; DB 1; Length 215;
Pred. No. 2.30e-06;
75; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Streut Street Tower, One Market Plaza CITY: San Francisco STATE: California
   LOCATION: 1..215
OTHER INFORMATION: /standard_name= "Deduced amir
OTHER INFORMATION: sequence of PGIP from bean."
SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC_Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/238,163
FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTATION UNDRER: 34,774
REFERENCE/DOCKET UNDRER: 2307E-540
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                          US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
                                                                                                                                                                                                                                                                                                                                                1146 GCGAAAGACTGTACCAAGAT 1165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 215 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                          Query Match 1.6%;
Best Local Similarity 14.0%;
Matches 28; Conservative
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unknown
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ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STAIE: California
                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                            1400 TAATTTGGGACCGAGCTCTTGGATTGCCGCTAGAGAGGCCAAAGAGTGTCACAATGGAGT 1459
                                                                                                                                                                                                                                                      851 TAVYYCVRGRSYDSDGGDYWGGTTVTVSSHUVKDMTSSSSASVGDRVTTCRSSTTHGNGN 910
                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                            Score 34; DB 3; Length 965; Pred. No. 2.31e-08; 42; Mismatches 25; Indels
                                                                                                                               TOPOLOGY: unknown MOLECULE TYPE: DNA (genomic) SEQUENCE 965 BP; 192 A; 170 C; 226 G; 200 T; 177 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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US-08-238-163-5 STANDARD; DNA; UNC; 215 BP
REFERENCE/DOCKET NUMBER: LUD 5409
TELECOMMUNICATION INFORMATION:
TELEPAN: 212-688-9200
TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LEGITH: 965 base pairs
TYPE: nucleic acid
STRENDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/238,163
ETLING DATE: 03-MAY-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
Patent No. 5569830
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TELEPHONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: BENNETT, Alan
APPLICANT: LABAVITCH, JOHN M.
APPLICANT: POWELL, Ann
APPLICANT: STOIZ, Henrik
                                                                                                                                                                                                                                                                                                                                    1460 GGCTTGAGAACCAGTGCAAGA 1480
                                                                                                                                                                                                                                                                                                                911 TYYWYKGKAKYRVSNRSGVSR 931
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                                                                                                                                                                                               1.8%;
                                                                                                                                                                                                          Best Local Similarity 17.3%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 94105-1493
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SEQUENCE 965 BP; 192 A; 170 C; 226 G; 200 T; 177 OTHER

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291 ATCAACTGTGATGTTCCCAATTGAACCTTTCATATCTGACTTGATCTTTTTCAGGCGATC 232
                                                                                                                                                                                                           61 YSSANYNYGGNNVGAAKTHYYTHTNVSGADSKTVTDSYNASGTSSSNGGTDGNRSGADSY 120
                                                                                                                                                                                                                                         231 CTGTTGTTCAGGAATCAAATTCTTGTACCAGCTCAGAACGCAGATCAAGACCGGAAGAGGT 172
                                                                                                                                                                                                                                                                        121 GSSKTAMTSRNRTGKTANNAVDSRNMGDASVGSDKNTKKHAKNSADGKVGSKNNGDRNNR 180
                                                                                                                                                                                                                                                                                                      171 TIGGACTIGAAGCCAGCGCACAGAATIGCTAACAITIGACIGIIGGACCGCTCGAGAGCG 112
                                                                                                                                             1 MINVIMSSSSVVSRIASCNDKAKKDGNIISSWIIDCCNRIWGVCDIDIIYRVNNDSGHNK 60
                                                                                                             0; Gaps
LOCATION: 1..215
OTHER INFORMATION: /standard_name= "Deduced amino acid OTHER INFORMATION: sequence of PGIP from bean."
SEQUENCE 215 BP: 15 A: 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                             80; Mismatches 104; Indels
                                                                          Score 31; DB 1; Length 215,
Pred. No. 2.30e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wallace, T. Paul
APPLICANT: Wallace, T. Paul
APPLICANT: Harris, William J.
APPLICANT: Old, Lloyd J.
APPLICANT: Welt, Sydney
APPLICANT: Kitamura, Kunio
TITLE OF INVENTION: Recombinant Human Anti-Lewis B
TITLE OF INVENTION: Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CUPRENT APPLICATION DATA.
FILING DATE: US/08/388,672A
FILING DATE: 14-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-388-672A-22 STANDARD; DNA; UNC; 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5409
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
TELEFAX: 212-838-384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22, Application US/08388672A Sequence 22, Application US/08388672A Patent No. 5795961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                    181 YGTGTKSNVSNNCGGGNKRDVSSYANNK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hanson, No. 5795961man D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                  111 GAGCTTTGACAGCAACGAAACGCTACGG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Felfe and Lynch STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 965 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 212-838-3884 INFORMATION FOR SEQ ID NO:
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                                                                               Query Match 1.6%;
Best Local Similarity 11.5%;
Matches 24; Conservative
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: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5795961
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1. CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY:
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1589 AAGGGCCGACCTATCTTGTCCCCCAAGAAAGGAGTGCTTTGTCAAGCAATTATTCATAGA 1530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1706 AATICCTC-ACACGCIGATCCAGCATGTAAAAATTAATAGGTCAATGCTATTAATCGCGT 1764
                                                                   836 ADTSSNSRSSVTAADTAVYYCVPGRSYDSDGGDYWGGTTVTVSSHIVKDMTSSSSASVGD 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 704 INYINGAYYINWSNCCNGCNTAYGGNGCNTTYYTNGGNGGNGINGINYTNGGNAAYWSNG 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  754 CNCARMGNGAYATGYINYTNAARMGNGCNCARCCNATHGGNWSNGTNYTNYTNATGGTNT 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: PROTEIN-BOUND MAGNETIC PARTICLES AND ITLE OF INVENTION: PROCESS OF PRODUCING THE SAME WINDER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS: ADDRESS: PILLSBURY MADISON & SUTRO, L.L.P.
STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match
1.5%; Score 28; DB 3; Length 1302;
Local Similarity 32.2%; Pred. No. 1.95e-04;
les 49; Conservative 26; Mismatches 76; Indels
Score 28; DB 3; Length 965; Pred. No. 1.95e-04; 38; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 1302 BP; 143 A; 118 C; 259 G; 216 T; 566 OTHER.
                                                                                                                                                                                                                                            US-08-529-600D-3 STANDARD; DNA; UNC; 1302 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           824 TYTTYYTNWSNATHGGNYTNYTNYTNGAYTTY 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,600D
FILLMO DATE: 18 SEP-1995
                                                                                                                                                                         1529 GATTATACATTGTGTTTTATGCTCGCGAG 1501
                                                                                                                                        896 RVTTCRSSTTHGNGNTYYWYKGKAKYRVS 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-248700
ELING DATE: IG-SEP-1994
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08529600D Sequence 3, Application US/08529600D Patent No. 5861285
                                                                                                                                                                                                                                                                                                                                                                  Tadashi MATSUNAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1302 base pairs
Query Match 1.5%;
Best Local Similarity 21.3%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Tadash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 18 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: WASH
STATE: D.C
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CITY: New York
STATE: New York
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Best Local Similarity
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Sequence 98, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                           APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
CORRESPONDENCE: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
1.4%; Score 26; DB 4; Length 74;
Best Local Similarity 9.1%; Pred. No. 3.40e-03;
Matches 6; Conservative 20; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 74 BP; 6 A; 6 C; 1 G; 1 T; 60 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .T 9
PCT-US95-11934-98 STANDARD; DNA; UNC; 81 BP.
                                                                                                                                                                                                       ADDESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTRY READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OMPUTER: SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE TO THE STATE OF THE S
PCT-US95-11934-100 STANDARD; DNA; UNC; 74
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US95/11934 FILING DATE: 20-SEP-1995 CLASSIFICATION:
                                                       Sequence 100, Application PC/TUS9511934
Sequence 100, Application PC/TUS9511934
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
New York
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STATE: Ne
COUNTRY:
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COMPUTER RANGEL FORM:

MENINA TYPE: IN PROPERTY PROPERTY
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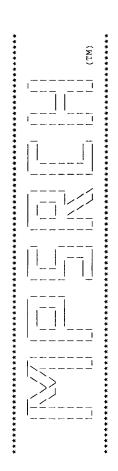
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                  STREET:
CITY: Ne
STATE: N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                           907 AGTGCTCACACCGGTCACTTGGTTGCTAGTGCTTTGTCTGATCCTTACCTCTCTTTGCT 966
                                                                                                                                                       0; Gaps
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                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From TITLE OF INVENTION: Peptide Libraries
UMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                             Ouery Match 1.3%; Score 24; DB 4; Length 75; Best Local Similarity 7.5%; Pred. No. 5.36e-02; Matches 5; Conservative 20; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y match 1.3%; Score 24; DB 4; Length 81; Local Similarity 17.1%; Pred. No. 5.36e-02; hes 13; Conservative 16; Mismatcher 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
SEQUENCE 81 BP; 3 A; 5 C; 6 G; 4 T; 63 OTHER.
                                                                               MOLECULE TYPE: DNA (genomic)
SEQUENCE 75 BP; 1 A; 1 C; 7 G; 5 T; 61 OTHER.
                                                                                                                                                                                                                                                 T 11
PCT-US95-11934-92 STANDARD; DNA; UNC; 81 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18,872
EF: 1101-196-228
                                                                                                                                                                                                                                                                                                                                                                      SSEE: Pennie & Edmonds
:: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
                                                                                                                                                                                                                                                                                     Sequence 92, Application PC/TUS9511934 Sequence 92, Application PC/TUS9511934 GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TELEFAX (212) 869-9741/8964
TELEX: 66141 PENNTE
INFORMATION FOR SEQ 1D NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH. 75 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ 1D NO: 92:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY ACENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
PEFERENCE/POCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
                                                                                                                                                                                                                  967 GCTGCTT 973
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                                                                                                                                                                                               64 NNBGGTT 70
                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                             CITY: N
STATE:
                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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907 AGIGCICACACGGICACIIGGIIGCIAGIGCIIIIGICIGAICCIIACCICICCIIIIGCI 966
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                                                                                                                                                                                                                                                                  Sequence 97, Application PC/TUS9511934
Sequence 97, Application PC/TUS9511934
Sequence 97, Application PC/TUS9511934
Sequence 97, Application PC/TUS9511934
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.3%; Score 24; DB 4; Length 82; 7.5%; Pred. No. 5.36e-02; ative 20; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 20-SEP-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
SEQUENCE 82 BP; 1 A; 2 C; 10 G; 8 T; 61 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-353-372A-16 STANDARD; DNA; UNC; 92 BP.
                                                                                                                                                                             .T 12
PCT-US95-11934-97 STANDARD; DNA; UNC; 82 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1101-196-228
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Sequence 16, Application US/08353372A
Patent No. 5840479
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (212) 790-9090
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/POCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 97:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 82 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                            1704 CGAATTCCTCACACGC 1719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 7,5%;
Matches 5; Conservative
                                                               63 NBNNBNNBNACGC 78
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APPLICANT: Marcia M. Miller
TITLE OF INVENTION: Restriction Fragment Length
TITLE OF INVENTION: Polymorphism Test For Haplotyping Domesticated Fowl
NUMBER OF SEQUENCES: 14
CORRESPONDENCE_ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        416 CAAAGCCTGGGGGTGAGCCCTTGCCTGAAGGTCTTCTGGGCTTCTTTTAACAGGAAAGG 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 SNNNKSNNAVKNGNNAKNSCKNKSANAVNNGNNAKNSNNNKSNNMGTREDNKNNRNAAKNN 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 24; DB 1; Length 105;
Pred. No. 5.36e-02;
27; Mismatches 53; Indels
                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3M Double Density 5 1/4" diskette
COMPUTER: Wang PC
OPPERATING SYSTEM: MS DOS Version 3.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA CRIGIALLY Prepared CRIGINAL SOURCE: Synthetically Prepared SEQUENCE 105 BP: 15 A; 0 C; 8 G; 1 T; 81 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .r 15
US-08-137-175A-7 STANDARD; DNA; UNC; 1958 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5451670e
                                                                                 STATE: 1000 CITY: Duarte STATE: California STATE: United States of America ZIP: 91010-0269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 NSGVADNKNNASNNYDNGSGVADNKNAAKNNY 103
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                                                                                                                                                                                                                      SOFTWARE: Microsoft
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/865,662F
FILING DATE: 07 April, 1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/068,176
FILING DATE: 30 June 1987
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                               FILING DATE: 07 April, 1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/688,326
FILING DATE: 22 April 1991
APPLICATION NUMBER: 07/588,922
FILING DATE: 27 September 1990
APPLICATION NUMBER: 07/210,405
                                                                                                                                                                                                                                                                                                                                                                                                   US 07/130,529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Irons, Edward S.
REGISTRATION NUMBER: 16,541
REFERENCE/DOCKET NUMBER: NO. 54
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELERAX: (202) 783-6031
TELERAX: NO. 5451670e
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08137175A Sequence 7, Application US/08137175A Patent No. 5777095 GENERAL INFORMATION:
APPLICANT: BARBOUR, Alan G. APPLICANT: BERGSTROEM, Sven
                                                                              ADDRESSEE: City of Hope
STREET: 1500 East Duarte Road
                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 33 June 1988
APPLICATION NUMBER: US 07/13
FILING DATE: 9 December 1987
APPLICATION NUMBER: US 07/06
FILING DATE: 30 June 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.3%;
Best Local Similarity 13.0%;
Matches 12; Conservative
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TYPE: Nucleic Acid
STRANDEDNESS. Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IOPOLOGY: Linear
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   APPLICANT: Little, Melvyn
APPLICANT: Breitling, Frank B
APPLICANT: Breitling, Frank B
APPLICANT: Stedan
APPLICANT: Klewinghaus, Iris
APPLICANT: Klewinghaus, Iris
TITLE OF INVENTION: Preparation and Use of Gene Banks of
TITLE OF INVENTION: Synthetic Human Antibodies ("Synthetic Human-Antibody
NUMBER OF SEQUENCES: 39
COPPESSONDENCE, ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 5.36e-02;
24; Mismatches 13; Indels
                                                                                                                                                  Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          753 GAIGTACAAGAATGGTGACACTATACCTAAGGATGAATCCCTGGA 797
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                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CUPPENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,372A
FILING DATE: 02-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
SEQUENCE 92 BF; 13 A; 10 C; 17 G; 17 T, 35 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05552.1032-02000
                                                                                                                                                                             STREET: 1300 I Street, N.W., Suite 700 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 40 02 897.6
FILING DATE: 01-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 40 03 880.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: DE P 40 03 880.7
FILING DATE: 09-FEB-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .r 14
US-07-865-662F-13 STANDARD; DNA; UNC; 105
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Sequence 13, Application US/07865662F
Patent No. 5451670
                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUBER: 08/247,393
FILING DATE: 23-MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                         07/654,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: FOTMan, David S.
REGISTRATION NUMBER: 33,694
PEFERENCE/POCKET NUMBER: 055
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/6:
FILING DATE: 30-JAN-1991
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 92 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 1.3%;
Best Local Similarity 17.8%;
Matches 8; Conservative
                                                                                                                                                                   Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 xxxxx
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Gaps
APPLICANT: HANSSON, Lennart
TITLE OF INVENTION: IMPROVEMENT IN BORRELIA BURGDORFERI AND
TITLE OF INVENTION: PROPHYLAXIS
CORRESPONDENCE: 22
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                      COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NAMER: 26-OCT-1993
CLASSIFICATION NAMER: PCT/US92/08972
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 28.005
REGISTRATION NUMBER: 28.005
REGISTRATION NUMBER: BARBOUR-1B
TELEPHONE: 202-737-3528
TELEPHONE: 203-737-3528
TELEPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: 959..1843
OTHER INFORMATION: /product-"OspB"
SEQUENCE 1958 BP, 837 A, 284 C, 340 G, 497 I, 0 OTHER.
                                                                                                                     ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY USA
21P: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.3%; Score 25; DB 3; Len Best Local Similarity 83.8%; Pred. No. 1.37e-02; Matches 31; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 TITITITAATITGCTAFITGTTATITGTTGATCTTAT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: /product- "Ospa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: Sat Oct 23 16:34:16 1999 Job time : 141 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Borrelia burgdorferi
STRAIN: Ip90
INDIVIDUAL ISOLATE: Isolate fr
INDIVIDUAL ISOLATE: Soviet Unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 125..949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Fri Oct 22 16:36:55 1999; MasPar time 7.33 Seconds 752.832 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-702-718-2 (1-471) from USO8702718.pep 3466 1 MVFYRSVSLLSKLRSRAVQQ......PLERPKSVTWEWLENGCKKA 471 Title:

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

119857 segs, 11713122 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-issued 1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1

Mean 33.654; Variance 162.896; scale 0.207 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Pred. No.	.42e+00	2.42e+00	77e+00	•	2.80e+01	2.80e+01	2.80e+01	5.85e+01	5.85e+01	.05e+01	4.36e+01	5.85e+01	5.85e+01	9.04e + 01	7.82e+01	6.77e + 01	5.77e+01	9.04e+01	1.39e + 02	60e+02	20e+02	60e+02	60e+02
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Description	Sequence 10, Applicat	Sequence 10, Applica	7			ď,	'n	Sequence 29, Applica	10	Sequence 127, Applicat	7	7	7, Applica	Patent No. 5320958.	ü	Sequence 2, Applicatio	148,	36, A	2, A	, Appli	56,	Sequence 27, Applicati	
QI	US-08-063-	PCT-US93-0	ns-07-689-	5320958-6		PCT-US95-0	-08-012-	-245-	-245-	-637-	-08-844-	-463-	S-08-460-		-08-742-	-742-	US-08-592-	-149-	-818-	-08-761-	US-08-933-	,	US-08-279-
DB	7	m	Н	4	П	m	٦	C1	C1	7		~	7	4	C1	7	7	C)	7	C	C a	C a	٦
Length	CA	220	3031	268	Ω	355	S	98	108	225	587	4	54	485	9	771	1312	2265	170	335	340	509	550
% Query Match	3.3	3.3	3.3				2.8	2.7	2.7	2.7	2.7	2.7		5.6					2.5				2.5
Score	113	113	115	100	97	26	46	85	92	93	94	92	92	68	06	91	91	68	86	85	87	85	82
Result No.	7	2	3	4	S	9	7	œ	o	10	11	12	13	14	15	16	17	18	19	20	21	Ci	23

1.39e+002 1.39e+002 1.39e+002 1.39e+002 1.39e+002 1.20e+002 1.20e+002 1.20e+002 1.20e+002 1.20e+002 1.30e+002	
Sequence 1, Applicatio Sequence 5, Applicatio Sequence 2, Applicatio Sequence 2, Applicatio Sequence 3, Applicatio Sequence 3, Applicatio Sequence 3, Applicatio Sequence 4, Applicatio Sequence 4, Applicatio Sequence 4, Applicatio Sequence 45, Applicatio Sequence 5, Applicatio Sequence 5, Applicatio Sequence 5, Applicatio Sequence 6, Applicatio Sequence 2, Applicatio	ane Transport Proteins Ninth Floor , Version #1.25 52
US-08-745- US-08-205- US-08-205- US-08-395- VG-08-395- VG-08-395- VG-08-395- VG-08-395- VG-08-395- VG-08-395- VG-08-144- VG-08-	4.1 v
2.55 2.55	STATE OF THE PROPERTY OF THE P
224 225 227 227 227 233 333 331 331 331 331 331 331 331 331	XXXXX  Sequence 10, Applical APPLICANT: EdwarION UNMER OF SEQUENCE ADDRESSEE: Share STREET: 225 Street: Palone STRYE: COUNTRY: USA STRYE: COUNTRY: USA STRYE: Galifo STRYE: Galifo SOFTWARE: Patt COMPUTER READABLI MEDIUM TYPE: COMPUTER SEADABLI NETLECANTION NO REFERENCE/POCK TELECOMUNICATION TYPE: AMINO A TOPOLOGY: lin MOLECULE TYPE: HYPOTHETICAL: N FRAGMENT TYPE: ORIGINAL SOURCE: ORIGINAL SOURC
	# 6 * * * * # * 8 8 8 8 8 8 8 8 8 8 8 8 8 8

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84 VGPLTNRIGYHIPMFVGFMIMF-LSTLMFAFSGTYALLFVARTLQGIGS 131
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                                                                                        209 DSMNLIAQVPLVAAYVYRRMYKNGDT-IPKDESLDYGANFAHM-LGFSSSEMHELLMRLY 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 DSMNLIAQVPLVAAYVYRRMYKNGDT-IPKDESLDYGANFAHM-LGFSSSEMHELLMRLY 266
                                                                    24 DNMLLTVVVPIVPTFLYATEFKDSNSSLHRGPSVSSQEENVRIGILFASKALMQLLVNPF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 DNMLLTVVVPIVPTFLYATEFKDSNSSLHRGPSVSSQEENVRIGILFASKALMQLLVNPF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.
                                                                                                                                                                                                                                                            GENEFAL INFORMATION -
APPLICANT: Edwards, Robert H
TITLE OF INVENTION: Vesicle Membrane Transport Proteins
NUMBER OF SEQUENCES: 17
                                                                                                                         267 VIIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGL-AG-PLHGLAN 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 3.3%; Score 113; DB 3; Length 220; Local Similarity 20.2%; Pred. No. 2.42e+00; les 22; Conservative 41; Mismatches 41; Indels
                              Length 220;
                                                                                                            84 VGPLTNRIGYHIPMFVGFMIMF-LSTLMFAFSGTYALLFVARTLQGIGS 131
                            3.3%; Score 113; DB 1; Length 220:
20.2%; Pred. No. 2.42e+00;
ative 41; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Pelease #1.0, Version #1.25
CURRENT APPLICATION DATA:
FITTAL CATTLE NOT NUMBER: PCT/US93/05704
                                                                                                                                                                       220 AA
                                                                                                                                                                                                                                                                                                               E: Sheldon & Mak
225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                         UP930611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9067-1PCT
                                                                                                                                                                       PRT;
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220 AA; 23695 MW; 270630 CN;
                                                                                                                                                                                                                                                    Application PC/TUS9305704
 NISM: Rattus rattus
220 AA; 23695 MW; 270630 CN;
                                                                                                                                                                                                                                 Sequence 10, Application PC/TUS9305704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Farber, Michael B
REGISTATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9067-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 795-6321
INFORMATION FOR SEO ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 220 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide HYPOTHETICAL: NO FRANCES
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                     Local Similarity 20.2%;
nes 22; Conservative
                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS.
                                                                                                                                                                                                                                                                                                                       STREET: 225 South
CITY: Pasadena
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: i ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                      PCT-US93-05704-10
                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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 ORGANISM:
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          SEQUENCE
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                              Query Match
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                                                 Matches
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420 PLAFLFFGQNIIAASPLAVLAYAIPHMFHSIATA-AKV-NKG-WRYSFWSEVYETTMALF 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wong, Hing
APPLICANT: Benziman, Moshe
TITLE OF INVENTION: METHODS AND NUCLEIC ACID SEQUENCES FOR THE
TITLE OF INVENTION: EXPRESSION OF CELLULOSE SYNTHASE OPERON
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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267 VIIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGL-AG-PLHGLAN 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McCutchen, Doyle, Brown & Enersen
                                                                                           3031 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
JENCE 3031 AA, 328497 MW; 44365167 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/07/689,008
FILING DATE: 19910422
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 337,194
FILING DATE: 12-APP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 496,236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: McCutchen, Jugers
STREET: Three Embarcadero Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.24
                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                     Sequence 2, Application US/07689008
Patent No. 5268274
                                                                                                                                                                                                                           Sequence 2, Application US/07689008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Murphy, Lisabeth Feix REGISTRATION NUMBER: 31547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                         Ben-Bassat, Arie
Calhoon, Roger D
                                                                                                                                                                                                                                                                                                                                                                                                           Gelfand, David H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 393-2000
TELEFAX: (415) 393-2286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 340817 MACPAG SFO INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 23-MAR-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3031 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                           Meade, James H
Tal, Rony
                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                      Fear, Anna L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Three Embarc
CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                          Patent No. 5268274
GENERAL INFORMATION:
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                                                                   RESULT 3
ID US-07-689-008-2
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                   214 IAQVPLVA-AYVYRRMYKNGDT--IPRDESLDYGANFAHMLGFSSSEMHELLMRLY-VTI 269
                                                                                                                                                                                                                                                                                                                                        95 KGLLRKGGLREGISTLLSLLSTEAPREAVQFRGKLLHVAKGPRALPQGAPTTSPGITNAL 154
477 LVRVTIITLMFPSKGKFNVTEKGGVLEEEFFDLGATYPNII-FAGIMTLGLLIGLFELTF 535
                                                                                                                                                                                                                                                                   Score 100; DB 4; Length 268;
Pred. No. 1.79e+01;
25; Mismatches 51; Indels 9; Gaps
                                                                                                                                                                                                                                                                                                      35 KAAQRWVLSNVVERLPVHGAAHGFVAGRSILTNALAHQGADVVVKVDLKDFFPSVTWRRV 94
                                                                                                                                                                                                                                                                                                                 APPLICANT: INOUYE, SUNIKO; HSU, MEI-YIN; EAGLE, SUSAN;
INOUYE, MASAYORI
TITLE OF INVENTION: ISOLATED BACTERIAL REVERSE TRANSCRIPTASE
NUMBER OF SEQUENCES: 24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/315,316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08450393A
Patent No. 5707815
GENERAL INFORMATION
GENERAL INFORMATION: Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                            355 AA
                                                                                      290 AA
                                                                                                                                                                                                             APPLICATION NUMBER: US/07/315,316
FILING DATE: 24-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                         LENGTH: 268
CE 290 AA; 32072 MW; 450220 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08450393A
                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                   2.9%;
Local Similarity 29.2%;
Les 35; Conservative
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STREET: 5 Falc
CITY: Palo Alto
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                                                                                       STANDARD;
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ZIP: 94306-2155
                                                                                                                                           Patent No. 5320958.
                                                                                                                                                            5320958
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US-08-450-393A-5
                                   536 HFNQLAG 542
                                                    270 HSDHEGG 276
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                                                                                                                         01-JAN-1900
                                                                                                                                                              Patent No.
                                                                                     5320958-6
                                                                                                                                                                                                                                                  SEQUENCE
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373 MKHLPEDPLFQL-VSKLYEVFLL-FLQNLAKLKP-WPNVDAHSGVLLN-YY-GLTEARYY 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: The Regents of the University of California IIILE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT IIILE OF INVENTION: PROTEIN RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 2.8%; Score 97; DB 1; Length 355; Local Similarity 31.9%; Pred. No. 2.80e+01; nes 23; Conservative 14; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US95/00476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     355 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Robbins, Berliner & Carson
201 N. Figueroa Street, 5th Floor
                                                                                                                                        UCAL-237/02US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REERENCE/DOCKET NUMBER: 5555-291
TELECOMMINICATION INFORMATION:
TELEPHONE: 310-977-1001
TELEFAX: 310-977-1003
APPLICATION NUMBER: US/08/450,393A FILING DATE: May 25, 1995 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application PC/TUS9500476 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                             355 AA; 41172 MW; 710742 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application PC/TUS9500476
                                                                                                             REGISTRATION NUMBER: 31,822
REPERENCE/DOCKER NUMBER: UCAL-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5165
TELEEX: 415-8857-0663
TELEEX: 380816CooleyPA
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                           TOPOLOGY: 11--
                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, 1
                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                               Cserr, Luann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             428 TVLFGVSRALGI 439
                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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6; Gaps

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23; Conservative 14; Mismatches 29; Indels
                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                           COMPUTER PEADABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.78:
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: USA
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IMMEDIATE SOURCE:
                                                         124 IILLTIDRYLAI 135
                                                                            428 TVLFGVSRALGI 439
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                                                                                                                   US-08-245-511-29
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                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
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Matches
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TITLE OF INVENTION: Cloning and Expression of Human

TITLE OF INVENTION: Macrophage Inflammatory Protein-1 alpha (MIP-1

TITLE OF INVENTION: alpha)/RANTES Receptor

NUMBER OF SEQUENCES: 2
                                                                                                                                        65 LKNMTSIYLLNLAISDLLFLFTLPFWIDY-KLKDDWVFGDAMCKILSGFYYTGLYSEIFF 123
                                                                                                                                                    6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                            y Match 2.8%; Score 97; DB 3; Length 355; Local Similarity 31.9%; Pred. No. 2.80e+01; hes 23; Conservative 14; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.8%; Score 97; DB 1; Length 355; Best Local Similarity 31.9%; Pred. No. 2.80e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/012,988A
FILING DATE: 19930128
                                                                                                                                                                                                                                        355 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15280-118
                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
JENCE 355 AA; 41172 MW; 710742 CN;
                                                                             355 AA; 41172 MW; 710742 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08012988A Patent No. 5652133
                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08012988A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 152
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-543-5043 INFORMATION FOR SEQ ID NO: 2:
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Weber,, Kenneth A. PEGISTRATION NUMBER: 31,
                 LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
                                                                                                                                                                                                                                         STANDARD;
          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415-543-5043
                                               MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 199301;
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                 428 TVLFGVSRALGI 439
                                                                    ANTI-SENSE: NO
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373 MKHLPEDPLEQL-VSKLYEVFLL-FLQNLAKLKP-WPNVDAHSGVLLN-YY-GLTEARXY 427
65 LKNMTSIYLLNLAISDLLFLFTLPFWIDY-KLKDDWVFGDAMCKILSGFYYTGLYSEIFF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 29, Application US/08245511
Patent No. 5928900
GENERAL INFORMATION:
APPLICANT: Masure, H Robert
APPLICANT: Pearce, Barbara J
APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Elaine
TITLE OF INVENTION: RACTERTAL EXPORTED PROTEINS AND
TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 98;
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                                                                                                                                                                                                                                                                   98 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,511
FILING DATE: 18-MAY-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,541
FILING DATE: 01-SEP-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae
                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: SPRU87
98 AA; 10496 MW; 48418 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 29, Application US/08245511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REPERENCE/DOCKET NUMBER: 600 TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
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87 IIPETLPSQM 96 | : : | 70 ITVDMVLGGM 79

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 LSKLRSPAVQQSNVSNSVPWLQVQTSSGLDLRSELVQELIPEQQDRLKKIKSDMKGSIGN 59
Best Local Similarity 24.3%; Pred. No. 5.85e+01;
Matches 17; Conservative 20; Mismatches 31; Indels 2; Gaps
                              26 MTRLRVTVKDADKVGNAEQW-KAEGAMGLVMKGQGVQAIYGPKADILKSDIQDILDS-GE 83
                                           10 LSKLRSRAVQQSNVSNSVRWLQVQTSSGLDLRSELVQELIPEQQDRLKKIKSDMKGSIGN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Caps
                                                                                                                                                                                                    Sequence 10, Application US/08245511
Patent No. 5928900
GENERAL INFORMATION
APPLICANT: Masure, H Robert
APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Elaine
TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 2.7%; Score 92; DB 2; Length 108; Best Local Similarity 24.3%; Pred. No. 5.85e+01; Matches 17; Conservative 20; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                         SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                             108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Jackson Esq., David A. PEGISTPATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600-1-069 CIP
                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,511
FILING DATE: 18-WAY-1994
CLASSIFFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
FENCE 108 AA; 11664 MW; 59621 CN;
                                                                                                                                                                                                                                                                                                      E: Klauber & Jackson
411 Hackensack Avenue
                                                                                                                                                                                    Sequence 10, Application US/08245511
                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SO, ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 108 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                   New Jersey
                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                         Hackensack
                                                                                                                                                                                                                                                                                                                                           USA
                                                                   84 IIPETLPSOM 93
                                                                                      70 ITVDMVLGGM 79
                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                            US-08-245-511-10
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366 TCQREFAMKHLPEDPLFQLVSKLYEVFLLFLQNLAKLKPWPNVDAHSGVLLNYYGLTEAR 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 93; DB 2; Length 225; Pred. No. 5.05e+01; 24; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARD STATES.

SOFTWARD APPLICATION DATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION 1435
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY AGBNT INFORMATION:
NAME: Pabet, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPWS 101
TELECOMMUNICATION 1072-0724
                  225 AA.
                                                                                                                                                                                                                                           APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   587 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                  STAIL:
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
--worder: IBM PC compatible
--worder: IPM PC compatible
--worder: IPM PC compatible
--worder: IPM PC compatible
                    FRT;
                                                                                                                                                                                                                                                                                                                                         ADDRESSE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                       Sequence 127, Application US/08637759B Patent No. 5876931 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 AA; 25356 MW; 275619 CN;
                                                                                                                                                Sequence 127, Application US/08637759B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 127:
                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 225 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 2.7%;
Local Similarity 23.0%;
hes 17; Conservative
                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            426 YYTVLFGVSRALGI 439
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                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Atlanta
STATE: Georgia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
J 10
US-08-637-759B-127
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US-08-844-280-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                XXXXXX
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MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
JENCE 1548 AA; 172282 MW; 12743552 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,092B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-007-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
                                                                                                                                                                                                                                                                                                             CONTEX: CANADA
ZIP: K7L 3N6
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 01546
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-2342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-07-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
CLASSIFICATION: 435
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NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 7:
SEGUENCE CHARACTERISTICS:
LENGTH: 1548 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.7%;
Best Local Similarity 28.2%;
Matches 22; Conservative
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                                                                                                                                                                                                                                                         CITY: Kingston STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-460-907B-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 VGRRRDLGGLIFI-D-LRDREGIM-Q-LVI-NPEKVSAEVMATAESLRSEFV-IEVTGQV 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.7%; Score 94; DB 1; Length 587;
28.4%; Pred. No. 4.36e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1548 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA: FILING DAMPS: US/08/844 ....
                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 5747315el Compounds
                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/844,280
18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: P31457-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
JENCE 587 AA; 66220 MW; 1692397 CN;
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PHOR APPLICATION DATA:
PPLOR APPLICATION NUMBER: 9607993.4
FILING DATE: 18-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08463092B Patent No. 5766880
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                                                                                                                                                                                                  Sequence 2, Application US/08844280 Patent No. 5747315
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                                                                                                                                            Sequence 2, Application US/08844280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1: 587 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHAPACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 610-270-5090
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                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 6
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Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: PA
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370 VGWLRVPGMAVLFVTLPL-QAVISKHVQDVSERMASVVDLRI-KRINEL-LSGVRIVKFM 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 92, DB 2, Length 1548,
Pred. No. 5.85e+01;
18; Mismatches 34; Indels 4; Gaps
GENERAL INFORMATION:
APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
STREET: Queen's University at Kingston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1548 AA
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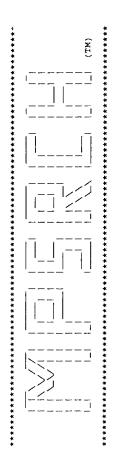
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370 VGWLRVPGMAVLFVTLPL-QAVISKHVQDVSERMASVVDLRI-KRTNEL-LSGVRIVKFM 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 92; DB 2; Length 1548;
Pred. No. 5.85e+01;
18; Mismatches 34; Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                  ADDRESSEE: PARTED RESEARCH & DEVELOPMENT INNOVATIONS STREET: Queen's University at Kingston CITY: Kingston STATE: Ontario STATE: Ontario ZIVIRY: CANADA ZIP: K7L 3N6
                                                                       Sequence 7, Application US/08460907B
Patent No. 5891724
GENERAL INFORMATION:
APPLICANT: Deeley, Roger G.
APPLICANT: Cole, Susan P.C.
TITLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUG
TITLE OF INVENTION: RESISTANCE ON A CELL
NUMBER OF SEQUENCES: 9
COPRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
ENCE 1548 AA; 172282 MW; 12743552 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,907B
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
CLASSIFCATION 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Steeg, CATOL Miernicki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: 01551
TELECOMMUNICATION:
TELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION NUMBER: 08/029,340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER PEADABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                      Sequence 7, Application US/08460907B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (613) 545-2342
TELEPAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1548 amino acids
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Best Local Similarity 28.2%;
Matches 22; Conservative
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RESULT

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204 KAAQRWVLSNVVERLPVHGAAHGFVAGRSILTNALAHQGADVVVKVDLKDFFPSVTWRRV 263
                                                                                                                                                                                                                                                                                                                        16 RAVQOSNVSNSVRWLQVQTSS-GL-DLRSELVQELIPEQQDRLKKIK-SDMKGSIGNITV 72
                                                                                                                                                                                                                                                                                                                                                               264 KGLLRKGGLPEGTSTLLSLLSTEAPRQAVQFRGKLLHVAKGPRALPQGAPTSPGITNAL 322
                                                                                                                                                                                                                                                                         8; Gaps
                                                                                                         APPLICANT: INOUYE, SUNIKO; HSU, MEI-YIN; EAGLE, SUSAN;
INOUYE, MASAYORI
TITLE OF INVENTION: ISOLATED RACTEPIAL REVERSE TRANSCRIPTASE
NUMBER OF SEQUENCES: 24
CURRENT PAPLICATION DATA:
APPLICATION NUMBER: US/07/315,316
FILING DATE: 24-FEB-1989
                                                                                                                                                                                                                                               Score 89; DB 4; Length 485; 
Pred. No. 9.04e+01; 
27; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08742753
Patent No. 5861278
GENERAL INFORMATION:
APPLICANT: WONG, Gordon G.
APPLICANT: YAO, Kwok-Ming
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                          763 AA
525 AA.
                                                                                                                                                                                                                       525 AA; 57562 MW; 1459426 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08742753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 52
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8260
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32,618
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R.
REGISTRATION NUMBER: 32,6
                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                               Query Match 2.6%;
Best Local Similarity 26.9%;
Matches 32; Conservative
STANDARD;
                                                                       Patent No. 5320958.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                               5320958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02140
                                                                                                                                                                                                             LENGIH: 485
                                                                                                                                                                                                                                                                                                                                                                                                                JT 15
US-08-742-753-4
                                                                                                                                                                                             SEQ ID NO:2:
                                                01-JAN-1900
                                                                                                Patent No.
5320958-2
                                                                                                                                                                                                                       SEQUENCE
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CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 76.3 maino acids
CC STRANDEDNESS: single
CC STRANDEDNESS: single
CC STRANDEDNESS: single
CC FEATURE: CDNA
CC FEATURE: CDNA
CC NAME/KEL: CDNA
CC NAME/KEL: CDNA
CC NAME/KEL: CDNA
CC LOCATION: 70.2358
SQ SEQUENCE 763 AA: 84252 MW; 3182536 CN;
CU LOCATION: 2.6%; SCOTE 90; DB 2; Length 763;
Best Local Similarity 27.1%; Pred. No. 7.82e+01;
Matches 19; Conservative 21; Mismatches 26; Indels 4; Gaps 4;
Db 334 LPEHLESQOKRPNPELRRNM-TIKTELPLGARRKMKPLLPRVSSYLVPIQFPVNGSLVLQ 392
III: : II: : II: : II: III: IIII
COY 49 IPEQ-ODRLKKIKSDMKGSIGNITVDMVLGGMRGMTGLL-WKPHYLDPDEGIRFRGLSIP 106
Db 393 PSVKVPLPLA 402
III | OY IOT ECOKV-LPAA 115
Search completed: Fri Oct 22 16:38:18 1999
Job time: 83 secs.
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Pelease 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

MasPar time 18.71 Seconds 535.432 Million cell updates/sec Fri Oct 22 16:20:42 1999; Run on:

>US-08-702-718-2 (1-471) from US08702718.pep

Tabular output not generated.

3466 Description: Perfect Score:

1 MVFYRSVSLLSKLRSRAVQQ......PLERPKSVTMEWLENQCKKA 471 Sednence:

PAM 150 Gap 11 Scoring table:

170751 seqs, 21266608 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38

Variance 166.895; scale 0.216 Mean 36.074; Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

					CHINESTOC		
		æ					
Result		Query					
NO.	Score	Match	Match Length DB	DB	ΩI	Description	Pred. No.
        	3466	100.0	471	15	R86383	Potato citrate syntha	0.00e+00
7	3466	100.0	471	14	R82838	Potato citrate syntha	0.00e+00
3	3098	89.4	469	14	R82840	Tobacco citrate synth	1.27e-270
4	2637	76.1	437	14	R82839	Sugar beet citrate sy	8.02e-228
S	310	6.8	436	m	R14357	Citrate synthase enco	1.16e-15
9	130	3.8	754	35	W69756	Acetobacter xylinum b	2.91e-01
7	113	3.3	220	σ	R47340	Fragment of chromaffi	4.63e+00
80	115	3.3	754	œ	R45000	Cellulose synthase op	3.37e+00
9	110	3.2	3084	35	W50891	Mouse laminin A chain	7.44e+00
10	105	3.0	355	24	W29179	Rat CC chemokine rece	1.63e+01
11	100	2.9	329	29	W55574	H. pylori ORF 06ep302	3.50e+01
12	100	2.9	329	53	W55330	H. pylori ORF hp3e110	3.50e+01
13	101	2.9	456	34	W38570	Methyl tetrahydropter	3.01e+01
14	100	2.9	4473	13	R97244	Virulence gene cluste	3.50e+01
15	64	2.8	355	25	W26588	Human MIP-1 alpha/RAN	5.51e+01
16	46	2.8	355	11	R52749	C-C chemokine recepto	5.51e+01

24444444444444444444444444444444444444	700+ 700+ 700+ 700+ 700+ 700+
Human MIP-lalpha/RANT Prostaglandin-EP3-9 r Prostaglandin-EP3-21 Prostaglandin-EP3-21 Prostaglandin-EP3-21 Human prostaglandin E Human EP3-V receptor. Streptococcus pneumon Streptococcus pneumon Streptococcus pneumon Streptococus pneumon Streptococus pneumon Streptococus pneumon Mouse novel secreted Leishmania antigen Lo T-lymphocyte TLiss An Human T-lymphocyte TL DNAX accessory molecu B. cepacia insertion Reverse transcriptase Mouse TRIDENT transcr Human hepatocyte nucle Rat hepatocyte nucle Human homologue of ye Human PADACO	a grade a grade
WA25751 R69517 R69517 R69517 R705110 R707110 R707110 R707110 R707110 R707110 R707110 R707110 R707110 R707110 R707110 R707110 R707110 R707110 R707110 R707110	215 215 313 373 234 234 131 131 787
3352 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	3 4 5 6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
355 365 365 398 399 399 390 390 100 100 100 100 100 100 100 100 100 1	1146676617
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11110222222222222222222222222222222222	

### ALIGNMENTS

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Inhibiting citrate synthase (CS) activity in plants - to inhibit flower formation and improve storage capacity, e.g. in potatoes, a lso new CS sense and anti-sense DNA sequences.

Talso new CS sense and anti-sense DNA sequences.

Claim 5; Page 15-19; 35pp; German.

The potato citrate synthase (CS) gene or cDNA sequence encoding CS (T03410) may be used to produce antisense CS sequences. CS DNA csequences are useful for altering CS activity in plants. Antisense CS sequences can be used to inhibit CS expression in plants and has the effect of inhibiting flower formation and by doing so improves the plant's storage capacity. This is partic. useful in crop plants of any kind but esp. useful in potatoes. In addition to altering CS activity the DNA sequences can also be used to identify similar sequences in the genomes of other plants and in the production of transgenic plants with altered CS activity. This sequence

represents the amino acid sequence of potato citrate synthase.
                                 R86383;
24.ARF-1996 (first entry)
Potato citrate synthase.
Citrate synthase; inhibitor; increased storage capacity; potato;
                                                                                                                                                                                                                                                                                         (AGRE ) HOECHST-SCHERING AGREVO GMBH.
La Cognata U, Landschutze V, Muller-Roeber B, Landschuetze V;
WPI: 95-321536/42.
N-PSDB; T03410.
T
R86383 standard; Protein; 471 AA
                                                                                                                                       Solanum tuberosum.
14-SEP-1995.
09-MAR-1994; 408629.
09-MAR-1994; DE-408629.
22-SEP-1994; DE-433366.
19-OCT-1994; DE-438821.
                                                                                                                         antisense DNA.
RESULT
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Gaps .. Score 3466; DB 15; Length 471, Pred. No. 0.00e+00; 0; Mismatches 0; Indels 0 Query Match 100.0%; Best Local Similarity 100.0%; Matches 471; Conservative

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1 mvfyrsvsllsklrsravggsnvsnsvrwlqvgtssgldlrselvgelipegqdrlkkik 60

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                                                                                                                                                                                 121 PLPEGLLWLLIGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPWTQFATGV 180
                                                                                                                                                                                                                                                                                                                                                  241 LDYGANFAHMLGFSSSEMHELLMRLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFAAA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 sdmkgsignitvdmvlggmrgmtgllwkphyldpdegirfrglsipecqkvlpaakpgge 120
                                                                                        61 SDMKGSIGNITVDMVLGGMRGMTGLLWKPHYLDPDEGIRFRGLSIPECQKVLPAAKPGGE 120
                                                                                                                                                   121 pipegllwllltgkvpskeqvnsivsgiaesgiisliimyttidalpvtahpmtgfatgv 180
                                                                                                                                                                                                                                        181 malgygsefgkayekgihkskyweptyedsmnliagyplyaayvyrrmykngdtipkdes 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA fragment of citrate synthase from Arabidopsis thallana was firstly amplified using A.thaliana cDNA and oligos T04202 and T04203 which are complementary to the 5' or 3' end of the coding region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 mvfyrsvsllsklrsravggsnvsnsvrwlgvgtssgldlrselvgelipeggdrlkkik 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A. thaliana cDNA for citrate synthase. The oligos additionally introduce BamHI cleavage sites at both ends of the amplified cDNA fragment. a cDNA library was prepd. from potato leaves and screened with A. thaliana citrate synthase cDNA. Positive clones were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels 0; Gaps
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Disclosure; Page 53-56; 87pp; English.
To identify a cDNA from potato which codes for citrate synthase, a
                                                                                                                                                                                                                                                                                181 MALQVQSEFQKAYEKGIHKSKYWEPTYEDSMNLIAQVPLVAAYVYRRMYKNGDTIPKDES
                    1 MVFYPSVSLLSKLRSRAVQQSNVSNSVRWLQVQTSSGLDLRSELVQELIPEQQDRLKKIK
Landschuetze V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ltearyytvlfgvsralgicsqliwdralglplerpksvtmewlengckka 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 LTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENQCKKA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   purified and sequenced. The nt sequence is given in T04199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Citrate synthase; flower formation; tuber storage. Solanum tuberosum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 3466; DB 14;
Pred. No. 0.00e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AGRE ) HOECHST-SCHERING AGREVO GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R82838 standard; Protein; 471 AA.
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Local Similarity 100.08;
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22-SEP-1994; DE-435366.
19-OCT-1994; DE-438821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-SEP-1995.
07-MAR-1995; E00859.
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DNA encoding plant citrate synthase - used to regulate flower formation, to improve storage of tubers, etc. and to reduce sprouting Disclosure; Page 60-63, 87pp; English.

To identify a cDNA from tobacco which codes for citrate synthase, a cDNA bank of leaf tissue from tobacco was prepd. Plaques of this cDNA bank were screened using a radioactive DNA probe which comprises Solamm tuberosum citrate synthase cDNA (T04199). One of the clones was sequenced. The nt. sequence is
                                                                                                                                                                                                                                                                                                                                                                                                           malgygsefgkayekgihkskyweptyedsmnliagyplvaayvyrrmykngdtipkdes 240
                                                                                                                                                                                                                                              241 LDYGANFAHMLGFSSSEMHELLMRLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFAAA 300
                                                                                                                                                                                                                                                                                                     Inglagplhglangevllwiksvveecgeniskeglkdyvwktlnsgkvvpgfghgvlrk 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 sehgkvqlgnitvdmvlggmrgmtgllwetslldpdegirfrglsiyecqkvlpaakpgg 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SDM-KGSIGNITVDMVLGGMRGMTGLLWKPHYLDPDEGIRFRGLSIPECQKVLPAAKPGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 eplpegllwllltgkvpskeqvdslsqelrsratvpdhv-yktidalpvtahpmtqfatg 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 mvfyrgvsllsklrsravggtnlsnsvrwlqvgtssgldlrsel-gelipeggdrlkklk 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MVFYRSVSLLSKLRSRAVQQSNVSNSVRWLQVQTSSGLDLRSELVQELIPEQQDRLKKIK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Gaps
                                                                                                                                                                  (AGRE ) HOECHST-SCHERING AGREVO GMBH.
La Cognata U, Landschutze V, Muller-rober B, Landschuetze V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 3098; DB 14; Length 469;
Pred. No. 1.27e-270;
23; Mismatches 22; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 ltearyytvlfgvsralgicsqliwdralglplerpksvtmewlengckka 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 LTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENQCKKA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tobacco citrate synthase.
Citrate synthase; flower formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .r 3
R82840 standard; Protein; 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match
Local Similarity 89.6%;
es 423; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35-JAN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-MAR-1995; E00859.
09-MAR-1994; DE-408629.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-SEP-1994; DE-435366
19-OCT-1994; DE-438821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 95-328278/42.
N-PSDB; T04201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    469 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mueller-roeber B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            given in T04201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R82840;
                                                                                                                                           181
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eeviylllngelpnkaqydtftntltnhtllheqir-nffngfrrdahpmailcgtvgal 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nyaenflsmmfarmsepykvnpvlaramnrililhadheq-naststvrlagstganpfa 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 DYGANFAHML-G-FSSS-EMHELLMR-LY-VII-HSDHEGGNVSAHTGHLVASALSDPYL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 ciaagiaalwgpahgganeavlk-mlarigk-kenip-afiaq-v-kdknsgvklmgfgh 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314 rvyknfdprakimgqtchevltelgikddplldlavel-ekialsddyfvqrklypnvdf 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 EGLLWLLLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATGVMAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 sa-f-ypdandiaip-an-rdla---amrliakiptiaawayk--ytggeafiyprnd-l 199
 274 EGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENISK 333
                                                                                                                                        394 LFLONLAKLK-PWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALGLP 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acetic acid resistant gene with in plasmid and transformed acetobacter - improves yield of acetic acid fermentation. Disclosure: Fig 5: 12pp. Japanese The aarA gene encodes the citrate synthase and is part of an acetic acid resistance operon comprising aarA, aarB and aarC. The DNA can be used to prepare an acetic acid resistant strain bacteria for use in acetic acid fermentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85; Mismatches 111; Indels 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 310; DB 3; Length 436; Pred. No. 1.16e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           373 ysgiilkamgiptsmf-tvlfavarttg 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           411 HSGVLLNYYGLTEARYYTVLFGVSRALG 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ā
                                                                                                                                                                                                                                                              .T
R14357 standard; Protein; 436 AA.
                                                                                                                                                                                                                                                                                                               23-JAN-1992 (first entry)
Citrate synthase encoded by aarA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W69756 standard; Protein; 754
                                                                                                                                                                       418 lerpksvtmewlekfckr 435
                                                                                                                                                                                                           453 LERPKSVTMEWLENQCKK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 8.9%;
Best Local Similarity 30.5%;
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NAKA-) NAKANO SUMISE KK.
WPI; 91-329112/45.
                                                                                                                                                                                                                                                                                                                                                                                                                   05-FEB-1990; 024395.
15-FEB-1989; JP-033776.
05-FEB-1990; JP-024395.
                                                                                                                                                                                                                                                                                                                                                  Acetic acid resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 436 AA;
                                                                                                                                                                                                                                                                                                                                                                      Acetobacter sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; 014367
                                                                                                                                                                                                                                                                                                                                                                                      J03219878-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W69756;
                                                                                                                                                                                                                                                                                                  R14357;
                                                                                                       358
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                                                                                                                                                                                                                                                              RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding plant citrate synthase - used to regulate flower formation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 ipdhv-yktidalpitahpmtqfctgvmalqtrsefqkayekgihkskfweptyedclsl 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 iaqvpvvaayvyrrmykngqviplddsldyggnfahmlgfdspqmlel-mrlyvtihsdh 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eggnvsahtghlvgsplsdpylsfaaalnglagplhglangevllwiksvvdecgenist 297
                   vmalqvqsefqkayekgihksklweptyedsmsliaqvplvaayvyrrmykngntipkdd 238
                                                                   239 sldyganfahmlgfsssdmhel-mklyvtihsdheggnvsahtghlvasalsdpylsfaa 297
                                                                                                                                      298 alnglagplhglangevllwiksvveecgeniskeglkdyawktlksgkvvpgfghgvlr 357
                                                                                                                                                                                                         358 ktdprytcgrefalkhlpedplfglvaklyevflgflgnlaklnpwpnvdahsgvllnyy 417
                                                                                                                                                                                                                                          360 KTVPRYICQREFAMKHLPEDPLFQLVSKLYEVFLLFLQNLAKLKPWPNVDAHSGVLLNYY 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to improve storage of tubers, etc. and to reduce sprouting Disclosure; Page 57-60; 87pp; English.

Disclosure; Page 57-60; 87pp; English.

Synthase, a cDNA from sugar beet which codes for citrate synthase, a cDNA bank of leaf tissue from sugar beet was prepd. Plaques of this cDNA bank were screened using radioactive DNA probes which comprise a mixture of Solanum tuberosum citrate synthase cDNA (T04199) and Nicotian tabacum citrate synthase cDNA (see T04201). One of the clones was sequenced. The nt. sequence is given in T04200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ssnldlrsel-qelipeqqerlkkikkefqsfqlqninvdmvlqqmrqmtqllwetslld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 SSGLDLRSELVQELIPEQQDRLKKIKSDMKG-SIGNITVDMVLGGMRGMTGLLWKPHYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peegirfrgfsipecqkllpaasagaeplpegllwllltgkvpskeqvdalsadlrkras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             La Cognata U, Landschutze V, Muller-rober B, Landschuetze V;
Mueller-roeber B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                                                                                                            418 gltearyytvlfgvsralgicsgliwdralglplerpksvtmewlenhckka 469
                                                                                                                                                                                                                                                                                                               420 GLTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVIMEWLENQCKKA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2637; DB 14; Length 4
Pred. No. 8.02e-228;
41; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sugar beet citrate synthase.
Citrate synthase; flower formation.
Best vulgaris strain Zuchtlinie 5S 0026
W09524487-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-WAR-1995; E00859.
09-WAR-1994; DE-408629.
22-SEP-1994; DE-438586.
19-OCT-1994; DE-438821.
(AGRE ) HOECHST-SCHERING AGREVO GMBH.
                                                                                                                                                                                                                                                                                                                                                                    T
R82839 standard; Protein; 437 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 81.3%;
Matches 356; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   25-JAN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 95-328278/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            437 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; T04200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-SEP-1995
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                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                           qq
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Gaps 28;

of

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Claim 2; Page 34; 50pp; Japanese.

This represents the amino acid sequence of a Acetobacter xylinum subspecies sucrefermentans bcsA gene product. The invention provides a gene encoding a Acetobacter xylinum subspecies sucrefermentans derived cellulose synthesis complex produced protein. The gene sequence represents bcsA, bcsB, bcsC or bcsD, CMCase and a beta-glucosidase encoding gene. The novel gene and the enzyme participate in the synthesis of cellulose by microorganisms. Cells transformed with the genes may be sequence 754 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          420 plaflfaggniiaaaplavaayalphmfhsiata-akv-nkg-wrysfwsevyettmalf 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 SLIIMYTTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKYWEPTYEDSMNL- 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              477 lvrvtivtllfpskgkfnvtekggvlxeexfdlgatypnii-fatimmgglliglfeliv 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 IAQVPLVAA-YVYRRMYKNGDT--IPKDESLDYGANFAHMLGFSSSEMHELLMRLYVTIH 270
                                 bcsC; bcsD; CMCase; beta-glucosidase; enzyme; cellulose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Gaps
Acetobacter xylinum bcsA gene product.
Acetobacter xylinum; sucrofermentans; cellulose synthesis complex;
                                                                                                                                                                                                                                                                                                                                                                                                                      Gene encoding Acetobacter xylinum cellulose synthetase complex containing a group of genes including those for conventional and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New mammalian vesicle membrane transport protein - and corresp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fragment of chromaffin granule amine transporter protein. Vesicle membrane transport protein; gene therapy; screening; Parkinsons disease; neurotoxin; identification; detection; antibody; probe; chromaffin granule amine transporter protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 130; DB 35; Length 754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                  (BIOP-) BIO-POLYMER RES CO LTD.
Hayashi T, Tahara N, Tonouchi N, Tsuchida T, Yano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 2.91e-01;
                                                                                                                                                                                                                            /label= unspecified
/note= "encoded by AAG"
                                                                                                                                      note* "encoded by GAG"
                                                                                                                                                                                         /note= "encoded by GAG"
                                                                                                                       /label= unspecified
                                                                                                                                                                         /label= unspecified
                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R47340 standard; Protein; 220 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    536 rfnql-dviarnayllnca 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 SDHEGGNVSAHTGHLVASA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.8%;
Best Local Similarity 19.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JUN-1992; US-899074
30-JUL-1992; US-923096.
(REGC ) UNIV CALIFORNIA.
Edwards RH;
                                                                                                                                                                                                                                                                                                             JP-063927
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                                                                    Acetobacter xylinum.
                                                                                                                                                                                                                                                                              11-SEP-1998.
09-OCT-1997; J03633.
04-MAR-1997; JP-0639
                                                                                                                                                        Misc_difference 506
                                                                                                     Misc_difference 503
                                                                                                                                                                                                          Misc_difference 573
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 98-495854/42.
N-PSDB; V52831.
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                                                     microordanism
                                                                                                                                                                                                                                                               409839455-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                        Yoshinaga F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09325699-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-DEC-1993.
                                  bcsA; bcsB;
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The sequences given in R45000-03 represent the proteins encoded by The sequences given in R45000-03 represent the proteins encoded by the bacterial cellulose synthase operon. The sequence given in R45004 is the begining of an open reading frame overlapping the end of this operon. The bacterial cellulose synthase operon contains four genes, genes A-D. The operon sequence may be used in a transcription vector for the expression of the cellulose synthase operon to increase cellulose production in a recombinant microorganism. This system may be used as an important tool for exploring mechanisms of cellulose synthesis and for enhancing production of cellulose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 SLIIMYTTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKYWEPTYEDSMNL- 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420 plaflffggniiaasplavlayaiphmfhsiata-akv-nkg-wrysfwsevyettmalf 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 DSMNLIAQVPLVAAYVYRRMYKNGDT-IPKDESLDYGANFAHM-LGFSSSEMHELLMRLY 266
DNA, vectors, transformed cells and antibodies, for diagnosis and treatment of neurological disorders, e.g. Parkinson disease Example 2; Page 114-115; 181pp; English.

The CDNA encoding the chromaffin granule amine transporter protein is useful in gene therapy and as a probe for detecting genomic sequences. The protein is used for screening cytotoxic compounds implicated in Parkinsons disease, diseases associated with activity of neurotoxins or psychiatric disorders and to identify compounds which selectively inhibit or activate its action. Antibodies raised against this protein are useful as immunoassay reagents for detecting the protein and as affinity reagents for purification. This fragment of the transporter protein shares homology with the Neterminal domains of the methlenomycin; tetracycline and multi-drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 dnmlltvvvpivptflyatefkdsnsslhrgpsvssqeenvrigilfaskalmqllvnpf 83
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contiguous nucleic acid sequences - encoding bacterial cellulose synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cellulose synthase operon, gene A product.

Bacterial; cellulose synthase; operon; gene A; gene B; gene C; gene D; transcription vector; recombinant microorganism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Calhoon RD, Fear AL, Gelfand DH;
                                                                                                                                                                                                                                                                                                                                                                Query Match 3.3%; Score 113; DB 9; Length 220; Best Local Similarity 20.2%; Pred. No. 4.63e+00; Matches 22; Conservative 41; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 vgpltnrigyhipmfvgfmimf-lstlmfafsgtyallfvartlggigs 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 VIIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGL-AG-PLHGLAN 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46; Mismatches 49; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               л 8
R45000 standard; Protein; 754 AA.
                                                                                                                                                                                                                                                                                                      transporter proteins.
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Best Local Similarity 18.1%;
Matches 23; Conservative
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Tal R, Wong H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-DEC-1993.
12-APR-1989; 337194.
04-APR-1990; WO-U01811.
09-APR-1990; IL-094053.
10-APR-1990: NS-014264.
11-APR-1990; NS-233312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cellulose synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acetobacter xylinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CETU ) CETUS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 93-404004/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       754 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; Q53522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JUN-1994
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                                                                                                                                                                                                                                                                                                      resistance
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3084 AA;

Sequence

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This is the amino acid sequence of the mouse laminin A chain. The primary object of the invention is to use laminin, laminin-derived primary object of the invention is to use laminin, laminin-derived protein fragments and/or laminin-derived polypeptides as potent inhibitors of amyloid formation, deposition, accumulation and/or persistence in Alzheimer's disease and other amyloidoses. The laminin products (see W50888-98) may include mouse or human laminin A or Al chain, laminin Bl or B2 chain, laminin A2 chain (merosin), aminin G1 chain, the globular repeats of the laminin A1 chain and the becamploid binding domain of the laminin A chain A chaimed method for treating an amyloid disease comprises administering a polypeptide having a conformational similarity to a fragment of a laminin protein. A method for diagnosing an amyloid disease comprises administering of involves determining levels of laminin in a sample. Production of laminin or its fourth globular repeat in vivo provides a method for involves can be used for the diagnosis, prognosis, monitoring and treatment of amyloidoses such as Alzheimer's disease, Down's
                   14 IAQVPLVA-AYVYRRNYKNGDT--IPKDESLDYGANFAHMLGFSSSEMHELLMRLY-VTI 269
477 lvrvtiitlmfpskgkfnvtekggvleeeefdlgatypnii-fagimtlglliglfeltf 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AL amyloid), the amyloidosis associated with type II diabetes (amylin or islet amyloid), the amyloidosis associated with prion diseases including Creutzfeldt-Jacob diseases, Gertstnann-Straussler syndrome, kuru and animal scrapie (PrP amyloid), the amyloidosis associated with long-term haemodialysis and carpal tunnel syndrome (beta 2-microglobulin amyloid), the amyloidosis associated with senile cardiac amyloid and Familiah Amyloidotic Polyneuropathy (prealbumin or transthyretin amyloid), and the amyloidosis associated with endocrine tumours such as medullary carcinoma of the thyroid (variant of procalcitonin).
                                                                                                                                                                                                                                                           syndrome and hereditary cerebral haemorrhage with amyloidosis of the Dutch type (where the specific amyloid is the beta-amyloid protein), the amyloidosis associated with chronic inflammation, various forms of malignancy and Familial Mediterranean Farma amyloid or inflammation-association amyloidosis), the amyloidosis associated with multiple myeloma and other B-cell abnormalities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
2746..2922
/note= "fourth globular domain repeat (Claim 13)"
2690..2700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       wrl: y=24033471.
Use of laminin and fragments - for developing products for use in
the diagnosis and treatment of amyloid disease, e.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "beta-amyloid protein binding region (Claim 12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 74-79; 132pp; English.
                                                                                                                                                                                                     W50891 standard; Protein; 3084 AA.
                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-APR-1998.
08-OCT-1997; U18145.
08-OCT-1996; US-027981.
(UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Snow AD;
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                                                                           536 hfnqlag 542
                                                                                                                     270 HSDHEGG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease or CJD
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                                                                                                                                                                                                                                              07-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                    therapy
                                                                                                                                                                                                                             W50891;
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This sequence is a rat CC chemokine receptor. The receptor can be used
to screen for novel binding compounds and for preparation of antibodies
                                                              1884 selqsragaldrdlenvrwvslnatsaahvhsn-iqtlt-eeaewla-adahktanktdl 1940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 lfnlavsdlvflftlpfwidy-klkdnwvfgdamckllsgfyylglyseiffiilltidr 131
                                                                                           11 SKLRSRAVQQSNVSNSVRWLQVQTSSGLDLRSELVQELIPEQQDRLKKIKSDMKGSIGNI 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 105; DB 24; Length 355;
Pred. No. 1.63e+01;
15; Mismatches 38; Indels 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUN-1998 (first entry)
L pylori ORF Obep30223_23557202_c2_130 cytoplasmic protein.
Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                          CC chemokine receptor protein - useful to screen for novel binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent {\rm H.}\ {\rm pylori}
   Length 3084;
                                30; Mismatches 33; Indels
                                                                                                                                                                                                                                                19-DEC-1997 (first entry)
Rat CC chemokine receptor.
rat; CC chemokine receptor; screen; binding; ligand.
Score 110; DB 35;
Pred. No. 7.44e+00;
                                                                                                                            1941 ise-slas-rgkavlqrssrflkesvgtr 1967
                                                                                                                                                         71 TVDMVLGGMRGMTGLLWKPHYLDPDEGIR 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 ylaivhavfslrartvtfgiitsiii-w 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            436 ALGICSQLIWDRALGLPLERPKSVTMEW 463
                                                                                                                                                                                                       T 10
W29179 standard; Protein; 355 AA.
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W55574 standard; Protein; 329 AA.
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22-FEB-1996; 035192.
22-FEB-1996; JP-035192.
(TAKE) TAKEDA CHEM IND LTD.
WPI; 97-486426/45.
N-PSDB; T86839.
 3.2%;
Local Similarity 23.6%;
hes 21; Conservative
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US-625811.
US-758731.
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25-OCT-1996; US-736905.
28-OCT-1996; US-738859.
(ASTR ) ASTRA AB.
Alm RA, Smith D;
WPI: 97-503122/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-1997; U05223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355 AA;
                                                                                                                                                                                                                                                                                                 Rattus rattus.
J09227599-A.
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 Query Match
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polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection and for diagnosis of H. pylori infection and for diagnosis of H. pylori infection of the pylori brotein may be used in a vaccine to prevent or treat H. pylori protein polypeptide binding compounds, infection or to identify H. pylori plotpeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The DNA and probes derived from it may be used for the identification of H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic and sequences complementary to the DNA act as antisense sequences and can be used to prevent the translation of H. pylori mRNA. Antibodies against the protein can be used in immunoassays to evaluate the abundance and distribution of H. pylori-specific antigens. The genomic sequence of H. pylori (ATC. 55479) was determined from overlapping contigs generated by mochanically shearing the bacterial DNA. The sequences were analysed for OR or ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF
infection and for diagnosis of H. pylori infection

Claims 14,96; Page 779-779; 1145pp; English.

This sequence is a H. pylori cytoplasmic protein involved in cofactor.

This sequence is a Protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The DNA and probes derived from it may be used for the identification of H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and can be used to prevent the translation of H. pylori mRNA. Antibodies against the protein can be used in immunoassays to evaluate the abundance and distribution of H. pylori-specific antigens. The genomic sequence of the pylori (ATCC 55679) was determined from overlapping contigs generated for DPP of at least 180 muclorides and the predicted coding regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli
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H. pylori ORF hp3el1024orf49 protein.
Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 100, DB 29; Length 329;
Pred. No. 3.50e+01;
15; Mismatches 8; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori nucleic acid sequences and encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 IAOVPLVAAYVYRRMYKNGDTIPKDESLDYGANFAH 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 veempliasvifnrl-kkgmplgmdgalny-gefsh 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 12
W55330 standard; Protein; 329 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.9%,
Best Local Similarity 30.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAR-1997; U05223.
06-DEC-1996; US-761318.
29-MAR-1996; US-625811.
02-APR-1996; US-758731.
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28-OCT-1996; US-738859.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      329 AA;
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Alm RA, Smith D;
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Claim 12; Pages 342-344; 483pp; English.

This sequence represents a Streptococcus pneumoniae protein that, based on homology with an E. coil protein, is a methyl tetrahydropteroyitri glutamate-homocysteine methyltransferase, and is encoded by a DNA of the invention. The DNA sequences were isolated from S. pneumoniae strain 0100993 (NCIMB 40794). The Streptococcus pneumoniae proteins of the invention can be used to identify compounds which interact with and inhibit or activate the activity of the proteins. Antaqonists can be used to treat diseases caused by S. pneumoniae proteins, through genetic inmunisation. They can also be used to induce an immunological response in a mammal by inoculation with the S. pneumoniae proteins or delivery of the encoding nucleic acids in a vector adequate to produce antibody and/or I cell immune responses to protect the animal from disease. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     profeins can also be used to identify antimicrobial compounds which are capable of inhibiting their bioactivity. In particular the proteins of the invention can be used to prevent adhesion of bacteria to mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            extracellular matrix proteins on in-dwelling devices or in wounds, to block protein-mediated mammalian cell invasion, and to block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or other surgical techniques.
were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 MYTTIDALPVJAHPMIOFATGVMALO-VOSEF--OKAYEKGIHKSKY-WEPTYEDSMNLI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 vyadlvnlpvdaigl-dfvegkktlelvkggfpadktlyvgivngkniwrnnyekslavl 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methyl tetrahydropteroyltriglutamate-homocysteine methyltransferase. Streptococcus pneumoniae protein; genetic immunisation; antagonist; immunological response; incoulation; antibody production; inhibitor; T cell immune response; antimicrobial compound; bacterial adhesion; extracellular matrix protein; protein mediated cell invasion, wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel Streptococcus pneumoniae proteins and related DNA - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 101; DB 34; Length 456;
Pred. No. 3.01e+01;
17; Mismatches 22; Indels 5; Gaps
                                                                                                                                                                                                                8; Indels 2; Gaps
                                                                                                                                                                Score 100: DR 29; Length 329;
Pred. No. 3.50e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosing anti-microbial agents for treatment of bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Black MT, Hodgson JE, Knowles DJC, Nicholas RO,
                                                                                                                                                                                                                                                               218 veempliasvifnrl-kkgmplqmdgalny-qefsh 251
                                                                                                                                                                                                                                                                                                             214 IAQVPLVAAYVYRRMYKNGDTIPKDESLDYGANFAH 249
                                                                                                                                                                                                                15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         W38570 standard; Protein; 456 AA.
W38570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-MAY-1997; U07950.
14-MAY-1996; US-017670.
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.9%;
Local Similarity 31.3%;
Les 20; Conservative
                                                                                                                                                                Query Match 2.9%;
Best Local Similarity 30.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae.
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                                                                                                                     329 AA;
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The first with insertion inactivated genes into environment and retrieval and analysis of mutants

Tetrieval and analysis of mutants

Claim 51; Figure 11; 319pp; English

Claim 51; Figure 11; 319pp; English

A method for identifying a microorganism having a reduced adaptation

to a particular environment comprising the steps of: (1) providing a plurality of microorganisms each of which is independently mutated by the insertional inactivation of a gene with a nucleic acid comprising a unique marker sequence so that each mutant contains a different marker sequence, or clones of the said microorganism; (2) providing individually stored nucleic acid comprising the unique marker sequence from each individual mutant; (3) introducing a providing individually stored nucleic acid comprising the unique marker sequence from each individual mutant; (3) introducing a convironment and allowing those microorganisms which are able to do so to grow in the said environment; (4) retrieving microorganisms from the said environment or a selected part thereof and isolating the nucleic acid from the retrieved microorganisms; (5) comparing any marker sequences in the nucleic acid isolated in step (4) to the marker sequences of each individual mutant stored as in step (2); and (6) selecting an individual mutant which does not contain any of the marker sequences as isolated in step (4). The products and and an individual mutant which does not contain and or the marker sequences of each individual mutant which does not contain and contain and contains a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 100; DB 19; Length 4473;
Pred. No. 3.50e+01;
25; Mismatches 35; Indels 4; Gaps 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2872 mrtixxrsrscherysms-lpdspl-qligilfilsilpl-iivmgtsflklavvfsilr 2928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the marker sequences as isolated in step (4). The products and methods can be used for identifying virulence genes in microorganisms. The mutant microorganisms can be used in vaccines or to screen for drugs which reduce virulence or compounds useful for preventing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :| :| :: :: ::| | : :: | | : : : | : : : : : : : ::| 358 LRKTVPRY-TCQREFAMKHLPEDPLFQLVSKLYEVFLLFLQNLAKLKPWPNVDAHSGVLL 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-57N-1998 (first entry)
Human MIP-1 alpha/RANTES receptor.
Macrophage inflammatory protein-1 alpha; MIP-1 alpha;
reduced upon activation normal T expressed and secreted; RANTES;
                                                            07-JAN-1997 (first entry)
Virulence gene cluster polypeptide product.
Mutant; adaptation; virulence factor; identification; screening;
vaccine; drugs; infection; treatment.
                                                                                                                                                                                                                                                         Noyer= "All x's in this sequence correspond to termination codons in the virulence gene cluster sequence given in T09224."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying virulence genes in microorganisms - by introducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ameliorating or treating infections in animals or plants. Sequence 4473 AA;
                                                                                                                                                                        Salmonella typhimurium.
Key Location/Qualifiers
R97244 standard; Protein; 4473 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2929 nalgiqqvppnialyglalvlsl 2951
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W26588 standard; Protein; 355 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                           09-DEC-1994; GB-024921.
31-JAN-1995; GB-001881.
05-MAY-1995; GB-009239.
(FPMS-) FPMS TECHNOLOGY LTD.
Holden DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.9%;
Best Local Similarity 22.9%;
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 13-JUN-1996.
11-DEC-1995; G02875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 96-287194/29.
N-PSDB; T09224.
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NW receptor; cytokine; antiinflammatory; inflammation; human.

NESSE2133-A.

PD 29-UUL-1997.

PF 28-JAN-1993; 012988.

PR 28-JAN-1993; US-012988.

R 28-JAN-1993; US-01298.

R 37-3945/36.

R 37-3945/36.

R 37-3945/36.

R 37-3945/36.

R 37-3945/36.

R 37-3945/36.

R 37-3946/36.

R 37-3
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Query Match 2.8%; Score 97; DB 25; Length 355; Best Local Similarity 31.9%; Pred. No. 5.51e+01; Matches 23; Conservative 14; Mismatches 29; Indels 6; Gaps

9

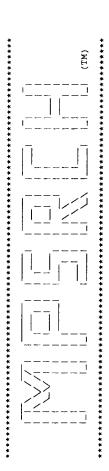
Db 124 iilltidrylai 135

QY 428 TVLFGVSRALGI 439

Search completed: Fri Oct 22 16:28:26 1999 Job time : 464 secs.

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. Sun Oct 24 10:10:33 1999



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MPsrch\_pp protein · protein database search, using Smith-Waterman algorithm

Fri Oct 22 16:28:44 1999; MasFar time 21.02 Seconds 897.635 Million cell updates/sec

Pun on:

Tabular output not generated

Title:

Description: Perfect Score: Sequence:

>US-08-702-718-2 (1-471) from US08702718.pep 3466 1 MVFYPSVSLLSKLPSPAVQQ.......PLEPPKSVTMEWLENGCKKA 471

PAM 150 Gap 11 Scoring table:

122810 seqs, 40068593 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

1:pirl 2:pir2 3:pir3 4:pir4 Database:

Mean 50.591; Variance 106.019; scale 0.477 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARTES

	No.	00+6	00e+00	00e+00	00e+00	00e+00	09e-296	64e-284	46e-278	e-229	e-197	e-33	e-31	e-25	9-24	e-24	34e-24	e-22	3-22	5e-22	e-22	$\sim$	e-20	
	Pred.	00.00+00	00.0	0.0	0.00	0.00	60.6	2.64	4.46	8.43e-	9.90e-J	3.00e-	1.13e-	1.26e-2	1.336-2	4	6.	1.41e-	1.416-	9.75	4.51e-	4.54	1.43e	
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SUMMARIES	ID	S44316	T02390	YKMUM	YKPG	S42370	YKBY	S41563	YKBYC	JC5625	S52814	140717	YKOPC	YKPSCA	S53007	S74344	C69417	139506	JQ1392	A43936	E70782	YKRECP	E69658	
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œ	Query Match	100.0	81.4	99	55.4	49.7	48.0	46.3	45.4	38.3	33.7	9.1	6.8	7.8	7.7	7.6	7.5	7.3	7.3	7.2		7.1		
	Score	3466	2820	2305	1921	1722	1663	1606	1575	1329	1168	316	307	272	566	263	261	254	254	249	251	245	242	
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361 IVPRYICQREFAMKHLPEDPLFQLVSKLYEVFLLFLQNLAKLKPWPNVDAHSGVLLNYYG 420

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YKEC S41527 G69600 E64760 140380 D70380 YKYT P47033 YKYT P43033 YKYT P43033 YKYT P43033 YKYT P43033 YKYT P43033 YKYT P43033 YKYT P43033 YKYT P4303 YKYT P4303 YKYT P4303 YKYT P4303 YKYT P4303 YKYT P4303 YKYT P4303 YKYT P4303 YKYT P4003 YKYT P4003 YKYT P4003 YKYT P4003 YKYT P4003 YKYT P4003 YKYT YKYT P4003 YKYT YKYT YKYT YKYT YKYT YKYT YKYT YKY	ALIGNMENT	pe colan colan colan colan colan colan colan colan colan colon col	Score 3 Pred. N 0; Mis	NVSNSVRWL 	MTGLLWKP           MTGLLWKP	VNSIVSGIAE                VNSIVSGIAE	KYWEPTYEDS 	LLMRLYVTIH	SVVEECGE 	TA TAULT TO
наималинаминанинанин		s	.08; .08; ive	\$00A	GMRG  - -  GMRG	KEQV HEDI	HKSK 	EMHEI  - -  EMHEI	LWIK	700
7422 7422		Lam 119 2p- 2p- 2p- 2p- 2p- 2p- 2p- 2p- 2p- 2p-	100. ty 100. servati	KLRSRAV         KLRSRAV	VDMVLGC	TGKVPSF         TGKVPSF	AYEKGIH         AYEKGIH	GFSSSEN          GFSSSEN	LANQEVLI          LANQEVLI	TO THE DAY
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carbon-carbon lyase; oxo-acid-lyase; tricarboxylic acid cycle
#length 474 #molecular-weight 52782 #checksum 6960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana chromosome IÎ BAC F4II genomic sequence T02390
T02390 *type complete probable citrate (s1)-synthase (EC 4.1.3.7) - Arabidopsis
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Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter,
                                                                                                                                                                                                                                                                                                                  F4I1.16 protein
#formal_name Arabidopsis thaliana #common_name mouse-ear
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                                                                                                                                                                                                                                                                                                                                                                                                05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.;
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                                                                                                    421 LTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENQCKKA 471
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55; Mismatches 38;
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##cross_references EMBL:X17528; NID:g11243; PID:e1188578; FID:g2552924
##note the sequence from Fig. 2 is inconsistent with that from
Fig. 1 in having 47-Gly, 125-Trp, 141-Leu, 151-Ser,
185-Asn, 187-Asn, 191-Asn, 348-Leu, an additional Gly
after 89-Trp, an additional Val after 393-Cys and two
additional Arg after 228-Arg, in lacking 114-Leu and
residues 233 to 241
                                                                                                                        citrate (si)-synthase (EC 4.1.3.7) precursor, mitochondrial Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                               Unger, E.A.; Hand, J.M.; Cashmore, A.R.; Vasconcelos, A.C. Plant Mol. Biol. (1989) 13:411-418
Isolation of a cDNA encoding mitochondrial citrate synthase
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#active_site His, His, Asp *status predicted
#length 472 #molecular-weight 52941 #checksum 9626
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418 YYGLTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENQCKKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 66.5%; Score 2305; DB 1; Length 472; Best Local Similarity 68.9%; Pred. No. 0.00e+00; Matches 328; Conservative 60; Mismatches 76; Indels 1:
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                                                                                                                                                                                                                                                                                                                                                                                                     from Arabidopsis thaliana
#cross-references MUID:91370823
                                                                                                   *type complete
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##residues 1-472 ##label UNG
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#### \*authors Evans, C.T.; Owens, D.D.; Sumegi, B.; Kispal, G.; Srere, P.A. #journal Blochemistry (1988) 27.4680-4686 | Isolation nucleotide sequence, and expression of a cDNA encoding pig citrate synthase. pig citrate (si)-synthase (EC 4.1.3.7) precursor - pig #formal\_name Sus scrofa domestica #common\_name domestic 15-Oct-1982 #sequence\_revision 30-Sep-1992 #text\_change Bloxham, D.P.; Parmelee, D.C.; Kumar, S.; Wade, R.D.; Ericsson, L.H.; Neurath, H.; Walsh, K.A.; Titani, K. Proc. Natl. Acad. Sci. U.S.A. (1981) 78:5381-5385 Primary structure of porcine heart citrate synthase. Aci347 Bloxham, D.P.; Parmelee, D.C.; Kumar, S.; Walsh, K.A.; Titani, K. Biochemistry (1982) 21:2028-2036 Complete amino acid sequence of porcine heart citrate 416 LNYYGLTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENQCKKA 471 Remington, S.; Wiegand, G.; Huber, R. J. Mol. Biol. (1982) 158:111-152 Crystallographic refinement and atomic models of two different forms of citrate synthase at 2.7 and 1.7 angstroms resolution. ##cross-references EMBL:M21197; NID:g164418; PID:g164419 NCE A90457 #type complete ##molecule\_type protein ##residues 28-464 ##label BLO ##molecule\_type protein ##residues ##molecule\_type mRNA ##residues 1-464 ##label EVA A29966; A01109; A61347 #cross-references MUID:82231993 #accession A01109 18-Sep-1998 synthase A29966 A61347 A29966 A92884 #accession #accession #authors #journal #authors #journal #journal ACCESSIONS REFERENCE #title REFERENCE REFERENCE REFERENCE TITLE ORGANISM RESULT ENTRY DATE

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                           annotation; X-ray crystallography, 2.7 and 1.7 angstroms clrate (si)-synthase is found in nearly all cells capable of catalyte metabolism. It catalyzes the condensation of oxaloacetate and acetyl-CoA to form citrate in the tricarboxylic
                                                                                                                                                                         It is synthesized in the cytoplasm but functions in the mitochondrion of eukaryote cells. This molecule is a dimer of identical chains. Each dimer binds two
                                                                                                                                                                                                                                                                      molecules of acetyl-CoA and two molecules of oxaloacetate at two
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#modified_site N6,N6-trimethyllysine (Lys) #status
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#product citrate (si)-synthase #status experimental
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#cross-references MUID:83010291
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                                                                                                                                                    acid cycle.
                                                                                                                                                                                                                                                                                                                              CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301,347,402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                     *contents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-464
                                                                                                                                                                                                                                                                                                                                                         KEYWOPDS
                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                1-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARY
                                                                                                                                                                                                                                          COMMENT
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9

Gaps

Indels

86; Mismatches

254; Conservative

Matches

27 SASSTNLK-DILADLIPKEQARIKTFRQQHGNIVVGQITVDMMYGGMRGMKGLVYETSVL 85

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S42370 *type complete citrate (si)-synthase (EC 4.1.3.7) precursor - Caenorhabditis
                                                                                                                                                                                         205 LIAKLPCVAAKIYRNLYREGSSIGAIDSKLDWSHNFINMLGYIDAQFTEL-MRLYLTIHS 263
                                                                                                                                                                                                                                                                             324 SDEKLRDYIWNTLNSGRVVPGYGHAVLRKTDPRYTCQREFALKHLPHDPMFKLVAQLYKI 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384 VPNVLLEQGKAKNPWPNVDAHSGVLLQYYGMTEMNYYTVLFGVSRALGVLAQLIWSRALG 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 ISVLDPEEGIRFRGYSIPECQKLLPKAKGGEEPLPEAIWWLLCTGDVPSEAQTAAITKEW 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 NARADLPTHVV-RMLDNFPDNLHPMAQFIAAIAALNNESKFAGAYARGVAKASYWEYAYE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 DSMDLLAKLPTVAAIIYRNLYRDGSAVSVIDPKKDWSANFSSMLGYDDPLFAEL-MRLYL 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 DSMNLIAQVPLVAAYVYRRMYKNGDTIP-KDESLDYGANFAHMLGFSSSEMHELLMRLYV 267
                                                                   DPDEGIRFRGYSIPECQKMLPKAKGGEEPLPEGLFWLLVTGQIPTEEQVSWLSKEWAKPA 145
                                                                                                              93 DPDEGIRFRGLSIPECQKVLPAAKPGGEPLPEGLLWLLLTGKVPSKEQVNSIVSGIAESG 152
                                                                                                                                                            146 ALPSHVV-TMLDNFPTNLHPMSQLSAAITALNSESNFARAYAEGIHRTKYWELIYEDCMD 204
                                                                                                                                                                                                                                                                                                                                              264 DHEGGNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLVWLTQLQKEVGKDV 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332 SKEQLKDYVWKTLNSGKVVPGFGHGVLRKTVPRYTCQREFAMKHLPEDPLFQLVSKLYEV 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         392 FILFLQNLAKLK-PWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALG 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 LQVQTSSGLDLRSELVQELIPEQQDRLKKIKSDMKGSIG-NITVDMVLGGMRGMTGLLMK 88
34 ISSGLDLFSELVQELIPEQQDFLKKIKSDMKGSI-GNITVDMVLGGMRGMTGLLWKPHYL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 LSTSAEGSTNLKEVLSKK-IPAHNAKVKSFRTEHGSTVVQNVNIDMIYGGMRSMKGMVTE 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *sequence_revision 10-Nov-1995 *text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *superfamily citrate (si)-synthase carbon-carbon lyase; mitochondrion; oxo-acid-lyase #length 468 #molecular-weight 51540 #checksum 2659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #cross-references EMBL:Z30423; NID:g458479; PID:g458482
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Pred. No. 0.00e+00;
84; Mismatches 109;
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Best Local Similarity 54.0%;
Matches 236; Conservative
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S42370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     451 LPLERPKSVIME 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          444 FPLERPKSMSTD 455
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Isolation of the nuclear yeast genes for citrate synthase and fifteen other mitochondrial proteins by a new screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            citrate (si)-synthase (EC 4.1.3.7) precursor, mitochondrial yeast (Saccharomyces cerevisiae) protein NVO19; protein VNO01c #formal_name Saccharomyces cerevisiae 25.Feb-1985 #sequence_revision 10-Feb-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Verhasselt, P.; Aert, R.; Voet, M.; Volckaert, G.
submitted to the EMBL Data Library, January 1994
Twelve open reading frames revealed on the 23.6 kbp segment
flanking the centromere on the Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##cross-references EMBL:X77395; NID:q496717; PID:q496718
##note the nucleotide sequence was submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Twelve open reading frames revealed in the 23.6 kb segment flanking the centromere on the Saccharomyces cerevisiae
                             268 TIHSDHEGGNVSAHTGHLVASALSDFYLSFAAALNGLAGPLHCLANQEVLLMIKSVVEEC 327
                                                                                                                                 328 GENISKEQLKDYVWKTLNSGKVVPGFGHGVLRKTVPRYTCQREFAMKHLPEDPLFQLVSK 387
                                                                                                                                                                                                      382 LYKITPGILLEQGKAKNPWPNVDSHSGVLLQYFGMTEMSFYTVLFGVSRALG-CLSQLIW 440
                                                                                                                                                                                                                                262 VIHSDHEGGNVSAHTSHLVGSALSDPYLSFSAAMAGLAGPLHGLANQEVLVFLNKIVGEI 321
                                                                                                    322 GFNYTEEQLKEWVWKHLKSGQVVPGYGHAVLRKTDPRYECQREFALKHLPNDDLFKLVST 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aert, R.; Verhasselt, P.; Voet, M.; Volckaert, G. submitted to the Protein Sequence Database, April 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Verhasselt, P.; Aert, R.; Voet, M.; Volckaert, G.
Yeast (1994) 10:1355-1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##cross-references EMBL:223259; NID:9313749; PID:9313750
NCE S45118
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NCE S48338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, July 1993 835390
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##experimental_source strain D273-10B
NCE S62910
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EMBO J. (1984) 3:1773-1781
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##rosidues 1-479 ##label VER
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##residues 1-479 ##label LIN
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#accession A01110
                                                                                                                                                                                                                                                                                                                                        446 DRALGLPLERPKSVTME 462
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##residues 1-47
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##molecule_type DNA
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#submission

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##cross-references BMBL:271616; NID:g1302468; PID.e239778; FID:g1302469; MIPS:YNR001c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #domain transit peptide (mitochondrion) #status
predicted #label TNP\
#product citrate (si)-synthase #status predicted #label
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دع
                                                                                                                                                                                                                                                                                                                                   carbon-carbon lyase; catalyzes condensation of oxaloacetate and acetyl-CoA to form citrate; oxo-acid-lyase tricarboxylic acid cycle *superfamily citrate (si)-synthase
                                                                                                                                                                                                                                                                                                                                                                                                                               acetyl-CoA; carbon-carbon lyase; homodimer; mitochondrion;
oxo-acid-lyase; tricarboxylic acid cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 EIPEHVI-QLLDSLPKDLHPMAQFSIAVTALESESKFAKAYAQGVSKKEYWSYTFEDSLD 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 LLGKLPVIASKIYRNVFKDGKITSTDPNADYGKNLAQLLGYENKDFIDL-MRLYLTIHSD 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276 HEGGNVSAHTTHLVGSALSSPYLSLAAGLNGLAGPLHGRANQEVLEWLFKLREEVKGDYS 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 HEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENIS 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       396 PGVLTKHGKTKNPWPNVDSHSGVLLQYYGLTEASFYTVLFGVARAIGVLPQLIIDRAVGA 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 DPDEGIRFRGLSIPECQKVLPAAKPGGEPLPEGLLWLLLTGKVPSKEQVNSIVSGIAESG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 LIAQVPLVAAYVYRRMYKNGDTIPKDESLDYGANFAHMLGFSSSEMHELLMRLYVTIHSD 272
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#length 479 #molecular-weight 53360 #checksum 4782
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##cross-references SGD:S0005284; MIPS:YNR001c
#accession Sobor.

##molecule_type DNA

##molecule_type DNA

1-479 ##label AER
                                                                                                                                  ##experimental_source strain S288C
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P.A.; Guarente, L.P.
Mol. Cell. Biol. (1986) 6:4509-4515
Mitochondrial and nonmitochondrial citrate synthases in
Saccharomyces cerevisiae are encoded by distinct homologous
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Ferea, T.; Contreras, E.T.; Oung, T.; Bowman, E.J.; Bowman,
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                                       #journal Mol. Gen. Genet (1994) 242-105-110
#title Characterization of the cit.1 gene from Neurospora crassa encoding the mitochondrial form of citrate synthase.
#cross-references MUID:94104594
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                                                                                                                                                                                                                                     36/3; 58/2; 123/1; 453/2
superfamily citrate (si)-synthase
carbon-carbon lyase; mitochondrion; oxo-acid-lyase
#length 469 #molecular-weight 52002 #checksum 490
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*#molecule_type DNA
1-460 ##label ROS
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#accession A25393
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##residues 1-460 ##label AIG
##cross-references EMBL:X59720; NID:g1907116; PID:e264468; PID:g1907148;
MIPS:YCR005c
                                                                        #authors Biteau, N.; Fremaux, C.; Hebrard, S.; Menara, A.; Aigle, M.; Crouzet, M.

#journal Yeast (1992) 8:61-70

#title The complete sequence of a 10.8kb fragment to the right of the chromosome III centromere of Saccharomyces cerevisiae.

#cross_references MuID:92254505

#accession S26734
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CLASSIFICATION #superfamily citrate (si)-synthase
    acetyl-CoA; carbon-carbon lyase; homodimer; oxo-acid-lyase;
    REYWORDS
    peroxisome; tricarboxylic acid cycle
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Mol. Cell. Biol. (1991) 11:38-46
Intramitochondrial functions regulate normitochondrial
citrate synthase (CIT2) expression in Saccharomyces
cerevisiae.
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NID:9171226; PID:9171227
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predicted #label TNP\
#product 14-nm filament protein/citrate synthase #status
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##residues
1.462 ##label NUM
##rcsidues
1.462 ##label NUM
##cross-references GB:D90117; NID:9217406; PID:d1014848; PID:g1688046
##cross-references GB:D90117; NID:g217406; PID:d1014848; PID:g1688046
##more
part of this sequence, including the amino end of the
mature protein, was confirmed by protein sequencing
IT his protein is involved in oral morphogenesis preceding binary
fission, and in nuclear events during fertilization, such as
formation of gametic pronuclei and zygote formation of gametic
pronuclei. It also acts as a mitochondrial enzyme, citrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Numata, O.; Takemasa, T.; Takagi, I.; Hirono, M.; Hirano,
Chiba, J.; Watanabe, Y.
Biochem Biophys Res. Commun. (1991) 174·1028-1034
83 GIIFRGYTIPQLKEFLPKADPKAADQANQEPLPEGIFWLLMTGQLPTHAQVDALKHEWQN 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 GIRFRGLSIPECOKVLP-A-AKPG--G--EPLPEGLLWLLLTGKVPSKEOVNSIVSGIAE 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 RGTVNQDCVNFILN-LPKDLHSMTMLSMALLYLQKDSKFAKLYDEGKISKKDYWEPFYED 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 NLKK-VIAEIIPQKQAELKEVKEKYGDKVVGQYTVKQVIGGMRGLMSDLSRC-DPYQ 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 DLRSELVQELIPEQQDRLKKIKSDMKGSI-GNITVDMVLGGMRGMTGLLWK-PHYLDPDE 96
                                                                                                                                                                                                                                                                                                                     #formal_name Tetrahymena thermophila
14-Oct-1997 #sequence_revision 07-Nov-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem Biophys Res Commun (1997) 237:205-210
Direct demonstration of the bifunctional property of
Tetrahymena 14-nm filament protein/citrate synthase
following expression of the gene in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tetrahymena 14-nm filament-forming protein has citrate
                                                                                                                                                                                                                                            14-nm filament protein/citrate synthase (EC 4.1.3.-)
    Tetrahymena thermophila (SGC5)
49K filament-forming protein
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oxo-acid-lyase
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larity 46.8%; Pred. No. 8.43e-229;
Conservative 95; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Takeda, T.; Watanabe, Y.; Numata, O.
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                                                                      428 LITDRAIGASIERPKSYSTE 447
                                                                                                                     443 LIWDRALGLPLERPKSVTME 462
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Wang, Y.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, T.D.;
Hall, J.; Storms, R.K.; Vo. D.H.; Winnett, E.
submitted to the EMBL Data Library, July 1995
The sequence of Saccharomyces cerevisiae chromosome XVI right
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NNCE S57724
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                                                                                                 321 KVSDKDIEDYVDHVISSGRVVPGYGHAVLRDTDPRFHHQVDFSKFHLKDDQMIKLLHQCA 380
                                                                                                                                                                                                                                                                     381 DVIPKKLLTYKKIANPYPNVDCHSGVLLYSLGLTEYQYYTVVFAVSRALG-CMANLIWSR 439
                                                                                                                                                                                                                                                                                              80 SLDPEHGIKFQGLTIEECQNRLPNTGIDGDNFLPESMLWLLMTGGVPTFQQAASFRKELA 139
                                                                                                                                                                                                                    330 NISKEQLKDYVWKTLNSGKVVPGFGHGVLRKTVPRYTCQREFAMKHLPEDPLFQLVSKLY 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        citrate (si)-synthase (EC 4.1.3.7) - yeast (Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 IIKSSALTLKEAL-ENVIPKKPDAVKKLKACYGSTFVGPITISSVLGGMPGNQSMFWQGT 79
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19-May-1995 #sequence_revision 01-Sep-1995 #text_change
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#molecular-weight 53811 #checksum 9998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein LPZ1w; protein YP9723.01; protein YPR001w
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98; Mismatches 125;
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##residues 1-486 ##label PEA
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##residues 1-486 ##label JIA
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Matches 207; Conservative
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249 HML-GFSS-S-EMHELLMR-L--YVTIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALN 302

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Microbiology (1994) 140:1817-1828
Mucleotide sequence, expression and transcriptional analysis of the Corynebacterium glutamicum gltA gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 316; DB 2; Length 437;
Pred. No. 3.00e-33;
91: Mismatches 111; Indels 24; Gaps 20;
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                                         150 ESGIISLIIMYT-TI-DALPVTAHPMTQFATGVMALQVQSEFQKAYEKG-IHKSKYWEPT 206
                                                                                                           318 AAQEVVRFLIEMNSNIS-SIAREQEIKDYLWKILNSNRVIPGYGHAVLRKPDPRFTAMLE 376
                                                                                                                                                                                                                                                                                                          312 ANQEVLLMIKSVVEECGENISKEQ-LKDYVWKTLNSGKVVPGFGHGVLRKTVPRYTCQRE 370
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                                                                                    198 LEDSLNLIASLPLLTGRIYSNITNEGHPLGQYSEEVDWCTNICSLLGMTNGTNSSNTCNL 257
                                                                                                                                                                            258 TSQQSLDFINLMRLYTGIHVDHEGGNVSAHTTHLVGSALSDPYLSYSSGIMGLAGPLHGL 317
                                                                                                                                                                                                   377 FAQKRPIEFENDKNVLLMQKLAEIAPKVLLEHGKSKNPFPNVDSASGILFYHYGIRELLF 436
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16_Aug-1996 #sequence_revision 16-Aug-1996 #text_change
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#length 437 #molecular-weight 48929 #checksum 2093
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carbon-carbon lyase; homohexamer; oxo-acid-lyase;
tricarboxylic acid cycle
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Best Local Similarity 28.5%;
Matches 90; Conservative
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carbon-carbon lyase; oxo-acid-lyase; catalyzes synthesis of citrate from acetyl-CoA and oxaloacetic acid tricarboxylic acid cycle fsuperfamily citrate (s1)-synthase allosteric regulation; carbon-carbon lyase; homohexamer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #journal J. Bacteriol. (1990) 172:2096-2104
*title Cloning of genes responsible for acetic acid resistance in Acetobacter aceti.
#cross-references MUID:90202732
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267 ALSGPLHGGANQAVLEMLEDIKSNHGGD-ATEFMNK-V-KNKEDGVRLMGFGHRVYKNYD 323
                                         303 GLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYVWKTLNSGKVVPGFGHGVLRKTV 362
                                                                                             324 PRAAIVKETAHEILEHLGGDDLLDLAIKLEEIALA-DDYFISRKLYPNVDFYTGLIYRAM 382
                                                                                                                                         363 PRYTCOREFA---MKHLPEDPLFQLVSKLYEVFLLFLQNLAKLKPWPNVDAHSGVLLNYY 419
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Pred. No. 1.13e-31;
85; Mismatches 111; Indels 32; Gaps
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#length 436 #molecular-weight 48196 #checksum 9071
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##cross-references GB:M34830; NID:q141729; PID:q141730
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Best Local Similarity 30.5%;
Matches 100; Conservative
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Plant Mol. Biol. (1995) 27:377-390
Molecular characterization of a glyoxysomal citrate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                         the citrate synthase of gram-negative bacteria is an allosteric enzyme whose activity is inhibited strongly and specifically by NADH
                                                                                                                                                                 *authors Donald, L.J.; Molgat, G.F.; Duckworth, H.W.

*journal J. Bacteriol. (1989) 171:5542-5550

*title Cloning, sequencing, and expression of the gene for NADH-sensitive citrate synthase of Pseudomonas aeruginosa.
YKPSCA #type complete citrate (si)-synthase (EC 4.1.3.7) - Pseudomonas aeruginosa #formal_name Pseudomonas aeruginosa 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 17-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps 26;
                                                                                                                                                                                                                                                                                                                                                                                                   carbon-carbon lyase; oxo-acid-lyase; catalyzes synthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 LLLNGELPTAAQKEQFVGTIKNHTMVHEQLK-TFFNGFRRDAHPMAVMC-GVIG-ALSAF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255 SGIAALWGPAHGGANEAVLRMLDEIGDVSNIDKFVEKAKDKNDPFKLMGFGHRV--YKNF 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 313 DPRAKVMKQTCD-E-VLQELGINDPQLELAMKLEEI-ARHDPYFVERNLYPNVDFYSGII 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 LLLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 YHDSLD--ITNPKHREVS-AHR--LIAKMPIIAAMVYK--YSKGEPMMYPRND-LNYAEN 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 FLHMM-FNTPCETKPISPVLAKAMDRIFI-LHADHEQ-NASTSTVRLAGSSGANPFACIA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 FAHMLGFSSS-E-MH-E-LL.---M-RLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 AALNGLAGFLHGLANQEVLLWIKSVVEECG-EN-ISKEQLKDYVWKTLNSGKVVPGFGHG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     357 VLRKTVPRYTCQREFAMKHLP-EDPLFQLVSKLYEVFLLFLQNLAKLKPWPNVDAHSGVL 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *Superfamily citrate (si)-synthase allosteric regulation; carbon-carbon lyase; homohexamer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #formal_name Cucurbita sp. #common_name cucurbit
14-Jul-1995 #sequence_revision 03-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #active_site His #status predicted
#length 428 #molecular-weight 47681 #checksum 7548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 7.8%; Score 272; DB 1; Length 428; Local Similarity 27.9%; Pred. No. 1.26e-25; es 90; Conservative 93; Mismatches 107; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                  citrate from acetyl-COA and oxaloacetic acid tricarboxylic acid cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oxo-acid-lyase; tricarboxylic acid cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S53007 #type complete citrate synthase - cucurbit
                                                                                                                                                                                                                                                                                                                 1-428 ##label DON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       416 LNYYGLTEARYYTVLFGVSRALG 438
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                                                                                                                                                                                                                                                                                                                                                          homohexamer
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##molecule_type DNA
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##residues
##cross-references EMBL:D64001; GB:AB001339; NID:g1001102; PID:d1010913;
PID:g1001122
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Library, June 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 LLLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATGVMALQV-QS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 DANPALRGODLYKSK--QVRDKQIARIIGKAPTIAAAAYLRLAGRPPVLPSSN-LSYSEN 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 EFQKAY-EKGIHKSKYWEPTYEDSMNLIAQVPLVAAYVYRRMYKNGDTIPKDESLDYGAN 246
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                                                                                                                                                                                                                                                                                                                                                                                                                           *superfamily citrate (si)-synthase
#length 516  #molecular-weight 56759  #checksum 9186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 266; DB 2; Length 516;
Pred. No. 1.33e-24;
85; Mismatches 132; Indels
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                                                                                                                                                                                                                                                                                                                                                                       1-516 ##label KAT
                                                                                                                          *cross-references MUID:95195164
                                                                                                                                                                                                                                                    preliminary
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hes 103; Conservative
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57 LLIWGKLPTQAEIEEFEYEIRTHRRIKYHIR-DMMKCFPETGHPMDALQTSAAALGL--- 112
                                                                                                                                                                                                                                                                                                                                    367 CQREFA--M-KHLPEDPLFQLVSKLYEVFLLFLQNLAKLKPWPNVDAHSGVLLNYYGL-T 422
                                                                                                                                                                         129 LLLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSE 188
                                                                                                                                                                                                                    113 FY-A-RRALDDPKY-IRA--AVVRLLAKIPTMVA-AFH-MIREGNDPIQPNDKLDYASNF 165
                                                                                                                                                                                                                                             166 LYMLTEKEPDPFAAKVFDVCLTLHAEH-TMNASTFSARVTASTLTDPYAVVASAVGTLAG 224
                                                                                                                                                                                                                                                                                                                                                                                           225 PLHGGANEEVL----NMLEEIG-SV--ENVRPYVEKCLANKQRIMGFGHRVYKVKDPRAI 277
                                                                                                                                                                                                                                                                                                                                                                                                                    278 ILQDLAEQLFAKMGHDEYYEIAVELEKVVEEYV-G-QK-GIYPNVDFYSG-LV-YRKLDI 332
#length 397 #molecular-weight 44830 #checksum 904
                                      Ouery Match 7.6%; Score 263; DB 2; Length 397; Best Local Similarity 30.1%; Pred. No. 4.28e-24; Matches 95; Conservative 73; Mismatches 118; Indels 30;
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423 EARYYTVLFGVSRALG 438
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    SUMMARY
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Oct 22 16:31:39 1999; MasPar time 14.47 Seconds 920.365 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-702-718-2 (1-471) from US08702718.pep 3466 1 MVFYRSVSLLSKLRSRAVQO......PLERPKSVIMEWLENQCKKA 471 Description: Perfect Score: Title:

Sequence:

PAM 150 Gap 11 Scoring table:

77977 seqs, 28268293 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot37 1:swissprot Database:

Mean 51.825; Variance 92.291; scale 0.562 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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Pred. No.	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	8.03e-26	3.93e-23	2.97e-39	2.08e-37	9.64e-30	2.41e-29	3.80e-29	3.80e-29	9.47e-29	1.49e-28	1.496-28
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Description	CITRA	CITRATE SYNTHASE,	CITRATE SYNTHASE,	CITRATE SYNTHASE,	PROBABLE CITRATE	PROBABLE CITRATE	CITRATE SYNTHASE,	CITRATE SYNTHASE	CITRATE SYNTHASE,	CITRATE SYNTHASE	CITRATE SYNTHASE	CITRATE SYNTHASE											
ID	CISY_CITMA	CISY_ARATH	CISY_PIG	CISY_CHICK	CISY_CAEEL	CISY_SCHPO	CISY_YEAST	CISY_EMENI	CISY_ASPNG	CISY_CANTR	CISY_NEUCR	CISZ_YEAST	CISY_TETTH	CISX_YEAST	CISY_CORGL	CISY_ACEAC	CISY_PSEAE	CISY_RICCA	CISY_RICJA	CYSZ_CUCMA	CISZ_STRMU	CISY_SYNY3	CISY_ASTRI
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Query Match	80.2	66.5	55.4	53.1	49.7	49.5	48.0	47.7	47.4	47.3	46.3	45.4	38.3	33.7		e. 8		7.7	7.7	7.7	7.6	7.6	7.6
Score	2779	2305	1921	1842	1722	1716	1663	1652	1642	1639	1606	1575	1329	1168	316	307	269	267	266	266	264	263	263
Result No.	H	C3	m	4	S	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	CI CI	23

80.2%; Score 2779; DB 1, Length 471;

Query Match

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15-DEC-1999 (REL. 37, LAST ANNOTATION UPDATE)
15-DEC-1999 (REL. 37, LAST ANNOTATION UPDATE)
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EURARYOTA: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA;
EUPHYLLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES: RPASSICACEAE: ARABIDOPSIS.
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                                                                                                                                                                60 SDLGKAQLGNITIDVVIGGMRGMTGLLWETSLLDPDEGIRFRGLSIPECOKLLPAAKPDG 119
                                                                                                                                                                                                                      120 EPLPEGLLWLLLTGKVPSKEQVDGLSKELRDRATVPDYV-YKAIDALPVSAHPMTQFASG 178
                                                                                                                                                                                                                                                          120 EFLPEGLLWLLLTGKVFSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATG 179
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                                                                               1 MASLRSATALSFLRSFAGGGSNLSNSVFWLQMQSSADLDLHSQL-KEMIPEQGERLKKVK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNGER E.A., HAND J.M., CASHWORE A.R., VASCONCELOS A.C.; "Isolation of a cDNA encoding mitochondrial citrate synthase from Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  418 FGLAEARYYTVLFGVSRSLGICSQLIWDRALGLPLERPKSVTLDWIEKNCKKA 470
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-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O
                 56; Mismatches 41; Indels
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Best Local Similarity 78.4%; Pred. No. 0.00e+00;
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                 371; Conservative
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BLOXHAM D.P., PARMELEE D.C., KUMAR S., WALSH K.A., TITANI K.;
"Complete amino acid sequence of porcine heart citrate synthase.";
BIOCHEMISTRY 21:2028-2036(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Isolation, nucleotide sequence, and expression of a cDNA encoding pig citrate synthase.";
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                                     HSSP; P23007; 5CSC.
LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE,
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                                                                                                                                                                                                Length 472;
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MEDLINE; 89000665.
EVANS C.T., OWENS D.D., SUMEGI B., KISPAL G., SRERE P.A.;
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01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTHON UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                 Score 2305; DB 1;
NO. 0.00e+00;
                                                                                                                                              BY SIMILARITY. 954AFA81 CRC32;
                                                                                              CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
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 PS00480; CITRATE_SYNTHASE; 1.
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                PFAM; PF00285; citrate_synt; 1.
HSSP; P23007; 5CSC.
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68.9%;
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                                                                 MULTIGENE FAMILY.
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                                                                                                                                           SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX. CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
            MEDINE; 83010291...

REMINGTON S., WIEGAND G., HUBER R.;

"Crystallographic refinement and atomic models of two different forms of citrate synthase at 2.7 and 1.7-A resolution.";

J. Mol. BIOL. 158:111-152(1982).
                                                                      MEDINE: 91104711.
ALTER G.M., CASAZZA J.P., ZHI W., NEMETH P., SRERE P.A., EVANS C.T.;
"Mutation of essential catalytic residues in pig citrate synthase.";
BIOCHEMISTRY 29:7557-7563(1990).
-! CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                             PIR: A29966; YRRG.
PDB: 1CTS: 10-JUL-88.
PDB: 2CTS: 09-OCT-88.
PDB: 4CTS: 16-JUL-88.
PDB: 4CTS: 16-JUL-88.
PROSITE: PSO0480: CITRATE_SYNTHASE; 1.
PROSITE: PSO0480: CITRATE_SYNTHASE; 1.
LYASE: TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; 3D-STRUCTURE;
                                                                                                                                                            METABOLISM. SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                  CITRATE SYNTHASE. METHYLATION (TRI-).
        X-RAY CRYSTALLOGRAPHY (2.7 AND 1.7 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                          MITOCHONDRION.
                                                                                                                           PATHWAY: TRICARBOXYLIC ACID CYCLE. SUBUNIT: HOMODIMER.
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                                                                                                                                                                                                                                                                                          Score 1921; DB 1; Length 464;
Pred. No. 0.00e+00;
86; Mismatches 86; Indels 6
                                                                                                                                                                                                                                                                             51629 MW; 3BC38D25 CRC32;
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Best Local Similarity 58.8%;
Matches 254; Conservative
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CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE, 91255228.
LIAO D.-I., KARPUSAS M., REMINGTON S.J.;
Crystal structure of an open conformation of citrate synthase from chicken heart at 2.8-A resolution.";
BIOCHEMISTRY 30:6031-6036(1991).
-: CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                          KARPUSAS M., BRANCHAUD B., REMINGTON S.J.;
"Proposed mechanism for the condensation reaction of citrate sypthase: 1.9-A structure of the ternary complex with oxaloacetate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE CITPATE SYNTHASE FAMILY.
CAUTION: THIS IS AN X-RAY DETERMINED SEQUENCE WHICH WAS
ESTABLISHED USING THE SEQUENCE OF PIG CITRATE SYNTHASE AND
MODIFYING IT BASED ON THE OBSERVED ELECTRON DENSITY.
1CSC: 15-APR-91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDB: 1AM2: 24-DEC-97.
PROSITE: PS00480; CITRATE_SYNTHASE; 1.
PFAM: PF00285; citrate_synt; 1.
LYASE: TRICARBOXYLIC ACID CYCLE: MITOCHONDRION; 3D-STRUCTURE.
                                                                                                                                                                                                                                                                               EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2 R ANGSTROMS) OF OPEN CONFORMATION
                                                                                                                                             01-AUG-1991 (REL. 19, CREATED)
01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
01-5UC-1998 (REL. 36, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL (EC 4.1.3.7).
                                                                                                        433 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATHWAY: TRICARBOXYLIC ACID CYCLE. SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)
                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and carboxymethyl coenzyme A."; BIOCHEMISTRY 29:2213-2219(1990).
                                                                                                        STANDARD;
                                                                                                                                                                                                                                                          GALLUS GALLUS (CHICKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|||||||: : 451 LPLERPKSVTME 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-APR-91.
15-APR-91.
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24-DEC-97.
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30-APR-94.
15-OCT-95.
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                                                                                                                                                                                                                                                                                                                                                                   TISSUE-HEART MUSCLE;
MEDLINE; 90248434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2CSC; 15-APR-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JAN-93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OXALOACETATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDR: 1CSC; 10 PDB: 2CSC; 10 PDB: 2CSC; 10 PDB: 4CSC; 10 PDB: 5CSC; 10 PDB: 5CSC; 10 PDB: 5CTS; 10 PDB: 1CST; 10 PD
                                                                                                      CISY_CHICK
P23007;
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94 PDEGIRFRGLSIPECOKVLPAAKPGGEPLPEGLLWLLLTGKVPSKEQVNSIVSGIAESGI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 IAKLPCVAAKIYRNLYRAGSSIGAIDSKLDWSHNFTNMLGYTDAQFTEL-MRLYLTIHSD 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358 PNVLLEQGAAANPWPNVDAHSGVLLQYYGMTEMNYYTVLFGVSRALGVLAQLIWSRALGF 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 PDEGIRFRGFSIPECQKLLPKGGXGGEPLPEGLFWLLVTGQIPTGAQVSWLSKEWAKRAA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 LPSHVV-TMLDNFPTNLHPMSQLSAAITALNSESNFARAYAEGILRTKYWEMVYESAMDL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 HEGGNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLGWLAQLQKAXXXAGA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 HEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENIS 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DASLPDYIWNTLNSGRVVPGYGHAVLRKTDPRYTCQREFALKHLPGDPMFKLVAQLYKIV 357
                                                                                                                                                                                                                                                                                                                                                                                                              1 ASSTNLK-DVLAALIPKEQARIKTFRQQHGGTALGQITVDMSYGGMRGLVYETSVLD 59
                                                                                                                                                                                                                                                                                                                                                                                                                         35 SSGLDLRSELVQELIPEQQDRLKKIKSDMKGS-IGNITVDMVLGGMRGMTGLLWKPHYLD 93
                                                                                                                                                                                                                                                                                                                                                                        Score 1842; DB 1; Length 433;
Pred. No. 0.00e+00;
85; Mismatches 94, Indels 6, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 IAQVPLVAAYVYRRMYKNGDTI-PKDESLDYGANFAHMLGFSSSEMHELLMRLYVTIHSD
                                                                                                                                                                                                                                                                                                                                                       47373 MW; 6E24FE58 CRC32;
                                                                                                                                                                                                                                                                                                                                                                        / Match 53.1%;
Local Similarity 57.1%;
hes 246; Conservative
343
364
365
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375
385
390
415
427
433 AA;
SEQUENCE
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METABOLISM.
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                                                                                                                                                                                                                                                                                                                                               LT 6
CISY_SCHPO
Q10306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPAC6C3.03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation the European Bioinformatics Institute. There are one restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- PATHWAY: TPICAPBOXYLIC ACID CYCLE.
--- SUBUNIT -- HOMODIMBR (BY SIMILARITY)
--- SUBCELLULAR LOCATION- WITCHOMDRIAL MATRIX (BY SIMILARITY)
--- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00285; citrate_synt; 1.
HSSP; P23007; 5CSC.
HYPOTHETICAL PROTEIN; LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 NARADLPTHVV-RMLDNFPDNLHPMAQFIAAIAALNNESKFAGAYARGVAKASYWEYAYE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 AESGIISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKYWEPTYE 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203 DSMDLLAKLPTVAAIIYRNLYRDGSAVSVIDPKKDWSANFSSMLGYDDPLFAEL-MRLYL 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 VIHSDHEGGNVSAHTSHLVGSALSDPYLSFSAAMAGLAGPLHGLANQEVLVFLNKIVGEI 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 TSVLDPEEGIRFRGYSIPECQKLLPKAKGGEEPLPEAIWWLLCTGDVPSEAQTAAITKEW 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 LSTSAEGSTNLKEVLSKK-IPAHNAKVKSFRTEHGSTVVQNVNIDMIYGGMRSMKGMVTE 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 LQVQTSSGLDLRSELVQELIPEQQDRLKKIKSDMKGSIG-NITVDMVLGGMRGMTGLLWK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1722; DB 1; Length 468;
Pred. No. 0.00e+00;
84; Mismatches 109; Indels 8; Gaps
                                                                                                                                                                                                                                               CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                  01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
PROBABLE CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                 SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -! - SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
IN ADA3A630 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WORMPEP; T20G5.2; CE00513.
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51540 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 49.7%;
1 Similarity 54.0%;
236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z30423; G458482; -.
                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
468
303
349
452 PLERPKSVTME 462
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                                                                                                                                                                                                                                                                                                                                                                STRAIN=BRISTOL N2;
BERKS M., SMITH A.
SUBMITTED (MAR-199
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303
349
404
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                                                                                    CISY_CAEEL P34575;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- SURCELLULAR LOCATION: MITOCHONDRIAL MATRIX (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 RFRGYTIPECQKLLPSSPNGKQPLPESLFWLLVTGEIPTLSQVQALSADWAARSQLPKFV 169
                                                                                                                                                                                                         382 LYKITPGILLEQGKAKNPWPNVDSHSGVLLQYFGMTEMSFYTVLFGVSRALG-CLSQLIW 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 LKDRLA-ELIPEKQAEIKKFRAEHGQDVIGEVTINOMYGGARGVRSLIWEGSVLDPNEGI 109
268 TIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLMIKSVVEEC 327
                                                                                   322 GFNYTEEQLKEWVWKHLKSGQVVPGYGHAVLRKTDPRYECQREFALKHLPNDDLFKLVST 381
                                                                                                                                            328 GENISKEQLKDYVWKTLNSGKVVPGFGHGVLRKTVPRYTCQREFAMKHLPEDPLFQLVSK 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL PROTEIN; LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVLIN K., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.; SUBMITTED (FEB-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O + OXALOACETATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 LRSELVQELIPEQQDRLKKIKSDM+KGSIGNITVDMVLGGMRGMTGLLWKPHYLDPDEGI 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST MINOTATION UPDATE)
PROBABLE CITRATE SYNTHASE, MITOCHOMORIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 482;
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83; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
SCHIZOSACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITRATE SYNTHASE.
BY SIMILARITY
BY SIMILARITY.
BY SIMILARITY.
A: 18145A7D CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               482 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00480; CITRATE_SYNTHASE; 1.
PFAM; PF00285; citrate_synt; 1.
HSSP; P23007; 5CSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PATHWAY: IRICARBOXYLIC ACID CYCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.58;
                                                                                                                                                                                                                                                                                                                               441 ARGMGLPLERPKSHSTD 457
                                                                                                                                                                                                                                                                                                                                                                                      446 DRALGLPLERPKSVTME 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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482 AA;
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nes 237, Conserv
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PATHWAY: TRICAPBOXYLIC ACID CYCLE SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX. CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
170 E-ELIDRCPPTLHPMAQFSLAVTALEHDSAFAKAYERGMNKHDYWKYEYEDCMDLIAKTV 228
                                    159 MYTTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKYWEPTYEDSMNLIAQVP 218
                                                                                                             219 LVAAYVYRRMYKNGDTIPKDESLDYGANFAHMLGFSSSEMHELLMRLYVTIHSDHEGGNV 278
                                                                                                                                                   289 SAHTGHLVGSALSSPFLSMAASLNCLAGPLHGLANQEVLNFLITMKKEIGDDLSEETIKS 348
                                                                                                                                                                                          279 SAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKD 338
                                                                                                                                                                                                                                349 YLWKLLNSGRVVPGYGHAVLRKTDPPYTAQREFALEHLPKDPMFQLVSPLYEIVPGVLTE 408
                                                                                                                                                                                                                                                                                                                               399 LAKLK-PWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPK 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERHASSELT P , AERT R., VOET M , VOLCKAERT G.; "Twelve open reading frames revealed in the 23.6 kb segment flanking the centromere on the Saccharomyces cerevisiae chromosome XIV right
                                                                                                                                                                                                                                                  229 PIAGRIYRNLYRDGVVAPIQMDKDHSYNFANVLGFANNEEFVELMRLYLTIHADHEGGNV
                                                                                                                                                                                                                                                                                                         409 HGKTKNPYPNVDSHSGVLLQYYGLKEQSFYTVLFGVSRTLGVASQLIWDRALGLPIERPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (REL. 01, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE, MITCHONDETAL PRECURSOR (EC 4.1.3.7).
CITL OF LYSS OF GLU3 OF YNRONIC OR N2019.
SACCHAROWYCES CEREVISIAE (BAREY'S YEAST).
EUKARYOTA, FUNGI, ASCOMYCOTA, HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETAGEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Isolation of the nuclear yeast genes for citrate synthase and fifteen other micochondrial proteins by a new screening method.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Organization of the centromeric region of chromosome XIV in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY - CITPATE + COA - ACETYL-COA + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STETTLEP S , MAPIOTTE S., GENDREAU E , THUPIAUX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBMITTED (JUL-1993) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     479 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUISSA M., SUDA K., SCHATZ G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-D273-10B;
LINDNER P., PLUECKTHUN A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBO J 3:1773-1781(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YEAST 10:523-533(1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 95028151.
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                                                                                                                                                                                                                                                                                                                                                                                      469 SFSTE 473
                                                                                                                                                                                                                                                                                                                                                                                                                          458 SVTME 452
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P00890;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 LLGKLPVIASKIYRNVFKDGKITSTDPNADYGKNLAQLLGYENKDFIDL-MRLYLTIHSD 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 HEGGNVSAHTTHLVGSALSSPYLSLAAGLNGLAGPLHGRANQEVLEWLFKLREEVKGDYS 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              396 PGVLTKHGKTKNPWPNVDSHSGVLLQYYGLTEASFYTVLFGVARAIGVLPQLIIDRAVGA 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   393 LLFLQNLAKLK-PWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALGE 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 DPEEGIRFRGRTIPEIQRELPKAEGSTEPLPEALFWLLLTGEIPTDAQVKALSADLAARS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 DPDEGIRFRGLSIPECQKVLPAAKPGGEPLPEGLLWLLLTGKVPSKEQVNSIVSGIAESG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 IISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKYWEPTYEDSMN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273 HEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENIS 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION: TRANSIT PEPTIDE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 0.00e+00;
90; Mismatches 106; Indels
SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY
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E -> O (IN REF. 2).
E -> E (IN REF. 2).
W: C6896385 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MITOCHONDRION
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HSSP; P23007; 5CSC.
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Conservative
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EMBL; X77395; G496718; -.
EMBL; Z71616; E239778; -.
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PIR; S35390; S35390.
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                                                                                                                                                                                                                                                                                                                              -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 ITVDMVLGGMRGMTGLLWKPHYLDPDEGIRFRGLSIPECQKVLPAAKPGGEPLPEGLLWL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 LLTGEVPSEQOVRDLSAEWAARSDLPKFIE-ELIDRVPSTLHPMAQFSLAVTALEHESAF 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 LLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSEF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 AKATAKGINKKDYWNYTFEDSMDLIAKLPTIAAKIYRNVFKDGKVAPIQKDKDYSYNLAN 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 OLGFADNKDFVEL-MRLYLTIHSDHEGGNVSAHTTHLVGSALSSPMLSLAAGLNGLAGPL 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250 MLGFSSS-EMHELLMRLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPL 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310 HGLANQEVLNWLTEMKKVVGNDLSDQSIKDYLWSTLNAGRVVPGYGHAVLRKTDPRYTSQ 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 HGLANQEVLLWIKSVVEECGENISKEQLKDYVWKTLNSGKVVPGFGHGVLRKTVPRYTCQ 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               370 REFALRKLPDDPMFKLVSQVYKIAPGVLTEHGKTKNPYPNVDAHSGVLLQYYGLTERNYY 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 LTLDQAYGGARGVKCLVWEGSVLDSEEGIRFRGLTIPECQKLLPKAPGGEEPLPEGLFWL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 STLAAKPVVQSVAFNGLR--CYSTGKTKSLKETFADKL-PGELEKVKKLRKEHGNKVIGE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 SKLRSRAVQOSNVSNSVRWLQVQTSSGLDLRSELVQELIPEQQDRLKKIKSDMKGS-IGN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYASE; TRICARROXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE TRANSIT 135 MITOCHONDRION (POTENTIAL).
                                                                                                                                                                               MEDILINE, 97306446.

PARK B.W., HAN K.H., LEE C.Y., LEE C.H., MAENG P.J.;

Park B.W., and characterization of the citA gene encoding the mitochondrial citate synthase of Aspergillus nidulans.";

MOL. CELLS 7:290-295(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.7%: Score 1652; DB 1; Length 474; larity 54.1%; Pred. No. 0.00e+00; Conservative 85; Mismatches 116; Indels
                                                            EMERICELLA NIDULANS (ASPERGILLUS NIDULANS).
EUKARYOTA: FUNGI: ASCOMYCOTA; EUASCOMYCETES; PLECTOMYCETES;
                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MITOCHONDRION (POTENTIAL).
CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W: D97PIE91 CRC32;
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PSG048G; CITRATE_SYNTHASE; 1.
PFAM; PF00285; Citrate_synt; 1.
HSSP; P23007; SCSC
                                                                                                     EUROTIALES; TRICHOCOMACEAE; EMERICELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411 411 B
474 AA; 52223 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U89675; G2138332; -
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356
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                                                                                                                                            SEQUENCE FROM N.A.
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310
356
411
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                                                                                                                                                                    STRAIN-FGSC 4;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (BY SIMILARITY). CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 SDLPKFIE-ELIDRCPSTLHPMSQFSLAVTALEHESAFAKAYAKGINKKDYWNYTFEDSM 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 DLIAKLPTIAAKIYRNVFKDGKVAPIQKDKDYSYNLANQLGYGDNNDFVELMRLYLTIHS 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 DHEGGNVSAHTTHLVGSALSSPMLSLAAGLNGLAGPLHGLANQEVLNWLTKMKAAIGNDL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 DSEBGIRFRGRTIPECQELLPKA-PGGQEPLPEGLFWLLLTGEIPTEQQVRDLSAEWAAR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 NLIAQVPLVAAYVYRRMYKNGDTIPKDESLDYGANFAHMLGFSSSEMHELLMRLYVTIHS 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            272 DHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENI 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 TSSGLDLRSELVQELIPEQQDRLKKIKSDMKGS-IGNITVDMVLGGMRGMTGLLWKPHYL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 TGKAKSLKETFAEKL-PAELEKVKKLRKEHGSKVIGEVTLDQAYGGARGVKCLVWEGSVL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PLECTOMYCETES;
EUROTIALES; TRICHOCOMACEAE; MITOSPORIC TRICHOCOMACEAE; ASPERGILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93 DPDEGIRFRGLSIPECQKVLPAAKPGG-EPLPEGLLWLLLIGKVPSKEQVNSIVSGIAES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OSHIDA Y., MIYAKE K., KANAYAMA S., KIRIMURA K., USAMI S.;
SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MITOCHONDRION (BY SIMILARITY) CITRATE SYNTHASE.
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82; Mismatches 107, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                         01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4 1:3 7)
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4; 48D237BC CRC32;
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Pred. No. 0.00e+00;
                                    428 TVLFGVSRALGICSQLIWDRALGLPLERPKSVTME 462
430 TVLFGVSRALGVLPQLIIDRAFGAPIERPKSFSTE 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00480; CITRATE_SYNTHASE; 1. FFAM; PF00285; citrate_synt; 1. HSSP; P23007; 5CSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
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Local Similarity 54.9%;
les 237, Conservative
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                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                ASPERGILLUS NIGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310
356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METABOLISM
                                                                                                                                                                                                           CISY_ASPNG
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
-!- CITRATE SYNTHASE IS FOUND IN NEAPLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                   392 FLLFLQNLAKLK-PWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSOLIWDRALG 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              333 SDEAIKNYLWSTLNAGQVVPGYGHAVLRKTDPRYVSQREFALRKLPDDPMFKLVSQVYKI 392
                                    332 SKEQLKDYVWKTLNSGKVVPGFGHGVLRKTVPRYTCQREFAMKHLPEDPLFQLVSKLYEV 391
                                                                             393 APGVLTEHGKTKNPYPNVDAHSGVLLQYYGLTEANYYTVLFGVSRALGVLPQLIIDRALG 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 EQAYGGMRGIKGLVWEGSVLDPIEGIRFRGRTIPDIQKELPKAPGGEEPLPEALFWLLLT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 DMVLGGMRGMTGLLWKPHYLDPDEGIRFRGLSIPECQKVLPAAKPGGEPLPEGLLWLLLT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 GEVPTEAQTRALSEEFAARSALPKHVE-ELIDRSPSHLHPMAQFSIAVTALESESQFAKA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 RSSNVAKSTLKNSVR--TYATAEP-TLKQRL-EEILPAKAEEVKQLKKDYGKTVIGEVLL 64
                                                                                                                                                                                                                                                                                                                                                                                                                           FUNGI: ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE TRANSIT 1 PATIOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UEDA M., SANUKI S., KAWACHI H., SHIMIZU K., ATOMI H., TANAKA A. SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
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CITRATE SYNTHASE.
BY SIMILARITY.
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                       CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
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                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                         467 AA
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                                                                                                                                                                                                                                                                                                          01-NOV-1997 (REL. 35, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                402 402 F 467 AA; 52004 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                         CANDIDA TROPICALIS (YEAST)
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301
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                                                                                                                                                        453 APIERPKSYSTE 464
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P79024;
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184 YAKGVHKSEYWKYTYEDSIELLAKLPTIAAKIYRNVFHDGKLPAQIDSKLDYGANLASLL 243
                                                                         302
                                                                                                            252 GFSSS-EMHELLMRLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHG 310
                                                                                                                                                303 RANQEVLEWLFKLREELNGDYSKEAIEKYLWDTLNAGRVGPGYGHAVLRKTDPRYTAQRE 362
                                                                                                                                                                                      311 LANQEVLLWIKSVVEECGENISKEQLKDYVWKTLNSGKVVPGFGHGVLRKTVPRYTCQRE 370
                                                                                                                                                                                                                           363 FALKHMPDYELFKLVSNIYEVAPGVFDQHGMTK-NPWPNVGSHSGVLLQYYGLTEESFYT 421
                                                                                                                                                                                                                                               FEREA I., CONTRERAS E.T., OUNG T., BOWMAN E.J., ROWMAN B.J.;
"Characterization of the cit-1 gene from Neurospora crassa encoding
the mitochondrial form of citrate synthase.";
MOL. GEN. GENET. 242:105-110(1994).
-!- CATALYTIC ACTIVITY: CITRATE + GOA = ACETYL-GOA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-i- SUBCELLULAR LOCATION MITOCHONDRIAL MATPIX.
-i- DEVELOPMENTAL STAGE: ABUNDANT AFTER 6-12 HRS OF GROWTH. IT IS
NOT SIGNIFICANTLY EXPRESSED AFTER 24 HRS, WHICH IS SEVERAL HRS
AFTER ENTERING THE STATIONARY PHASE OF GROWTH.
                     244 GFGENKEFLEL-MRLYLTIHSDHEGGNVSAHTTHLVGSALSSPFLSLAAGLNGLAGPLHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-ROV-1995 (REL. 32, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE, MITOCHONDPIAL PRECURSOP (EC 4 1 3 7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MITOCHONDRION (POTENTIAL) CITRATE SYNTHASE.
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                                                                                                                                                                                                                                                                                                                        BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE: PS00480; CITRATE_SYNTHASE; 1. PFAM; PF00285; citrate_synt; 1. HSSP; P23007; SCC.
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469
352
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P34085;
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46.3%; Score 1606; DB 1; Length 469;

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CISY_TETTH P24118;
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                                                                                                                                                                                                                                              281 HLVGSALSSPFLSVAAGLNGLAGPLHGLANQEVLNWLTEMKKVIGDDLSDEAITKYLWDT 340
                                    44 ELLPENIEKIKALRKEHGSKVVDKVTLDQVYGGARGIKCLVWEGSVLDAEEGIRFRGKTI 103
                                                             47 ELIPEQODRLKKIKSDMKGSI-GNITVDMYLGGMRGMTGLLWKPHYLDPDEGIRFRGLSI 105
                                                                                                    162 RCPSDLHPMAQLSLAVTALEHTSSFARAYAKGINKKEYWGYTFEDSMDLIAKLPTIAARI 221
                                                                                                                                                         225 YRRMYKNGDTIPKDESLDYGANFAHMLGFSSS-EMHELLMRLYVTIHSDHEGGNVSAHTG 283
                                                                                                                                                                                                                                                                     284 HLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYVWKT 343
                                                                                                                                                                                                                                                                                                341 LNAGRVVPGYAHAVLRKTDPRYSAQRKFAQEHLPEDPMFQLVSQVYKIAPRVLTEHGKTK 400
                                                                                                                                                                                                                                                                                                             401 NPYPNVDAHSGVLLQHYGLTEANYYTVLFGVSRAIGVLPQLIIDRAVGAPIERPKSYSTD 460
                                                                                                                                                                                                                                                                                                                                                                  104 PECQELLPKA-PGGKEPLPEGLFWLLLTGEVPSEQQVRDLSAEWAARSDVPKFIE-ELID 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mitochondrial and nonmitochondrial citrate synthases in Saccharomyces cerevisiae are encoded by distinct homologous genes."; MOL. CELL. BIOL. 6:4509-4515(1986).
              9; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EURARYOTA; FUNG1; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 92254505.

BITEAU N., FREWAUX C., HEBRARD S., MENARA A., AIGLE M., CROUZET
"The complete sequence of a 10.8kb fragment to the right of the
chromosome III centromere of Saccharomyces cerevisiae.";
YEAST 8:61-70(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIAO.X., SMALL W.C. SPEPE P.A., BUTOW R.A.;
LIACTAMILOCHONDIAL functions regulate nonmitochondrial citrate
synthase (CIT2) expression in Saccharomyces cerevistae.";
MOL. CELL. BIOL. 11:38-46(1991).
-!- CATALYTIC ACTIVITY CITRATE + COA - ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROSENKRANTZ M., ALAM T., KIM K.-S., CLARK B.J., SRERE P.A.,
             79; Mismatches 106; Indels
Best Local Similarity 54.8%; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1988 (REL 06, CPEATED)
01-JAN-1988 (REL 06, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL 37, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 460 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE CITRATE SYNTHASE, PEROXISOMAL (EC 4.1.3.7).
CIT2 OR YCRO05C OR YCRSC OR YCRONS.
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             235; Conservative
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CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 GLLWKPHYLDPDEGIRFRGLSIPECQKVLPAAKPGGEPLPEGLLWLLLTGKVPSKEQVNS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 IVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKYW 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        324 VEECGENISKEQLKDYVWKILNSGKVVPGFGHGVLRKIVPRYTCQREFAMKHLPEDPLFQ 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264 RLYVIIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSV 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              308 KEEVNDDYSKDTIEKYLWDTLNSGRVIPGYGHAVLRKTDPRYMAQRKFAMDHFPDYELFK 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             368 LVSSIYEVAPGVLTEHGKTKNPWPNVDAHSGVLLQYYGLKESSFYTVLFGVSRAFGILAQ 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 NVASYLQSNSSQEKTLK-ERFSEIYPIHAQDVRQFVKEHGKTKISDVLLEQVYGGMRGIP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 NSVRWLQVQTSSGLDLRSELVQELIPEQQDRLKK-IKSDMKGSIGNITVDMVLGGMRGMT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
BY SIMILARITY.
MICROBODY TARGETING SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEROXISOME; MULTIGENE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93; Mismatches 120; Indels
                                                             SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. 45.4%; Score 1575; DB 1;
Similarity 50.5%; Pred. No. 0.00e+00;
222; Conservative 93; Mismatches 120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9E93E2FD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REL. 21, CREATED)
(REL. 21, LAST SEQUENCE UPDATE)
(REL. 28, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                462 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YEPD; 5440; -. SGD; LO000342; CIT2.
SGD; LO000342; MICROBODIES_CTER; 1.
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYASE; TRICARBOXYLIC ACID CYCLE;
ACT_SITE 293 BY S
ACT_SITE 339 BY S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 460 AA; 51413 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443 LIWDRALGLPLERPKSVIME 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                428 LITDRAIGASIERPKSYSTE 447
                                                                                                                                                                                                                                                                                                                                                                                EMBL; M14686; G171227; -.
EMBL; M54982; G171229; -.
EMBL; X59720; E264468; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                    EMBL; Z11113; G3299; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          339
394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A25393; YKBYC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P23007; 5CSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            394
                              METABOLISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ma.
Local Sim
222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1992 (
01-MAR-1992 (
01-FEB-1994 (
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440 AFGLPIERPGSADLKWFHDKYR 461

330 NISKEQLKDYVWKTLNSGKVVPGFGHGVLRKTVPRYTCQREFAMKHLPEDPLFQLVSKLY 389

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95; Mismatches 124; Indels 16; Gaps 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 GIIFRGYTIPQLKEFLPKADPKAADQANQEPLPEGIFWLLMTGQLPTHAQVDALKHEWQN 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 GIRFRGLSIPECQKVLP-A-AKPG--G--EPLPEGLLWLLLTGKVPSKEQVNSIVSGIAE 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 RGTVNQDCVNFILN-LPKDLHSMTMLSMALLYLQKDSKFAKLYDEGKISKKDYWEPFYED 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 SMPLIAKIPRVAAIIYPHKYPDSKLIDSDSKLDWAGNYAHMMGFEQHVVKECI-RGYLSI 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 HSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGE 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 KVSDKDIEDYVDHVISSGRVVPGYGHAVLRDTDPRFHHQVDFSKFHLKDDQMIKLLHQCA 380
                                                             EUKARYOTA; ALVEOLATA; CILIOPHORA, OLIGOHYMENOPHOREA; HYMENOSTOMATIDA,
TETPAHYMENINA; TETRAHYMENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 NLKK-VIAEIIPQKQAELKEVKEKYGDKVVGQYTVKQVIGGMRGMKGLMSDLSRC-DPYQ 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 DLRSELVQELIPEQQDRLKKIKSDMKGSI-GNITVDMVLGGMRGMTGLLWK-PHYLDPDE 96
                                                                                                                                                                                                                                                                                                      BIOCHEM. BIOPHYS. RES. COMMUN. 174:1028-1034(1991).
-!- FUNCTION: STRUCTURAL PROTEIN INVOLYED IN ORAL WORPHOGENESIS AND
IN PRONUCLEAR BEHAVIOR DURING CONJUGATION. RESPIRATORY ENZYME.
-!- CATALYTIC ACTIVITY. CITRAIE + COA - ACETYL. COA + H(2)O +
                                                                                                                                                                                                   NUMATA O., TAKEMASA T., TAKAGI I., HIRONO M., HIRANO H., CHIBA \mathcal{J}., WATANABE Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 SGIISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKG-IHKSKYWEPTYED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 SMNLIAQVPLVAAYVYRRMYKNGDTIPKDESLDYGANFAHMLGFSSSEMHELLMRLYVTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 HCDHEGGNVSAHTTHLVGSALSDPYLSYSAGVNGLAGPLHGLANQEVLKWLLQFIEEKGT
                                                                                                                                                                                                                                                      'Tetrahymena 14-nm filament-forming protein has citrate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX AND CYTOPLASMIC
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7) (14 NM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No. 8.03e-269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
17 7B6A39BC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1329; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MITOCHONDRION
                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 22-40.
                                                                                                                                                                                                                                                                                                                                                                                                                                    PATHWAY: TRICARBOXYLIC ACID CYCLE. SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; JN0130; JN0130.
PROSITE; PSOUAG0; CITRATE_SYNTHASE; 1.
PFAM; PF00285; Citrate_Synt; 1.
HSSP; P23007; SCSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52575 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n
Similarity 46.8%;
                             FILAMENT-FORMING PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D90117; E33571; -.
                                                TETRAHYMENA THERMOPHILA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    462 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOSKELETON.
                                                                                                                                                                              91128358
                                                                                                                                                                                                                                                                                                                                                                                                              OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOSKELETON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
SEQUENCE
                                                                                                                                                                                MEDLINE;
                                                                                                                                                                                                                                                                                   activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
SOURCE SERVING COURSE SERVING COURSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-:- CITPATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYASE; TRICARBOXYLIC ACID CYCLE; MULTIGENE FAMILY.

ACT_SITE 315 BY SIMILARITY.

ACT_SITE 419 BY SIMILARITY.

SITE 484 486 MICROBODY TARGETING SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEARSON D., BOWMAN S., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
SUBMITTED (APR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WANG Y., AHMED A., BUSSEY H., FORTIN N., FRIESEN J.D., HALL J. STOWNS R.K., VO D.H., WINNETT E.; SUBMITTED (XXX-1995), TO EMEL/GENBANK/DDBJ DATA BANKS.

-1. CATALITIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METABOLISM.
-!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JIA Y.K., BECAM A.-M., SLONIMSKI P.P., HERBERT C.J.; SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No. 3.93e-231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              806F987D CRC32;
                                                                                                                                                               01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 32, LAST ANNOTATION UPDATE)
CITAATE SYNTHASE 3 (EC 4.1.3.7).
CITAATE SYNTHASE 3 (EC 4.1.3.7).
                                                                                                                  486 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00342; MICROBODIES_CTER; PROSITE; PS00480; CITRATE_SYNTHASE;
                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                                                                                                                                                                                       SACCHAROMYCETACEAE; SACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00285; citrate_synt; 1.
HSSP; P23007, 5CSC.
448 ALGLPLERPKSVTMEWLENOCK 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53811 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.78;
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207; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 248951; G763000; -.
EMBL; 271255; E236811; -.
EMBL; U31900; G939735; -.
                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              486 AA;
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                                                                                                            CISX_YEAST
P43635:
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Best Local S:
Matches 200
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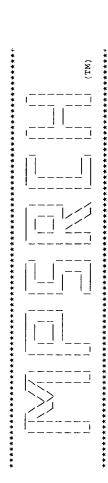
21 IIKSSALTLKEAL-ENVIPKKRDAVKKLKACYGSTFVGPITISSVLGGMPGNQSMFWQGT 79

US-08-702-718-2.rsp

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are estrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATHWAY: TRICARBOXYLIC ACID CYCLE.
SUBUNIT: HOMOHEXAMER (BY SIMILARITY).
CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                  80 SLDPEHGIKFQGLTIEECQNRLPNTGIDGDNFLPESMLWLLMTGGVPTFQQAASFRKELA 139
                                                                                                   91 YLDPDEGIRFRGLSIPECQKVLPAAKPGGEP-LPEGLLWLLLTGKVPSKEQVNSIVSGIA 149
                                                                                                                                          140 IRGR-KLPH-YTEKVI,SSLPKDMHPMTQLAIGLASMNKGSLFATNYQKGLIGKMEFWKDT 197
                                                                                                                                                                107 YEDSMNLIAQVPLVAAAYVRRMYKNGDTIPK-DESLDYGANFAHMLGFS----SSE---M 258
                                                                                                                                                                                                                                                                                                          258 TSQQSLDFINLMRLYTGIHVDHEGGNVSAHTTHLVGSALSDPYLSYSSGIMGLAGPLHGL 317
                                                                                                                                                                                                                                                                                                                                                 259 -- HE-L----LMRLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGL 311
                                                                                                                                                                                                                                                                                                                                                                                          318 AAQEVVRFIJEMNSNIS-STAREQEIKDYLWKILNSNRVIPGYGHAVLRKPDPRFTAMLE 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          377 FAQKRPIEFENDKNVLLMQKLAEIAPKVLLEHGKSKNPFPNVDSASGILFYHYGIRELLF 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               371 FAMKH-LP-E-DPLFQLVSKLYEVFLLFLQNLAKLK-PWPNVDAHSGVLLNYYGLTEARY 426
                                                                                                                                                                                                                          198 LEDSLNLIASLPLLTGRIYSNITNEGHPLGQYSEEVDWCINICSLLGMINGINSSNTCNL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EIKMANNS B.J., THUM-SCHMITZ N., EGGELING L., LUEDTKE K.U., SAHM H.; "Nucleotide sequence, expression and transcriptional analysis of the Corynebacterium glutamicum gltA gene encoding citrate synthase."; MICROBIOLOGY 140:1817-1828(1994).
: ||:| |: ||::|| :| :|| :| :|| 32 VQTSSGLDLRSELVQELIPEQQDRLKKIKSDMKGS-IGNITVDMVLGGMRGMTGLLWKPH 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENZYME REGULATION: WEAKLY INHIBITED BY ATP (APPARENT KI - 10 MM
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ACTINOMYCETALES; CORYNEBACTERINEAE; CORYNEBACTERIACEAE;
CORYNEBACTERIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  437 FTVIFGCSRAMGPLTQLVWDRILGLPIERPKSLNLEGLE 475
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LAST ANNOTATION UPDATE)
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PFAM: PF00285; citrate_synt; 1.
HSSP; Q53554; 1AJ8.
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CISY_CORGL SIGN...
P44457;
01-NOV-1995 (REL. 32, LAST SEQUE)
01-NOV-1995 (REL. 32, LAST SEQUE)
01-NOV-1995 (REL. 32, LAST ANNOT)
01-NOV-1995 (REL. 32, LAST ANNOT)
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91; Mismatches 111; Indels 24; Gaps 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 HML-GFSS-S-EMHELLMR-L--YVTIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALN 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303 GLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYVWKTLNSGKVVPGFGHGVLRKTV 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 PRYTCQREFA---MKHLPEDPLFQLVSKLYEVFLFLQNLAKLKPWPNVDAHSGVLLNYY 419
                                                                                                                                                                                                                                                                                                       129 LLLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSE 188
                                                                                                                                                                                                                                                                                                                                                                                                                  189 FOKAYEKGIHKSKYWEPTYEDSMNLIAQVPLVAAYVYRRMYKNGDTIPKDESLDYGANFA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RMMFGYPTEPYEIDPIMVKALDKLLILHADHEQ-NCSTSTVRMIGSAQANMFVSIAGGIN 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267 ALSGPLHGGANQAVLEMLEDIKSNHGGD-ATEFMNK-V-KNKEDGVRLMGFGHRVYKNYD 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 PRAAIVKETAHEILEHLGGDDLLDLAIKLEEIALA-DDYFISRKLYPNVDFYTGLIYRAM 382
                                                                                                                                                                                                                                                                                                                                                              154 YQDQLN-PLDEAQL-D-K--ATVRLMAKVPMLAAYAHRAR-KGAPYMYPDNSLNARENFL 207
                                                                                                                                          DB 1; Length 437;
LYASE; TPICARROXYLIC ACID CYCLE; ALLOSTERIC ENZYME. ACT_SITE 316 BY SIMLLARITY. ACT_SITE 372 BY SIMLLARITY. SEQUENCE 437 AA; 48929 MW; B408BFAS CRC32;
                                                                                                                                                                    Pred. No. 2.97e-39;
                                                                                                                                       Score 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: Fri Oct 22 16:32:36 1999 Job time : 57 secs.
                                                                                                                                     9.1%;
Local Similarity 28.5%;
hes 90; Conservative
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- n.a. database search, using Smith-Waterman algorithm n.a. MPsrch\_nn

Sat Oct 23 15:30:25 1999; MasPar time 3195.79 Seconds 1386.485 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-702-718-1 (1-1891) from US08702718.seq 1891 Description: Perfect Score: Title:

1 TITITGGTTGCATCAGCCTA.......TTATTTGATGATATTATGAA 189...
AAAAAGCAAGGTAGTGGGAT......AATAAACTACTATAATACTT N.A. Sequence:

TABLE default Gap 6 Scoring table:

2883791 seqs, 1171580779 bases x Searched:

Dbase 0; Query 0

STD:

Nmatch

Post-processing:

Minimum Match 0% Listing first 45 summaries

1:em\_est10 2:em\_est11 3:em\_est17 4:em\_est18 5:em\_est2
6:em\_est9 7:em\_gss1
genbank-est111 embl-est58 Database:

Database:

8:9b\_est1 9:qb\_est10 10:9b\_est11 11:9b\_est12 12:9b\_est13 13:9b\_est14 14:1b\_est15 15:9b\_est16 16:9b\_est17 17:9b\_est18 18:9b\_est19 19:9b\_est2 20:9b\_est20 21:9b\_est21 22:9b\_est22 23:9b\_est2 20:9b\_est23 24:9b\_est24 25:9b\_est26 27:9b\_est27 28:9b\_est28 29:9b\_est29 30:9b\_est2 31:9b\_est2 31:9b\_est2 33:9b\_est5 33:9b\_est6 33:9b\_est6 33:9b\_est6 33:9b\_est8 34:9b\_est8 34:9b

Mean 11.716; Variance 1.945; scale 6.023 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result Query No. Score Match Length DB ID Description Fred. No.  2 200 10.6 562 17 471 20 AA896953 L30-38673 Ice plant La 0.009+00 2 200 10.6 562 17 144185 7448 Lambda-PRL2 Arabi 0.000+00 3 189 10.0 478 31 R90544 16899 Lambda-PRL2 Arabi 0.000+00 5 172 9.1 417 24 C96653 C96653 Rice callus Cry 0.000+00 5 173 9.1 676 23 A170686 EST220465 Normalized r 0.000+00 7 153 8.1 657 15 AA606966 vm94h09.rl Knowles Sol 3.250-287 8 150 7.9 307 10 AA213175 C00534 R COMA from cat 5.790-280 10 144 7.6 501 11 AA313713 EST18558 Colon carcin 1.680-280		. 0	00	00	00	00	00	00	287	280	280	265
Score Match Length DB ID 12 201 12.7 471 20 AA896953 1200 10.6 552 17 T44185 189 10.0 478 31 R90544 172 9.1 477 24 C96653 173 9.1 676 23 AI176862 150 7.9 527 31 R90561 150 7.9 501 11 AA313713		Pred. N			0.00e+	0.00e+	0.00e+	0.00e+	3.25e-	5.79e-	5.79e-	1.68e-
Score Match Length DB 241 12.7 471 20 200 10.6 502 17 189 10.0 478 31 172 9.1 4478 31 153 8.1 657 15 150 7.9 507 11 144 7.6 501 11		Description	L30-386T3 Ice plant La	7448 Lambda-PRL2 Arabi	16899 Lambda-PRL2 Arab	AU002699 Bombyx mori p	C96653 Rice callus Ory	EST220465 Normalized r	vm94h09.rl Knowles Sol	CD0534.R cDNA from oat	16916 Lambda-PRL2 Arab	EST185581 Colon carcin
Score 241 241 241 179 173 173 153 150 150 150			AA896953	T44185	R90544	AU002699	C96653	AI176862	AA606966	AA231705	R90561	AA313713
Score 241 241 241 179 173 173 153 150 150 150		DB	20	17	31	56		23	15	10	31	11
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;	æ	Query	12.7	10.6	10.0	9.5	9.1	9.1	8.1	7.9	7.9	7.6
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900	59b06.rl Stratagen	3417 Lambda	u0002G14	Jll.rl Barstea	5054.5prime GH	94h09.rl s	08g10.rl Soares	.sl Soar	65e02.rl Soares m⊂	58d01.s1 NCI_C	5h01.rl Soares m	3d11.r	ST36505 Embryo, 8 we	12223 Er	3q03.sl Soares_	59h08.rl Stratagen	2ZA101 norm	Oc03.rl Soares mel	LO.	3c01.rl Soares mou	3-A1-dp-g-06-0-UI.	Dictyostelium	27941 Cerebellu	th04.rl Sommer	Of10.xl Soares 2N	54627 Jurkat T-	q59h09.rl Stratage	554	r00324 Maize Lea	9c01.s1 Stratage	24544 Cerebellum	L10F11 Chris M	587 Mouse early
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11	13	14	15	97	17	18	19	c 20	21	c 22	23	24	25	56	27	28	53	30	31	32	c 33	34	35	36	c 37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

AA896953 471 bp mRNA EST 06-APR-1998 120-38673 Ice plant Lambda Uni-Zap XR expression library, 30 hours NaCl treatment Mesembryanthemum crystallinum cDNA clone L30-386 5' similar to Citrate synthase, mitochondrial precursor, mRNA Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.
1 (bases 1 to 471)
Cushman, J.C. An expressed sequence tag database for the common ice plant, Mesenbryanthemum crystallinum Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2150267. AA896953.1 GI:3033346 common ice plant. sequence. 93033346 RESULT 1 LOCUS DEFINITION ORGANISM REFERENCE AUTHORS TITLE ACCESSION JOURNAL VERSION KEYWORDS COMMENT SOURCE

Contact: Cushman JC
Department of Biochemistry and Molecular Biology
Oklahoma State University
350 Noble Research Center, Stillwater, OK 74078-3035, USA Email: jcushman@biochem.okstate.edu PCR PRimers 9 row: H column: Tel: 405-744-6207 Fax: 405-744-7799 Plate: L30-4 FORWARD: I7 BACKWARD:

Seq primer: T3

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Tel: 517-353-0854
Fax: 517-353-9168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, euphyllophytes, Spermatophyta, Magnollophyta, eudicotyledons, Rosidae, Capparales, Brassicaceae, Arabidopsis.
                                                      /organism="Mesembryanthemum crystallinum"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1
EcoRI; Site_2: XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      982 TTAGCCGGACCACTTCATGGTTTAGCCAATCAGGAAGTTTTGCTATGGATAAAATCTGTT 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1222 CIGGITTCAAAACICTACGAAGTTTTCCTCCTGTTCTTACAGAACTTGGCAAAGITAA·A 1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1281 ACCTTGGCCAAATGTTGATGCCCACAGTGG-TGTGTTGTTGAACTATTATGGTTTAACT- 133E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 AGATACTCTTGCCAGAGGGACTTTGCCCTTAAGCACTTACCTAATGATCCACTATTTCAA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 GTGGATGAATGTGGAGAAACATCAGCACGGAGCAGCTAAAAGATTATGTCTGGAAGACA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 TTAAAAAGTGGCAAGGTTGTACCTGGATATGGCCATGGAGTTCTGCGCAAGACGGATCCA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 CIGGITICGAAGCIGIATGAAIGGIGCCICCAATICTGACAGGCIGGGAAGGIAAAGA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T44185 502 bp mRNA EST 07-JAN-1998
7448 Lambda-PRL2 Arabidopsis thaliana cDNA clone 123C9T7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                            63 TTGGCTGGCCCACTTCATGGATTAGCCAATCAGGAAGTGTTGCTGTGGATCAAGTCAGTT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          363 ACCATGGCCGAATGTTGATGCCCACAGTGGGTGTATTGCTGAACTACTATGGTTTGACAA 422
                                                                                                                                                                                                                                                                                                                                                                                      3 CATTTGGTGGGTAGCGCACTTTCAGATCCTTACCTTTCATTTGCAGCTGCACTGAATGGG 62
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                /cloud_lb="lce plant Lambda Uni-Zap XR expression
library, 30 hours NaCl treatment"
/tissue_type="Leaf, 30 h 0.4M NaCl"
/dev_stage="Six week old"
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                                                                                                                                                                                                                                                                                        Score 241; DB 20; Length 471; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                              0; Mismatches 86; Indels
High quality sequence stop: 320.
Location/Qualifiers
                                                                                                            /db_xref="taxon:3544"
/clone="L30-386"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423 GAAAGCAAGATACTACACTGT 443
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Best Local Similarity 79.6%;
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                                                                                                                                                                                                                                                                                                                              351; Conservative
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                    FEATURES
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/strain-war columbia"
//strain-war columbia"
//strain-war columbia"
//strain-war columbia zip Lox; Site_1: Sal, Site_2: Not,
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark-rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques. The vector is BRL's lambda zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
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DEFINITION 16899 Lambda-PRL2 Arabidopsis thaliana cDNA clone 189D15T7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1088 AIGTIIGGAAAACAIIGAACAGGGCAAGGTIGICCCGGGTIIIGGACAIGGAGITCIGC 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              968 CTGCTTTGAATGGTTTAGCCGGACCACTTCATGGTTTAGCCAATCAGGAAGTTTTGCTAT 1027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 AIGTITGGGAAACAITAAACAGIGGCAAGGTIAITCCGGGGTAIGGICACGGIGTICINC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             788 AAICCCIGGAITAIGGIGCAAAITIIGCICACAIGCITIGGIIIICAGIAGCICIGGAAIGC 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 TGAAAGAGCTCATGAGGCTTTACATCACCATCCACAGGGATCATGAAGGTGGAAATGTTA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 GIGCICACACIGGICACCIGGIIGGIAGIGCACITICAGACCCAIAICIGICAITIGCAG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AATCTTTGGATTATGGTGCAAATTTTTCCCACATGTTGGGATTTGAT--GAI--GAAAGG 58
                                                                                                                                        Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg.,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Gaps
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On Jan 7, 1998 this sequence version replaced qi:948518
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90 c 118 g 149
                                                                                                             MSU-DOE Plant Research Laboratory
                                                                                                                                                                                                                                                                                                                      Email: 22313tcn@ibm.cl.msu.edu
Seg primer: T7.
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                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                       Contact: Thomas Newman
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R90544.1 GI:958084
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                    DEFINITION
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JOURNAL
COMMENT
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                                                            ACCESSION
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                                                                                                                                                                                                                    REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strain-"var columbia"

// Strain-"var columbia"

// Note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;

// Lambda PRL2 is a cDNA library derived from equal

// Apols of mRNA. The mRNA Sources were 1)

// day germinated etiolated seedlings; 2) tissue culture

// day germinated etiolated seedlings; 2) tissue culture

// Strain of the light, 8 hour dark-rosettes;

// Same plants as 3 but aerial tissue (stems, flowers and

// sliques. The vector is BRL's lambda Zip-Lox. The cDNA

inserts were directionally cloned with Sal-Not arms usin:
                                                                                                                                                                        large-scale partial sequencing of anonymous Arabidopsis cDNA cloness Plant Physiol. 106, 1241-1255 (1994)
                                                                                               Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., Carticosh, L., Ohltrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, F. and Somerville, C. Genes galore: a summary of methods for accessing results from
                Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis.

[ (bases 1 to 478)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             943 TCTGATCCTTACCTCTCCTTTGCTGCTGCTTTTGAATGGTTTAGCCGGACCACTTCATGGT 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1183 ITCGCTATGAAGCATTTGCCTGAAGATCCACTGTTTCAACTGGTTTCAAAACTCTACGAA 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 TITGCCITGAAGCAICTACCTGACGNCCCTCTTTTCCAGCTSGTCAAAGCTTTATGAA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 ATATCAAAAGAACAGTIGAAAGAATATGTTTGGAAAACATTAAACAGTGGCAAGGTTATT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 ITGGCTAATCAGGAAGTTTTGCTTTGGATCAAATCAGTCGTAGAGGAATGTGGAGAAGAT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 TCAGACCCATATCTGTCATTTGCAGCTGCATTAAATGGTTTAGCTGGGCCACTCCATGGT 63
                                                                                                                                                                                                                                                                                           MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Gaps
                                                                                                                                                                                                                                     On Apr 14, 1993 this sequence version replaced gi:693655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 189; DB 31; Length 478
Pred. No. 0.00e+00;
C; Mismatches 66; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Lambda-PRL2"
90 c 113 q 13
                                                                                                                                                                                                                                                                                                                                                                                                               Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7 dye primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oligo dT primed cDNA. /db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                            Contact: Thomas Newman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 10.0%;
Best Local Similarity 79.6%;
Matches 255; Conservative
                                                                                                                                                                                                                                                                                                                                                                          Tel: 517-353-0854
Fax: 517-353-9168
                                                                                                                                                                                                                                                                                                                                                           Lansing, Mi
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ORGANISM
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RESULT

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AU002699 620 bp mRNA EST 15-JAN-1999
AU002699 Bombyx mori p50(Daizo) Bombyx mori cDNA clone n0357, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1126 GGITTIGGACATGGAGTICTGCGAAAGACTGTACCAAGATATACATGCCAGAGAGAGTTC 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 TITGGAGIGICCCGAGCGIIGGGIGITCICGCICAGIIGAITIGGICCCGIGCGCICGGA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GCTAATCAAGAGGTTCTGGTATGGCTCGAGAACTGCGCAAACAAGTTGGTGATAATTTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 GGTTACGGTCATGCAGTACTTAGAAAAACTGATCCAAGATATACTTGCCAGCGTGAGTTT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 CATICGGGAGIICIIIIGCAGIAIIAIGGICIGAAGGAGAIGAACIACIAIACAGIAAIG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GATCCTTACTTATCTTTCGCCGCTGGACTCAATGGTCTTGCTGGACCACTTCACGGCCTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 886 GATCATGAAGGTGGTAATGTCAGTGCTCACACCGGTCACTTGGTTGCTAGTGCTTTGTCT 945
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                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Lepidoptera; Bombycoidea; Bombycidae; Bombyx.
1 (bases 1 to 620)
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                                                                                                                                                                                                                                                                                                                                                                                     Mita, K., Morimyo, M., Shimada, T., Okano, K., and Maeda, S.
Establishment of cDNA database of Bombyx mori
Unpublished (1999)
on Sep 1, 1995 this sequence version replaced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 179; DB 26; Length 620; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib-"Bombyx mori p50(Daizo)"
141 c 146 g 171 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    National Institute of Radiological Sciences Anagawa 4-9-1, Inage, Chiba 263-8555, Japan Email: kmita@uexs64.nirs.go.jp
PROJECT - 'CREST project by JST'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism-"Bombyx mori"
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/db_xref="taxon:7091"
/clone="n0357"
                                                                                                                                                             Ā世002599.1 GI:4159092
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Genome Research Group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.5%;
Best Local Similarity 66.4%;
Matches 392; Conservative
                                                                                                                                                                                                                              domestic silkworm.
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Query Match
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                                                                                                                                                                                                                                                                                   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain-"cultivar Nipponbare, sub_species Japonica"
/note="Vector: pBluescript II SK+; Site_1: SalI; Site_2:
NotI: cDNA prepared from rice callus mRNAs by using
oligo(dI) as a primer and ligating to the SalI-NotI site
of pBluescript II SK+ phagemid. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             979 GGTTTAGCCGGACCACTTCATGGTTTAGCCAATCAGGAAGTTTTGCTATGGATAAAATCT 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            799 TATGGTGCAAATTTTGGTCACATGCTTGGTTTCAGTAGCTCTGAAATGCATGAACTTCTT 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 ATGCGACTATATGTGACAATCCACACTGATCATGAAGGTGGAAATGTCAGTGCTCATACT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 GGACATCTGGTTGGAAGTGCTCTGTCAGATCCTTATCTTTTGCAGCTGCACTGAAT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 GGTTTAGCTGGACCATTGCACAGCCTAGGCTAATCAGGAAGTGCTGTTGTGGATCAAATGT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 739 TATGTTTATCGCAGGATGTACAAGAATGGTGACACTATACCTAAGGATGAATCCCTGGAT 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 TAIGCAGCAAACTTTTGAGACATGCTTGGGTTTGATGATGCCGAAAATGCTGGAG--T-TG 118
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                                                                                                                          19-0CT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 4; Gaps
                                                                                                                      LOCUS C96653 417 bp mRNA EST 19-OCT-19
DEFINITION C96653 Rice callus Oryza sativa cDNA clone C10531_5A, mRNA
                                    1423 TIGCCGCIAGAGAGGCCAAAGAGIGTCACAAIGGAGIGGCIIGAGAACCA 1472
541 CTTCCCATTGAGAGACCAAAGTCGCTCAGCACGGAGATGCTTATGAAACA 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 172; DB 24; Length 417;
Pred. No. 0.00e+00;
0; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Takuji Sasaki
National Institute of Agrobiological Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Aug 21, 1998 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 t
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76 c 108 g 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: tsasaki@abr.affrc.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rice Genome Research Program
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                                                                                                                                                                                                                                                                                                                                                                                     Sasaki,T. and Minobe,Y.
Rice cDNA from callus
Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2-1-2 Kannondai, Tsukuba
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Local Similarity 73.18;
Les 304; Conservative
                                                                                                                                                                                                                           C96653.1 GI:3758954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 0298-38-7441
Fax: 0298-38-7468
                                                                                                                                                                                                                                                                                                                                                     Oryza.
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                                                                                                                                                                                                                                                                    Oryza sativa.
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A1176862 676 bp mRNA EST 20-JAN-1999
EST220465 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
EST220465 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
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                                                                    1039 GITGTAGAAGAATGTGGGGAGAACATTTCCAAAGAGCAGTTGAAAGACTATGTTTGGAAA 1098
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299 GTAATAGGTGAGACAGGTAGTGATGTTACAACTGATCAACTCAAAGAGTATGTGTGGAAG 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 CAGIGCCCICGACACICCGAACAGGACIGIGIAGIAAFICATCICCCTVAIGCCATAGIA 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                353 CTTGGGGAGATGTTTCAGAGGAAACTCTCGCTGACAGGAATATCGTGGTGGATCAGTCTTCCT 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: ovary; Vector: pT7T3Pac; Site_1: EcoRI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eutheria: Rodentia, Sciurognathi, Muridae, Murinae, Rattus... i (bases 1 to 676)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
                                                                                                                                                                                    1099 ACATTGAACAGTGGCAAGGTTGTCCCTGGTTTTGGACATGGAGTTCTGCGAAAGAC 1154
                                                                                                                                                359 ACACTAAAAAGTGGAAAGGTTGTTCCTGGCTC-GGTCATGGAGTTCTACGTAAGAC 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Jan 19, 1998 this sequence version replaced gi:2152042.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA
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Local Similarity 67.8%; Pred. No. 0.00e+00;
nes 375; Conservative 0; Mismatches 173; Indels
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/db_xref="ATCC (inhost):2031570"
/db_xref="taxon:10118"
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Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene Index
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Score 153; DB 15; I Pred. No. 3.25e-287;
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Cornell University
Ithaca, Nr 14853-1901, USA
Tel: 607 255 6683
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AA231705
g1854091
AA231705.1 GI:1854091
                                    Query Match 8.1%;
Best Local Similarity 66.7%;
Matches 396; Conservative
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1 (bases 1 to 657)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLN: ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:570169
                                                                                                                                                                                                                                                                                                                                                                                                AA606966 657 bp mRNA EST 30-SEP-1997 wm94409.rI knowles Solter mouse blastocyst B1 Mus musculus cDNA clone IMAGE:1005953 5' similar to SW:CISY_PIG P00889 CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR ;, mRNA sequence.
                                                                                         1146 CAGAACTCCATGTCCAAAACCAGGGACAACCTTGCCACTGTTCAATGTTTTCCAAACATA 1087
423 TAGGACTGCATGACCATATCCTGGGACAACCCGTCCCGAGTTGAGTGTGTTTCCAGATGTA 482
                                                                                                                                            601
                                                                                                                                                                              1027 ATAGCAAAACTICCIGATIGGCIAAACCAIGAAGIGGICCGGCIAAACCAIICAAAGCAG 968
                                                                                                                                                                                                                                                    967 CAGCAAAGGAGGAGAGATCAGACAAAGCACTAGCAACCAAGTGACCGGTGTGAGCAC 908
                                                                                                                                                                                                                602 CTGCANAGGACAGGTAAGGGTCTGAAAGGGGGCTGCCCACCAACGAGTGGCTTGTGTGGGCAC
                                                                        542 AGACAAGCACCTCCTGGTTTGCTAGTCCATGCAGAGGCCCTGCCAGCCCATTCATAGCTG
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On Sep 12, 1996 this sequence version replaced gi:1328460
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(db_xref*'taxon:10090"

/clone="IMAGE:1005953"

/clone=lib="Knowles Solter mouse blastocyst B1"

/tissue_type="blastocyst"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stag6="embryo (pre-implantation)"
/lab_host="DH10B"
167 c 181 g 148 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST Project
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/organism="Mus musculus"
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The WashU-HHMI Mouse EST Project
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Location/Qualifiers
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
euphyllophytes, Spermatophyta, Magnollophyta; Liliopsida, Poales,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1330 GGTTTAACTGAAGCAAGATATTATACGGTCCTCTTTGGCGTATCAAGAGCTCTTGGCATT 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             976 AATGGTTTAGCCGGACCACTTCATGGTTTAGCCAATCAGGAAGTTTTGCTATGGATAAAA 1035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 AATGGGCTGGCGGGGT-CTACATGGACTAGCAAATCAGGAGGTGCTTGTCTGGCTGACA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 GAACACACTCAATTCAGGACGGGTGGTCCCAGGATACGGTCATGCAGTACTGAGGAAGAC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 TGACCCTCGCTATTCCTGTCAGCGAGGTTTGCTCTGAAACATCTGCCTAAGGGATTCCC 378
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                                                                                                                                                                                                                                                                                                82 ACAAGCCATTTGGTGGCGCAGCGCATT-TCAGACCCTTACCTGTCCTTTGCAGCAGCAGG 140
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                                                                       Gaps
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1 (bases 1 to 307)
VanDeynze, A.E., Sorrells, M.E., Park, W.D., Ayres, N.M., Fu, H., CartInhour, S.W. and McCouch, S.R.
Anchor Probes for Comparative Mapping of Grass Genera Unpublished (1997)
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CD0534.R cDNA from oat Avena sativa cDNA clone CD0534, mRNA
                                                                                                                                                  22 CTCATGCGTTTGTACCTCACCATCCATAGTGACCATGAGGGTGGTAATGTAAGTGCCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 -CAGCTACAGAAGGAAGTTGGCAAAGACGTGTCAGATGAGAAGTTACGAGACTACATCTG
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Length 657;
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COMMENT
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                                                                                                                                        Cultivar-"Brooks"

/cultivar-"Brooks"

/cultivar-"Brooks"

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/cultivar-"Brooks"

/cultivar-"Brooks"

/cultivar-"Brooks"

/collided leaf mRNA from the oat cultivar 'Brooks'

/collided leaf mRNA from the capture of the collided leaf mRNA from the maplification, use M13 forward and reverse primers.

/clones from this library are designated with the prefix 'Clon' 'Roote: Clone CD01081 was reclored into the TA cloning vector and carries kanamycin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   967 GCTGCTTTGAATGGTTTAGCCGGACCACTTCATGGTTTAGCCAATCAGGAAGTTTTGCTA 1026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R90561 527 bp mRNA EST 30-DEC-1997 16916 Lambda-PRL2 Arabidopsis thaliana cDNA clone 189H3T7, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 CGTAATACAGATCCACGATACTCGTGCCAAAGGGAGTTTGCACTTAAGTATTTACCCGAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 GACCCACTTTTCCAACTGGTCTCCAAGTTGTACGAAGTTGTGCCTCCTATCCTTACTGAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GCGGCACTGAACGGTTTAGCTGGGCCACTGCATGGCCTGGCTAATCAGGAAGTGTTGCTA 60
                         cDNA from oat (Avena sativa); reverse sequence of RFLP probe CDO534. Sequence determined by Nicola M. Ayres.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 150; DB 10; 1
Pred. No. 5.79e-280;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="cDNA from oat"
                                                                                                                         /organism="Avena sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="etiolated
                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="CD0534"
Email: srm4@cornell.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 7.9%;
Best Local Similarity 75.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231; Conservative
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SOURCE
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Astraha-"var columbia"

Ante-"var columbia"

Ante-"var columbia"

Lambda PRL2 is a cDN library derived from equal

quantities of 4 pools of mRNA. The mRNA sources were 1) 7

day germinated etiolated seedlings; 2) tissue culture

grown roots; 3) staged plants half with 24 hour light

grown roots; 3) staged plants half with 24 hour light

grown roots; 3) staged plants half with 24 hour light

grown roots; 3) staged plants half with 24 hour light

grie, half on 16 hr light, 8 hour dark- rosettes; 4)

same plants as 3 but aerial tissue (stems, flowers and

sliques. The vector is BRL's lambda Zip-Lox. The cDNA

inserts were directionally cloned with Sal-Not arms using

oligo dr primed cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCUS AA313713 501 bp mRNA EST BEST STATES COLON CARCINOMA (HCC) cell line Homo sapiens CDNA 5' end similar to similar to citrate synthase, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 GTCGAAAGACTTGGCGAACCGTGCTGC-TGTGCCAGATTATG-TGTACAATGCCATCGAT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 GCTCTGCCTTCCACAGCTCATCCAATGACTCAATTTGCTAGCGGTGTTATGGCCCTCCAG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 GTGCAAAGTGAGTTTCAAAAGGCATATGAGAATGGAATTCATAAGTCAAAGTTCTGGGAG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 CCAACATATGAGGATTGCCTCAACCTGATTTGCTCGTGTTNCCTGTTGTAGNCTGCATAA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               685 CCAACATATGAGGATTCCATGAATCTGATT-GCTCAAGTT-CCACTTGTTG-CTGCTTA- 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTTTATCCGAAGGGATGTATAANAATTGGTGGTTCCATTCCCTCAGGATAAAACCTTTG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTCTTTTGTGGGCTTCTCTTAACTGGAAAGGTACCTAGCAAAGAGCAAGTTGAAGCACT- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    505 GICICAGGAAITGCAGAGICGGCAICAIATCCCIGAICAICAIGIATACAACIAITGAI 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                565 GCCTTACCAGTCACAGCTCATCCAATGACCCAGTTTGCTACTGGAGTCATGGCTCTTCAG 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        385 ATACCTGAATGCCAAAAGGTATTACCTGCAGCAAAGCCTGGGGGTGAGCCCTTGCCTGAA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                445 GGTCTTCTCTGGCTTCTTTTAACAGGAAAGGTGCCATCAAAAGAGCAAGTGAATTCAATT 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 ATTCCTGAGTGCCAGAAAGTATTACCTACTGCCCAGTCTGGAGCTGAACCATTACCGGAG 62
                                                                                                                                                                        MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
On Apr 14, 1993 this sequence version replaced gi:693674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 527;
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0; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism-"Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /map="873F09; 1q21.3-1q23.2; 9"
/clone="189H3T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.9%; Score 150; DB 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Lambda-PRL2"
106 c 122 g 141
                                                                                                      MSU-DOE Plant Research Laboratory
                                                                                                                                                                                                                                                                                                                Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7 dye primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:3702
                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                    Michigan State University
                                                                     Contact: Thomas Newman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   796 GATTATGGTGCAAATTT 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 73.3%;
Matches 321; Conservative
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                                                                                                                                                                                                                                          7-353-0854
                                                                                                                                                                                                                                              Tel: 517-353-0854
Fax: 517-353-9168
                                                                                                                                                                                                                 Lansing, Mi
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Equivaled filiatures, cacalinger, nowes.

Sadams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Blutt, C.J., Lee, N.H., Kirkness, F.F., Wehistock, K.G., Gocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.C.,

Clayton, R.A., Cline, T.R., Octton, M.D., Earle-Hughes, J., Fine, L.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,

Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, F.S.T.,

Kelley, J.M., Kelley, J.C., Liulu, L.I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nquyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shriley, R.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Bolmke, D., Fengo, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,

He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P.S.,

Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Pillion, J.J., Fengo, P. F., Rosen, C.A., Haseltine, W.A., Fields, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995) 96026280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             963 IGCIGCIGCITIGAAIGGIIIAGCCGGACCACIICAIGGIIIAGCCAAICAGGAAGIIII 1022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: colon; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: Mon!
/db_xref="ArCC (inhost):109839"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 GAGACTACATCTGGAACACTCAACTCAGGACGGGTTGTTCCAGGCTATGGCCATGCAG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TGTCTGGCTAACA-CAGCTGCAGAAGGAAGTTGGCAAAGATGTGTCAGATGAGAAGTTAC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TGCAGCAGCCATGAACGGGCTGGCAGGGCCTCTCCATGGACTGGCAAATCAGGAAGTGCT 60
                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 144; DB 11; Length 501;
Pred. No. 1.68e-265;
0; Mismatches 153; Indels 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Apr 14, 1993 this sequence version replaced gi:693326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Colon carcinoma (HCC) cell line"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="colon"
/cell_type="KM12C"
/cell_line="KM12C(HCC)-parental human colon
carcinoma;Dukes B2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               =
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Kerlavage, AR
                                                       AA313713.1 GI:1966042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Other_ESTs: THC171646
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Best Local Similarity 67.4%;
Matches 327; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 3018699423
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                                                                                                                                                 Homo sapiens
                           q1966042
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                                                                                                                                              ORGANISM
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ACCESSION
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LOCUS AA237580 522 bp mRNA EST 03-WAR-1997
DEFINITION mxlld01.rl Soares mouse NML Mus musculus cDNA clone IMAGE:679873 5'
similar to SW:CISY_PIG P00889 CITRATE SYNTHASE, MITOCHONDRIAL
PRECURSOR;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Mylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:419577
                                                                                                                                                                                                                                                                                       1082 AAGACTATGTTTGGAAAACATTGAACAGTGGCAAGGTTGTCCCTGGTTTTGGACATGGAG 1141
                                                                                 1202 CIGAAGAICCACIGIIICAACIGGIIICAAAACICIACGAAGIIIICCICC-IGIICIIA 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360 TCCAGTATTATGGCATGACGGAGATGAATTACTACACGGTCCTGTTTGGGGTGTCACGAG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     420 CATIGGGIGTACTGGCACAGCICATCTGGAGCCGAGCCTTAGGGTICCCTCTAGAAAGGC 479
                                                                                                                                                        240 CTAATGACCCCATGTTTAAGTTGGTTGCTCAGCTGTACAAGATTGTGCCCAATGTCCTCT 299
                                                                                                                                                                                                                                                            300 TAGAGCAGGGTAAAGCCAAGAATCCTTGGCCCAATGTAGATGCTCACAGTGGGGTGCTGC 359
                                                   180 TACTAAGGAAGACTGATCCGCGATATACCTGTCAGCGAGAGTTTGCTCTGAAACACCTGC 239
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 522)
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On Sep 12, 1996 this sequence version replaced g1:1392879.
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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High quality sequence stop: 453.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                              1189 ATGAAGCATTTGCCTGAAGATCCACTGTTTCAACTGGTTTCAAAACTCTACGAAGTTTTC 1248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 ATCAGGAGGTGCTTGTCTGGCTGACA-CAGCTACAGAAGGAAGTTGGCAAAGACGTGTCA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 GATGAGAAGTTACGAGACTACATCTGGAACACACTCAATTCAGGACGGGTGGTCCCAGGA 236
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                                                                                                                                                                                                                                                                                                  1 ATGAGGGTGGTAATGTAAGTGCCCACACAAGCCATTTGGTGGG-AGCGCTGT-TCAGACC 58
                                                                                                                                                                                                                                                         8; Gaps
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Pred. No. 2.69e-246;
0; Mismatches 165; Indels
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                                                                             /db_xref="taxon:10090"
/map="3"
                                                             /clone="IMAGE:679873"
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Arabidopsis thaliana
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Local Similarity 66.9%;
nes 349; Conservative
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Inter-Vector: Lambda ZAPII; tissue-cell suspension culture of ecotype columbia; clone_library-AC16H; Cloning vector: Lambda ZAPII; Physiological condition: cycling cells."
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(Dases 1 to 466)

Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hollman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Pifkhin,L., Pohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R. Wabhy-Merck EST Project
Unpublished (1993 this sequence version replaced gi:693136.
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Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 213;
laboratoire de Biologie Moleculaire
BP 27,31336 Castanet-Tolosan cedex,France
Email: lescuredtoulouse.inra.fr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . match
Local Similarity 82.3%; Pred. No. 4.57e-220;
es 172; Conservative 0; Mismatcher 22
                                                                                                                                                      /organism="Arabidopsis thaliana"
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/clone_lib="AC16H"
1 40 c 52 g
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Contact: Thomas Newman
MSU-DDE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg.,E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Lambda-PRL2"
54 c 64 g 6
                                                                                                                                                        Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7 dye primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                               oligo dT primed cDNA./db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /map="21q"
/clone="158K12T7"
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                                                                                                 Lansing,Mi
Tel: 517-353-0854
Fax: 517-353-9168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   upland cotton.
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Retzel, E. and Somerville, C. Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
Rosidae; Capparales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Newman,T., deBrujn,F.J., Green,P., Keegstra,K., Kende,H.,
McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA720224 252 bp mRNA EST 30-DEC-1997 33417 Lambda-PRL2 Arabidopsis thaliana cDNA clone 158x12T7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        975 GAATGGTTTAGCCGGACCACTTCATGGTTTAGCCAATCAGGAAGTTTTGCTATGGATAAA 1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1035 ATCTGTTGTAGAAGAATGTGGGGAGA-ACATTTCCAAAGAGCAGTTGAAAGACTTTT 1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1094 GGAAAACATTGAACAGGGCAAGGTTGTCCCTGGTTTTGGACATGGAGTTCTGCGAAAGA 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274 A-CAGCTGCAGAAGGAAGTTGGCAAAGATGTGTCAGATGAGAAGTTACGAGACTACATCT 332
                                                                                                                                                                                                                                                                                                                                                                                                                                          95 CTCACGCGCGTGTACCTCACCATCCACAGTGACCATGAGGGTGGCAATGTAAGTGCCCAT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    856 CTTATGAGGCTCTATGTAACAATACACAGTGATCATGAAGGTGGTAATGTCAGTGCTCAC 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 ACCAGCCATTIGGIGGGCAGTGCGTNTTCCGACCCGTTACCTGTCCTTTGCAGCAGCCGT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               916 ACCGGTCACTTGGTTAGTTGTTGTCTGATCC-TTACCTCTCCTTTGCTGCTTGCTTT 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215 GAACGGGCTGGCAGGGCT-CTCCATGGACTGGCAAATCAGGAAGTGCTTGTCTGGCTAAC 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333 GGAACACACTCAACTCAGGACGGGTTGTTCCAGGCTATGG-CATGCAGTACTAAGGAAGA 391
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                                                                                                                                                                                                                                                                                                                                                                                                        5; Gaps
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On Sep 12, 1996 this sequence version replaced g1:1405146.
                                                                                                                                                                                                                                                                                                                                                                Length 466;
                                                                                                                                                                                                                                                                                                                                                              Score 120; DB 36; Length 466
Pred. No. 3.23e-208;
0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                     1 others
                                                                                                                                                                                                                                                                              /lab_host="SOLR (kanamycin resistant)"
116 c 122 g 110 t 1 oth
                                                                                                                                                                                                                     /clone_lib="Stratagene muscle 937209"
/tissue_type="muscle"
                                                                                                                                                                                                    /clone="IMAGE:562451"
                                                                                                                                                                             /db_xref="taxon:9606"
                                                                                                                                                                                                                                                             /dev_stage="adult"
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Best Local Similarity 69.3%;
Matches 259; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   452 TGTTTAAGTTGGTT 465
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/organism="Arabidopsis thaliana"
/strain="var columbia"
/strain="var columbia"
/note="Wector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
Lambda FRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1)
quantities of 4 pools of mRNA. The mRNA sources were 1)
quy germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
silnques. The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 585)
Wan,C.-H., Yu.Y., Sasinowski,M. and Wing,R.A.
Cotton EST Database: Sequence Analysis of 2000 cDNA Clones from an
Abscission Zone Library
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gossyplum hirsutum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
euphyllophytes, Spermatophyta, Magnollophyta, eudicotyledons,
Rosidae, Malvales, Malvaceae, Gossyplum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1366 GGCGTATCAAGAGCTCTTGGCATTTGCTCTCAGCTAATTTGGGACCGAGCTCTTGGATTG 1425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 AGTGGGGTCTTGCTGAACCACTATGGTCTAACCGAAGCAAGGTACTACACGGTGCTCTTT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 GGTGTTTCAAGGAGTCTTGGNATCTNCNCTCAGCTTATATGGGACCGAGCTCTTGGACTT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 CCTCCTGINCINACIGAGCTIGGAAAGGIGAAGAACCCGIGGCCAAAINITGAIGCTCAC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 252;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.1%; Score 115; DB 17; I Best Local Similarity 79.5%; Pred. No. 2.02e-196; Matches 159; Conservative 0; Mismatches 39;
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Score 116; DB 22; Length 585;
Pred. No. 8.91e-199;
0; Mismatches 90; Indels 15; Gaps 13;
                                                                                                                                            /organism-"Gossypium hirsutum"
/note-"Vector: Uni-ZAP XR; Site_1: EcoRI; Site_2: XhoI;
This is a Uni-ZAP XR custom cDNA library made by
Stratagene (U.S.A.: 1-800-424-5444): Stratagene cat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 GCGATGGTGTTTTTGAAGGGAGTATCAGCGCTATCCAGTCTAAGGTCACGTGTTAAACAG 109
                                                                                                                                                                                                                                                                                                                                                                                                                            70 GCAATGGTGTTCTACCGTAGCGTTTGCTGCTGCAAAGCTCCGCTCTGGGGGGCGTCCAA 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 CTTCATTCGCAGTTG--A-AGGAATTGATTCCTGAACAACAGGGGGGCGCTGAAGAAACTG 226
                                                                                                                                                                                                                         345 TTCGCTTTGGGGCCTTGTC-ATTCCGNAGTGTCAAAAACTATTACCAGCTGCAAA-CCTG 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        365 TICGCITCCGGGGGTTGTCTATACCTGAATGCCAAAAGGTATTACCTGCAGCAAAGCCTG 424
                                                                                                                                                                                                                                                                                            8 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       403 ATGGAGAACC-TT-CGINAGGGTCTT-TATGGCTTCTTT 438
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seg primer: SP030 (AACAGCTATGACTATA)
                                                                                                                                                                                                                                                                                         172 t
                                                                                               High quality sequence stop: 239.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                        Ouery Match 6.1%;
Best Local Similarity 73.7%;
Matches 294; Conservative
                                                                                                                               . 585
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Search completed: Sat Oct 23 16:24:08 1999

Job time : 3223 secs

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7:em_in 8:em_om 9:em_or 10:em_ov 11:em_pat 12:em_ph
13:em_pl 14:em_ro 15:em_sts 16:em_vi
genbank111
                                                                                                                                                                                                                                                                                                                                                                                    n.a. - n.a. database search, using Smith-Waterman algorithm
                                                                                                                                                                                                                                                                                Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd
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(1-1551) from US08702718.seq
1551
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Listing first 45 summaries
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Gap 6
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Perfect Score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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La Cognata, U., Landschuetze, V., Willmitzer, L. and Mueller-Roeber, B. Plant Cell Physiol In press (bases 1 to 1551)
La Cognata, U.
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Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
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Genbiologische Forschung, Berlin GmbH, Ihnestrasse 63, 14195
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Citrus maxima citrate synthase (cit) mRNA, nuclear gene encoding mitochondrial protein, complete cds.
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Charophyta/Embryophyta group; Embryophyta; Magnollophyta;
Magnollopsida; Rutanae; Sapindales; Rutaceae; Citrus.
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Canel, C., Bailey-Serres, J. and Roose, M. Physiological and molecular genetic studies of acid accumulation in
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VAAYVYQRIYKDGKIIPKDDSLDYGGNFSHMLGFDDPKMLELMRLYVTIHSDHEGGNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAHTGHLVASALSDPYLSFLAALNGLAGPLHGLANQEVILWIKSYVDECGENYTEQL
KYVWATLUSGKVVPGFGGYLRKTDPRYTCQREFALKHLPDDPLFQLVSKLYEVVPP
ILTKLGKVKNEWPNAHSGYLLNHFGLAEARYYTVLFGVSRSLGICSQLIWDRALGL
PLERPKSVILDWIEKNCKKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSIPECQKLLPAAKPDGEPLPEGLLWLLTGKVPSKEQVDGLSKELRDRATVPDYVYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MASLRSATALSRLRSRAGQGSNLSNSVRWLQMQSSADLDLHSQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEMIPEQQERLKKVKSDLGKAQLGNITIDVVIGGMRGMTGLLWETSLLDPDEGIRFRG
                                                                                                  Thesis (1994) Botany & Plant Sciences, University of California at
                                                                                                                                                                                                                       Submitted (04-JAN-1995) Camilo Canel, University of California at Riverside, Botany & Plant Sciences, Riverside, CA 92521-0124, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                       /strain="Siamese sweet (pummelo 2240)"
//strain="Siamese sweet (pummelo 2240)"
//note="There is a single copy of the cit gene in the citrus genome. A single transcript with an estimated length of 1,850 nucleotides can be detected in juice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function="synthesis of citrate from oxaloacetate and acetylCoA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 CTGATCTTGACCTTCATTCTCAGCTCAAGGAAATGATTCCAGAACAACAGGAGCGCCTGA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /function="synthesis of citrate from oxaloacetate and acetylcoa"
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Pred. No. 0.00e+00;
0; Mismatches 287; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    function = "targets the protein to the mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="citrate synthase precursor"
/protein_id="AAA82743.1"
/db_xref="PID:9624676"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="juice_cell"
/tissue_type="juice tissue"
/dev_stage="immature"
1. 56
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                                                                                                                                                                                                                                                                                                                               /organism="Citrus maxima"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:37334"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="hermaphrodite"
                                                                                                                                                                                                                                                                            Location/Qualifiers
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Canel,C.
Direct Submission
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1 (bases 1 to 1733)
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Best Local Similarity 78.2%;
Matches 1028; Conservative
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943 IGGCCGCATTAAATGGTTIAGCTGGACCACTCCATGGTTTGGCTAATCAGGAAGTTTTGC 1002
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                                                                                                                                             185 AGGGTATCCGGTTCAGGGGTTTTTCTATACCTGAATGCCAGAAACTTTTACCCGCTGCAA 244
                                                                                                                                                                                                        403 AGCCAGATGGAGAACCTTTGCCTGAGGGTCTTCTTTGGCTTCTTTTAACTGGAAAGGTAC 462
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                           125 TGGGCGGAATGAGAGGAATGACTGGTTTAGTTTTGGGAGACTTGGTTAGTGGACCAGAAG 184
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LSIYECQKVLPAAKPGGEPLPEGLLMLLLTGKVPSKEQVDSLSQELRSFATVPDHVYK
TIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKLMEPIYEDSMSLIAQVPL
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SAHTOHLVARALSDPYLSFAAALNGLANGYLLMYKRVYEGCEGNIGSKEQL
KDYAMKTLKSGKNGGFGHGVLKKUDPRYTCQREFANGYKHLPEDDLLGLYAKLYEVFLOF
FLONLAKLNPWPNVDAHSGVLLNYYGLTERRYYTVLFGVSRALGICSQLIMDRALGED
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/db_xref="GI:2300712"
/translation="MVFYRGVS1LSKLRSRAVQQTNLSNSVRWLQVQTSSGLDLRSEL
                                                                                                                                                                                                                                                                     Nicotiana tabacum
bularyota: Viridiantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
Asteridae; Solananae; Solanales; Solanaceae; Nicotiana.
I bases 1 to 1747)
Mueller-Roeber, B., Landschuetze, V. and La, C.U.
PROCESSES FOR INHIBITING AND FOR INDUCING FLOWER FORMATION IN
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1205 TIGGAATATGCTCACAGCTTATATGGGACCGAGCTCTTGGCTTGCCGCTAGAGAGGCCAA 1264
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                                   1423 AAAGTGTAACTTTAGATTGGATTGAGAAAATTGCAAGAAAGCAGCTTAGAATTG 1477
                                                                     1265 AGAGTGTCACTATGGAATGGCTTGAAAAGTTTTGTAAAAGAAGAGCATAACATTG 1319
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/protein_id="CAA02910.1"
/db_xref="PID:e306253"
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HOECHST SCHERING AGREVO GMBH (DE)
Other publication DE 4438821 960425
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Other publication AU 2067995 950925
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/clone="TCS"
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181 GAAGAGGGTATCCGGTTCAGGGGTTTTTCTATACCTGAATGCCAGAAACTTTTACCCGCT 240
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                                                                                   412 GCAAAGCCTGGGGGAGAGCCCTTGCCTGAAGGTCTTCTCTGGCTTCTTTTAACAGGAAAG 471
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SAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQL
SYDAWKTLKSGKVVPGFGHGYLRKTDPRYTCQREFALKHLPEDPLFQLYAKLYEVFLQ
FLQNLAKLNPWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALGLP
LEFRKSVTMEWLENKRA"

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GELIPEQORDEKKLKSHBRKVQLGNITVDWMLGGRRGWTGLMFTSLLBTERG
LSIYECOKVLPAARGGEPLPRGLLMLLLTGKVPSKPCOVDSLSGERRRATVEDHVYK
TIDALPVTAHPWTGFATGVWALQVQSEFQRAYEKGIHKSKLWEPTYEDSMSLIAQVPL
                                                                                                                                                                                                                  1 (bases 1 to 1747)
La Cognata,U., Landschuetze,V., Willmitzer,L. and Mueller-Roeber,B.
2 (bases 1 to 1747)
La Cognata,U.
La Cognata,U.
La Cognata,U.
                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; Asteridae; Solananae; Solanales; Solanaceae; Nicotlana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 GITCTIGGIGGAAIGAGAGAAIGACAGGAITACIGIGGGAAACCICAIIACIIGACCCC 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232 CTAAAGAAGCTCAAGTCAGAGCATGGAAAGGTTCAATTGGGAAACATCACAGTTGATATG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TCCTCTAACCTTGACCTTCGTTCAGAGTTACAAGAACTGATTCCTGAACAACAGGAACGA 60
                   07-0CT-1996
                                                                                                                                                                                                                                                                                                                                   Submitted (23-JAN-1995) U. La Cognata, Institute fuer
Genbiologische Forschung, Berlin GmbH, Ihnestrasse 63, 14195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          412 GCAAAGCCTGGGGGAGAGCCCTTGCCTGAAGGTCTTCTCTGTCTTTTTAACAGGAAAG
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                     PLN
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                                                                                                                                                                                                                                                                                                                                                                                                                             /organism-"Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product-"citrate synthase"
/protein_id="CAA59008.1"
/db_xref="PID:e137432"
                 NTCITSYNH 1747 bp mRNA N. tabacum mRNA for citrate synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="PID:91556429"
/db_xref="G1:1556429"
/db_xref="SPTREMBL:024135"
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                                                                                                             citl gene; citrate synthase. common tobacco.
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Best Local Similarity 78.5%;
Matches 1021; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1081 TTAGAGCTTGGAAAGGTAAAGAATCCATGGCCTAATGTTGATGCTCATAGTGGAGTTTTG 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1309 ITGAACIAITAIGGIITAACIGAAGCAAGAIAITAIACGGICCICITIGGIGIAICAAGA 1368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1072 AAAGACTACGCTTGGAAAACATTGAAAAGTGGCAAGGTTGTCCCTGGTTTCGGACATGGA 1131
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241 GCAAGTGCTGGTGCAGAGCCATTGCCTGAAGGTCTTGTTTGGCTTTTTTAACCGGAAAG 300
                                                                                                                              301 GTTCCTAGCAAAGAGCAAGTAGATGCTCTATCAGCAGATTTACGAAAACGTGCTTCTATC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGATTCACAAATCAAAGTTATGGGAACCGACATATGAGGATTCCATGAGTTTGATTGCT 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       712 CAAGITCCACTIGTIGCIGCTIAIGITIAICGCAGGAIGIACAAGAACGGCAACACATA 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           541 CAAGTTCCTGTTGTTGCAGCTTATGTTTATCGGAGGATGTATAAGAATGGACAAGTAATA 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   661 CCTCAGATGCTTGAGCTGATGCGCCTTTATGTCACAATTCACAGTGATCATGAGGGTGGA 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                             421 TITIGCACTGGTGTTATGGCCTTACAGACTCGAAGCGAATTTCAGAAGGCATATGAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       892 AACGICAGIGCICACACACAGGICACIIGGIIGCIAGIGCIIIGICAGACCCIIACCICICC
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                                                                472 GIGCCAICAAAAGAGCAAGIGGAIICAIIGICICAGGAAIIGCGAAGICGIGCIACIGIC
                                                                                                                                                                                                                                                                                                                                               592 ITTGCTACTGGAGTCATGGCTCTTCAGGTTCAAAGTGAATTTCAAAAGGCATATGAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     772 CCTAAGGAIGACICACIGGAITAIGGIGCAAAITITGCICACAIGCTIGGIITCAGIAGC
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1084 GAGCTIGGAAAGGIAAAGAAICCAIGGCCIAAIGIIGAIGCICAIAGIGGAGIIIIIGCIG 1143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       424 TGCACTGGTGTTATGGCCTTACAGACTCGAAGCGAATTTCAGAAGGCATATGAGAAGGG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 GAGGGTAICCGGTTCAGGGGTTTTTCTATACCTGAATGCCAGAAACTTTTACCCGCTGCA 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        925 AGCATGCAAGAGCTTATGAGGCTTTACGTTACTATCCATACTGACCATGAAGGTGGAAAC 984
                                                                                                         AAGCCCGGTGGAGAACCATTGCCTGAGGGTCTGCTCTGGCTTCTTTTAACTGGAAAGGTA 564
                                                                                                                                                                        244 AGTGCTGGTGCAGAGCCATTGCCTGAAGGTCTTCTTTGGCTTCTTTTAACCGGAAAGGTT 303
                                                                                                                                                                                                                                             CCAACTAAAGAGCAAGTAGATGCATTGTCCGCAGAGTTGCGAAGTCGTGCTGCTGTAACA 624
                                                                                                                                                                                                                                                                                                               304 CCTAGCAAAGAGCAAGTAGATGCTCTATCAGCAGATTTACGAAAACGTGCTTCTATCCCA 363
                                                                                                                                                                                                                                                                                                                                                                                    GAGCATGTATACAAAACCATGGATGCGTTACCTGTTACAGCTCATCCAATGACTCAATTT 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 GACCATGTGTACAAAACAATTGATGCTCTACCTATTACGGCTCATCCAATGACTCAGTTT 423
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1 (Dases 1 to 1859)
1 Takita, E., Koyama, H., Shirano, Y., Shibata, D. and Hara, T.
Direct Submission
Submitted (26-AUG-1998) to the DDBJ/EMBL/GenBank databases. Eiji
Takita, Gifu University, Laboratory of Plant Cell Technology, Faculty of Agriculture; Yanagido 1-1, Gifu, Gifu 501-1193, Japan (E-mail:takitaecc.gifu-u.ac.jp, Tel:+81-58-293-2911,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Takita,E., Koyama,H., Shirano,Y., Shibata,D. and Hara,T. cDNA encoding carrot mitochondrial citrate synthase Published Only in DataBase (1998) In press Location/Qualifiers
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/protein_id="BAA32557.1"
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LLFLQNLAKLKPWPNVDAHSGVLLNYYĞLTEARYYTULFGVSRALĞICSQLIMDRALĞ
                                                                                                                                                                                                                                                                                                                                         Forschung, Berlin GmbH, Ihnestr. 63, 14195 Berlin, FRG 2 (bases 1 to 1891)
Landschutze, V., Muller-Rober, B. and Willmitzer, L.
Mitochondrial citrate synthase from potato: predominant expression in mature leaves and young flower buds
Planta 196 (4), 756-764 (1995)
                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Asteridae; Solananae; Solanales; Solanaceae; Solanum; Potatoe;
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Direct Submission
Submitted (20-SEP-1993) V. Landschuetze, Inst. fuer Genbiologische
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Pred. No. 0.00e+00;
0; Mismatches 261; Indels 12;
                                    S.tuberosum mRNA for mitochondrial citrate-synthase.
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9483509
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/protein_id="CAA52976.1"
/db_xref="PID:9483510"
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/clone_lib="leaf library"
/clone="5-25-10"
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1264 AAGAGTGTCACTATGGAATGGCTTGAAAA 1292
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/db_xref="taxon:4113"
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/EC_number="4.3.1.7"
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Best Local Similarity 78.5%;
Matches 997; Conservative
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443 AAGGTCTTCTCTGGCTTCTTTTAACAGGAAAGGTGCCATCAAAAGAGCAAGTGAATTCAA 502
                                                                                                                                                                               TTGTCTCAGGAATTGCAGAGTCGGGCATCATATCCCTGATCATCATGTATACAACTATTG 562
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/db_xref="PID:92300708"
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/db_xref="GI:2300708"
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LLFLGNLAKLKPWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALG
LPLERPKSVTMEWLENQCKKA"
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Mueller-Roeber, B., Landschuetze, V. and La, C.U.
PROCESSES FOR INHIBITING AND FOR INDUCING FLOWER FORMATION IN
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/EC_number="4.1.3.7"
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Other publication DE 4438821 960425
Other publication DE 4435366 960328
Other publication AU 267995 950925
Other publication DE 4408629 950914.
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A46545
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/db_xref="taxon:4113"
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983 TAGCCGGACCACTICATGGTTTAGCCAATCAGGAAGTTTTGCTATGGATAAAATCTGTTG 1042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1281 A-CCTTGGCCAAATGTTGATGCCCACAGTGGTGTTGTTGAACTATTATGGTTTAACTG 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1103 AICCAIGGCCIAAIGITGAIGCTCAIAGIGGAGITITGCIGAACCACIAIGGITIGACAG 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1340 AAGCAAGATATTATACGGTCCTCTTTGGCGTATCAAGAGCTCTTGGCATTTGCTCTCAGC 1399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       923 TAAAACAGTGGCAAGGTTGTACCTGGATTTGGTCTAGGAGTATTGCGGAAGACAGATCCAA 982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               803 GTGCAAATTTTGCTCACATGCTTGGTTTCAGTAGCTCTGAAATGCATGAACTTCTTATGA 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          863 GGCTCTATGTAACAATACACAGTGATCATGAAGGTGGTAATGTCAGTGCTCACACCGGTC 922
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443 AAGGTCTTCTCTGGCTTCTTTTAACAGGAAAGGTGCCATCAAAAGAGCAAGTGAATTCAA 502
                                                                              269 AAGGICITCITITGGCTICITITAACCGGAAAGGITCCIAGCAAAGAGCAAGIAGAIGCIC 328
                                                                                                                                                                                                                             563 AIGCCITACCAGICACAGCICAICCAAIGACCCAGITIGCIACTGGAGICAIGGCTCTIC
                                                                                                                                                                                                                                                                                                                                                                                                   GIGGAAAITICGCACACAIGIIGGGAITIGAIAGCCCICAGAIGCTIGAGCIG---AIGC
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                                                                                                                                                                     503 ITGICTCAGGAATIGCAGAGICGGCCAICATAICCCIGAICAICAIGIATACAACIATIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGTTCAAAGTGAATTTCAAAAGGCATACGAGAAAGGGATTCACAAATCAAAGTATTGGG
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/translation="MVFFRSVSAFTRLRSRVQGQSSLSNSVRWIQMQSSTDLDLKSQ
LQELIPEHKDRLKKLKSEHGKVQLGNITVDMVIGGMRGWTGLLWETSLLDPEEVFALG
DCRLPECQKALLPTAQSGGLNHYRRSFVASLNWKGTLAKSKLKHCRKTWNRAAVSDYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YNAIDALPSTAHPMTOFASGVMALQVOSEFQRAYENGIHKSKFWEPTYEDCLNLIARV
PVAAYYYRKNYKNGDSIPEDSMELDYCRANESHALGFDDERKEKELMEKEPSEPSTYHHEGG
NVSAHTGHLVOSALESPATALNOLAGPHGELANDEVLIANESPSTYHHEGG
NVSAHTGHLVOSALESPATALNOLAGPHGLANDEVLIANESPSTYHHEGG
OLKEYVWKTLNSGKVIPGYGHGVLRNTDPRYVCQREFALKHHPDDPLFCQCKLMKLAS
CLTELESEEPWPNVDAHSGYLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRELLLA
LEPRSYYTMDWLEAHCKRASA*

3 45 C 40 9 4 88 t
                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, euphyllophytes, Spermatophyta, Magnoliophyta; eudicotyledons; Rosidae, Capparales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                                                                        1 (bases 1 to 1680)
Unger.E.A., Hand,J.M., Cashmore,A.R. and Vasconcelos,A.C.
Isolation of a cDNA encoding mitochondrial citrate synthase from
Arabidopsis thaliana
                                     Arabidopsis thallana mRNA for mitochondrial citrate synthetase, X17528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 ACCTGGACCTGAAGTCGCAGCTGCAAGAGTTAATTCCGGAACACAAGGACCGTCTGAAGA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 AACTGAAGTCAGAACATGGGAAGGTCCAACTGGGAAACATCACTGTTGATATGGTTATTG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290 GIGGAAIGAGAGGGAIGACIGGAIIGCIIIIGGGAAACCICAIIGCIIIGACCCGGAAGAGG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 AGTGCTGGTG-CA-GAGCCATTGCCTGAAGGTCTTCTTTGGCTTCTTTTAACCGGAAAGG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    468 TACCITAGCAAAGAGCAAGTIGAAGCACIGICGAAAGACTIG-GAAC-CGIGCIGCIGIG 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350 -TATTCGCTTTAGGGGATTGTCGACTTCCTGAGTGCCAAAAGCCCTATTACCTACTGCC 408
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                             26-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 GCGGAATGAGGAATGACTGGTTTACTTTGGGAGACTTCCTTACTCGACCCAGAAGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Arabidopsis thaliana'
                                                                                                                                                                                                                                                                                                                                                                                                        Plant Mol. Biol. 13 (4), 411-418 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product_citrate synthetase"
/protein_id="CGAA35570_1"
/db_xref="plD:e1188578"
/db_xref="PlD:e2652924"
/db_xref="GI:2652924"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="SWISS-PROT:P20115"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:3762"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58. .1476
/EC_number="4.1.3.7"
                             mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                          1680 bp
                                                                                                                                                                                                     Arabidopsis thaliana
                                                                                                                     X17528.1 GI:11243
citrate synthase.
thale cress.
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945 ATTTGCAGCTGCATTAAATGGTTTAGCTGGGCCACTCCATGGTTTGGCTAATCAGGAAGT 1004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1065 GAAAGAATATGTTTGGAAAACATTAAACAGTGGCAAGGTTATTCCGGGATATGGTCACGG 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1125 TGTTCTGCGCAATACTGATCCAAGATATGTATGCCAAAGAGAATTTGCCTTGAAGCATCA 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        960 AGTATIGCGGAAGACAGATCCAAGATACACATGCCAAAGAGAATITGCGTIGAAGCACTT 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1185 TCCTGACGACCC-TCTTTTCCAGTGTTG-CAA-GCT-TATGAAGTTG-GCCTCCTGTCTC 1239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACT-GAGCTIG-AAAG-IGAAGAACCC-IGGCCAAAIGTIGATGCTCACAGIGGGGTCTT 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1296 GCTGAACCACTATGGTCTAACCGAAGCAAGGTACTACACCGTGCTCTTTGGTGTTTCAAG 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1200 GAGTCTTGGAATATGCTCACAGCTTATATGGGACCGAGCTCTTGGCTTGCCGCTAGAGAG 1259
                                                                                                                                                                                                                                                                                                                                                                            TTTGCTAGCGGTGTTATGGCCCTCCAGGTGCAAAGTGAGTTTCAAAAGGCATATGAGAAT 645
                                                                                                               421 TITIGCACIGGIGITATGGCCTIACAGACICGAAGCGAATITCAGAAGGCATATGAGAAA 480
                                                                                                                                                                GGAATTCATAAGTCAAAGTTCTGGGAGCCAACATATGAGGATTGCCTCAACCTGATTGCT 705
                                                                                                                                                                                                            481 GGGATCCATAAGTCAAAGTTTTGGGAGCCAACATATGAGGACTGCCTTAGTTTGATTGCT 540
                                                                                                                                                                                                                                                          CGTGTTCCTGTTGTAGCTGCATATGTTTATCGAAGGATGTATAAGAATGGTGATTCCATT 765
                                                                                                                                                                                                                                                                                                      541 CAAGITCCTGTIGTIGCAGCTIAIGITIAICGGAGGAGGATGTAAAGAATGGACAAGTAATA 600
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Submitted (06-FEB-1998) Molecular Cardiology Institute, 75 Raritan Avenue, Highland Park, NJ 08904, USA Location/Qualifiers
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                                                                                                                  614 TTAAAGACTATGTTTGGAAAACATTAAATAGCGGAAAGGTTGIICCTGGAIITGGTCAIG 673
                                                                                                                                                                                                                                                                                                                                                              674 GAGTICTACGCAAAACIGIACCAAGATATACAIGICAAAGGGAGIIIIGCAIIGAAGCAII 733
                                                 719 GAAAIGITAGIGCACACACACGCCATITGGIGGGIAGICCACITICAGAICCITAITIGI 778
                                                                                                                                                                                 554 ITCICCIITGGAICAAAICCGIGGIAGAAGAGIGIGGAGAGATAIAAACCACAGAACAA 613
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1 (bases 1 to 1401)
Goldenthal, M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cloning and sequence analysis of human citrate synthase cDNA Unpublished
                                                                                                                                                                                                                899 IGAAAGAITAIGITIGGAAGACACIAAACAGIGGCAAGGITGIACCIGGAITIGGICIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              794 ITACCCAGCTGGGCAAGGTTAAAAACCCATGGCCTAATGTTGATGCTCACAGTGGGGTGT
       434 GGAATGTCAGTGCTCATACTGGTCACCTGGTTGCTAGTGCACTTTCAGATCCTTATCTTT
                                                                                             494 CATTIGCAGCIGCATIGAAIGGITIAGCIGGGCCACICCAIGGCIIGGCAAAICAGGAAG
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Homo sapiens citrate synthase mRNA, complete cds.
AF047042
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/product="citrate synthase"
/protein_id="AAC25560.1"
/db_xref="PID:93288815"
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/db_xref="taxon:9606"
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Goldenthal, M.J.
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//db_xref="SPTERMIL:024259"
//translation="MPTKEQVGALSKELRDRALVHDYVFKAIDALPVTAHPMTQFATG
//translation="MPTKEQVGALSKELRDRALVHDYVFKAIDALPVTAHPMTQFATG
//wallQVQSEPQKAYEKGIHKGKYWEPTYEDSLSLIARVPTVASYIYRRIYKDGKVIPM
NDSLVIGGRESHMGFDSPEMOELMRLYPVTVHSDHEGGNVSAHTGHLVASALSDPYLS
FAAALNGLAGFLHGLANQEVLLWIKGVVPEGCENITTEQLKDYWFTLNSGKYVPGFG
HGVLRKTVPRYTCQREFALKHLPDDPLFQLVSKLYEVVPPVTTQLGKVKNPWPWNVDAH
SGVILNYYGLTEARYTVLFGVSRSIGICSQLIWDRALGLPERPKSVTMELLENHCK
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; eudicotyledons; Bosidae; Violales; Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae; Violales; Salicaceae; Populus.

1 (bases 1 to 1378)
La Cognata,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                    Submitted (23-JAN-1995) U. La Cognata, Institute fuer
Genbiologische Forschung, Berlin GmbH, Ihnestrasse 63, 14195
                                                                                                                                                                                                                                                                                                               /organism="Populus balsamifera subsp. trichocarpa X
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/transl_except=(pos:16. .18,aa:Met)
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/protein_id="CAA59009.1"
/db_xref="PID:-257638"
/db_xref="PID:-31648926"
/db_xref="GI:1648926"
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/note="hybrid"
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Direct Submission
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KLLPKAKGGEEPLPEGLFWLLVTGCIPTEEQVSWLSKEWAKRAALPSHVVTMLDNFPT
NLHPWSQLSAAVTALNSESNFAQAYARGISRTKYWELIYEDSVDLIAKLPCVAAKIYR
                                                                                                                                                                                                                                   LVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLVWLTQLQKEVGKDVSDEKLRDYIWN
TLNSGRVVPGYGHAVLRKTDPRYTCQREFALKHLPNDPMFKLVAQLYKIVPNVLLEQG
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                                                                                                                                                                                             NLYWEGSGIGAIDSNLDWSHNFTNMLGYTDHQFTELMRLYLTIHSDHEGGNVSAHTSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 GTGGTGGGCCAAATCACTGTGGACATGATGTATGGTGGCATGAGAGGCATGAAGGGATTG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 CAGCIGGGGAATAICAAIGIIGACAIGGIAIIGGGCGGAAIGAGGGAAIGACIGGIITA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 GIGTATGAAACAICAGTTCTTGAICCTGATGAGGGCATCCGTTTCCGAGGCTTTAGTAIC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 CCTGAATGCCAGAAACTTTTACCCGCTGCAAGTGCTGGTGCAGAGCCATTGCCTGAAGGT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     355 TTATTTTGGCTGCTGGTAACTGGATGTATCCCAACAGAGGAACAGGTATCTTGGCTCTCA 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274 CTTCTTTGGCTTCTTTTAACCGGAAAGGTTCCTAGCAAAGAGCAAGTAGATGCTCTATCA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415 AAAGAGTGGGCAAAGAGGCAGCTCTGCCTTCCCATGTGGTCACCATGCTGGACAACTTT 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334 GCAGATITACGAAAACGTGCTTCTATCCCAGACCATGTGTACAAAACAAITGAIGCTCTA 393
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0; Mismatches 448;
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Best Local Similarity 63.5%;
Matches 785; Conservative
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/translation="mallfaaarlegaknasclvlaarhasasstnlkdiladlipke
QariktfroohgntvvgQitvDmmyGGmRGMKGLvYftSvLDpDeGirFRGYSIPECO
KMLPKAKGGEEPLPEGLFWLLVTGQIPTEEQVSWLSKEWAKRAALPSHVVTMLDNFPT
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LVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLVWLTQLQKGKDVSDEKLRDYIWN
TLNSGRVVPGYGHAVLRKTDPRYTCQREFALKHLPHDPMFKLVAQLYKIVPNVLLEQG
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Evans, C.T., Owens, D.D., Sumegi, B., Kispal, G. and Srere, P.A.
Isolation, nucleotide sequence, and expression of a cDNA encoding
955 GTTGGCAAAGATGTGTCAGATGAGAAGTTACGAGACTACATCTGGAACACCACTCAACTCA 1014
                                                                                       1015 GGACGGGTTGTTCCAGGCTATGGCCATGCAGTACTAAGGAAGACTGATCCGCGATATACC 1074
                                                                                                                                                                                                       1051 AAGTIGTATGAAGTGGTGCCTCCTATTCTATTAGAGCTTGGAAAGGTAAAGAATCCATGG 1110
                                                                                                                                                                                                                                                                                                                                                             1195 CCCAATGTAGATGCTCACAGTGGGGGTGCTCCAGTATTATGGCATGACGGAGATGAAT 1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACTACACGGTCCTGTTTGGGGTGTCACGAGCATTGGGTGTACTGGCACAGCTCATCTGG 1314
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                                                                                                                                  931 GGCAAGGTTGTACCTGGATTTGGTCTAGGAGTATTGCGGAAGACAGATCCAAGATACACA
                                                                                                                                                                               1135 CAGCTGTACAAGATTGTGCCCAATGTCCTCTTAGAGCAGGGTAAAGCCAAGAATCCTTGG
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="citrate synthase precursor (EC 4.1.3.7)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="citrate synthase signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Porcine citrate synthase mRNA, complete cds. M21197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M21197.1 GI:164418
citrate synthase.
Porcine kidney, cDNA to mRNA, clone PCS4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1231 GACCGAGCTCTTGGCTTGCCGCTAGAGAGGCCAAAG 1266
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/db_xref="PID:g164419"
/db_xref="G1:164419"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pig citrate synthase
Biochemistry 27, 4680-4686 (1988)
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/note="citrate synthase"
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/db_xref-"taxon:9823"
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                                                                                                                                                                                                                                                                                                                                                                                                             338 ATTIACGAAAACGIGCIICIAICCCAGACCAIGIGIACAAAACAAIIGAIGCICIACCIA 397
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                                                       185 IGGCCAAAICACIGIGGACAIGAIGIAIGGIGGCAIGAGAGGCAIGAAGGGAIIGGIGI 244
                                                                                                                                   245 ATGAAACATCGGTTCTTGATCCTGATGAGGGCATCCGTTTCCGAGGCTACAGTATCCCTG 304
                                                                                                                                                                                                                AATGCCAGAAAATGCTGCCCAAGGCTAAGGGTGGGGAAGAACCGCTGCCAGAGGGCTTAT 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           665 TCTACCGGGAAGGCAGCAGTATTGGGGCCATTGATTCTAAACTGGACTGGTCCCACAATT 724
                    5; Gaps
                                                                                                                                                          1084 CAAAGAGAGTITGCICIGAAACACCIGCCICAIGACCCCAIGIITAAGCIGGIIGCICAG
                                                                                                                                                                                                                                                                                            TITGGCTGCTGGTAACTGGACAGATCCCAACAGAGGAGGAGGTGTCTTGGCTCTCAAAAG
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                  0; Mismatches 410; Indels
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                  758; Conservative
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/db_xref-"SWISS-PROT:P00890"
/translation-"WSALLSTTSKSFLSRGSTROCONMOKALFALLNARHYSSASEQT
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/clone="Plasmid pFCS1 (Suissa et al., EMBO J. 3, 1773-1781
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.

    (bases 1 to 1481)

1114 AATGTTGATGCTCATAGTGGAGTTTTGCTGAACCACTATGGTTTGACAGAAGCAAGATAC 1173
                                         1264 TACACAGTCCTGTTCGGGGTATCACGGGCACTGGGTGTATTAGCACAGCTCATCTGGAGC 1323
                                                                  SCWICISNA 1481 bp DNA PLN 17-FEB-1997
S.Cerevisiae mitochondrial citrate synthase gene, complete CDS.
223259
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Isolation of the nuclear yeast genes for citrate synthase and
fifteen other mitochondrial proteins by a new screening method
EMBO J. 3 (8), 1773-1781 (1984)
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Lindner,P. and Plueckthun,A.
The effect of point mutations in the hinge of yeast citrate
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Submitted (05-JUL-1993) Peter Lindner, Protein Engineering,
Max-Planck-Institut fuer, Biochemie, Am Klopferspitz 18a,
Martinsried, D-82152, Fed. Rep., Germany
4 (bases 1 to 1481)
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Thesis (1993) Protein Engineering, Max-Planck-Institut fuer
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/protein_id="CAA80781.1"
/db_xref="PID:9313750"
/db_xref="GI:313750"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            direct N-terminal protein sequencing"
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                                                                                                                              1324 CGAGCCTTAGGCTTCCCTCTAGAGGGCCCAAG 1356
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mitochondrial citrate synthase
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JOURNAL
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SKETIEKYLMDTLNAGRVVPGYGHAVLRKTDPRYTAGREFALKHFPDYELFKLVSTIY
EVAPGVLTKHGKTKNPWPNVDSHSGVLLQYYGLTEASFYTVLFGVARAIGVLPQLIID
RAVGAPIERPKSFSTEKYKELVKKIESKN"
GKLPVIASKIYRNVFKDGKITSTDPNADYGKNLAQLLGYENKDFIDLMRLYLTIHSDH
EGGNVSAHTTHLVGSALSSPYLSLAAGLNGLAGPLHGRANQEVLEWLFKLREEVKGDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 GGTATCCGGTTCAGGGGTTTTTCTATACCTGAATGCCAGAAACTTTTACCCGCTGCAAGT 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 215; DB 27; Length 1481;
Pred. No. 2.56e-85;
0; Mismatches 462; Indels 0;
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/translation="MSAILSTTSKSFLSRGSTRQCQNMQKALFALLNARHYSSASEQT
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LGKLPVIASKIYRNVFKDGKITSTDPNADYGKNLAQLLGYENKDFIDLMRLYLTIHSD
HEGGNVSAHTTHLVGSALSSPYLSLAAGLNGLAGPLHGRANQEVLEWLFKLREEVKGD
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                                                                                                                                                                                                                                                                                      967 CGGAAGACAGATCCAAGATACACATGCCAAAGAGAATTTGCGTTGAAGACACTTGCCTGAT 1026
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                                                                                                                                                    1024 TACTTGTGGGATACTTTGAACGCAGGGAGAGTTGTTCCTGGTTATGGCCATGCGGTTTTG 1083
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Isolation of the nuclear yeast genes for citrate synthase and
fifteen other mitochondrial proteins by a new screening method
EMBO J 3 (8), 1773-1781 (1984)
787 GCAGCATTAAATGGTTTGGCTGGGCCACTCCATGGATTAGCCAACCAGGAAGTCCTGCTG 846
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                                                                                                  847 IGGATTAAATCAGTIGTIGATGAATGTGGAGAGAACATCTCGACAGAGCAGTTGAAAGAT
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/db_xref="taxon:4932"
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/db_xref="PID:93603"
/db_xref="GI:3603"
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13.9%; Score 215; DB 27; Length 2427;

Query Match

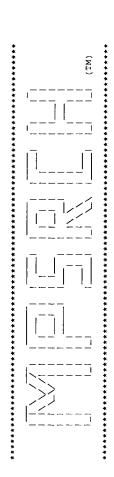
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AUTHORS
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Best Local Similarity 59.4%; Pred. No. 2.56e-85;
Matches 677; Conservative 0; Mismatches 462;
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EHVIQLLDSLPKDLHPMAQFSIAVTALESESKFAKAYAQGVSKKEYWSYTFEDSLDLL
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EGGNVSAHTTHLVGSALSSPYLSLAAGLNGLAGPLHGRANQEVLEWLFKLREEVKGDY
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RAVGAPIERPKSFSTEKYKELVKKIESKN"
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                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Fungi, Ascomycota, Hemiascomycetes; Saccharomycetales; Saccharomyceaceae; Saccharomyces.

1 (bases 1 to 4391)
Aert, R., Verhasselt, P., Voet, M. and Volckaert, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (29-APR-1996) Data collected by MIPS on behalf of the European yeast chromosome XIV sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152 Martinsried, FRG, E-mail: Mewes@mips.embnet.org
1702 GGIGTGTTACCCCCAATTAATCATCGATAGGGCTGTTGGTGCTCCAATCGAAAGGCCCAAA 1760
                                                                                                     1207 GGAATATGCTCACAGCTTATATGGCACCGAGCTCTTGGCTTGCCGCTAGAGAGGCCCAAA 1265
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                                                                                                                                                                                                             11-AUG-1997
                                                                                                                                                                                                                                 S.cerevisiae chromosome XIV reading frame ORF YNR001c. 271616 Y13139
91302468
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/gene="tP(AGG)NR - systematic name"
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complement(3382, 3497)
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235. .259
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3983, .4056
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1064 TITGGCCTTTCGATTGGAGCACCAACAGCCCTATCGATGATTAATTGGGGTAACACCA 1123 1205 AGACTCCTTGATACCCCAAACAAAAACCGTATAGTATCTTGCTTCTGTCAAACCATAGTGG 1146 TGCAATAAAACACCGGAATGTGAATCAACATTTGGCCATGGGTTCTTAGTTTTACCATGC 1243 1964 TCTGGAATTTCTGATCTGGCAGCTAAATCAGCAGAAAGGGCTTTAACTTGAGCGTCAGTA 2023 1265 TTTGGCCTCTCTAGCGGCAAGCCAAGAGCTCGGTCCCATATAAGCTGTGAGCATATTCCA 1206 1124 ATAGCTCTGGCAACACAAACAATACAGTGTAGAACGAAGCCTCAGTTAGACCATAGTAT 1183 TTAGTTAAAACCCCTGGGGCAACTTCATAAATGGTGGAGACCAACTTAAATAACTCGTAA 1303 TCTGGGAAATGTTTCAATGCGAATTCACGTTGAGCCGTATAACGAGGATCAGTTTTTCTC 1363 AAAACCGCATGGCCATAACCAGGAACAACTCTCCCTGCGTTCAAAGTATCCCACAAGTAC 1423 TITICAATIGITICTITIGAATAGICACCITICACTICTICTCTCAATITAAATAGCCAT 1483 1484 TCTAAAACTTCTTGATTGGCACGACCATGTAATGGGCCAGCTAAACCATTCAAACCAGG 1543 GCCAAAGATAAGTATGGCGAAGATAAGGCAGAACCCACTAAATGTGTATGGGCAGAA 1603 ACGITACCACCTICATGATCAGAATGAATAGTTAAATATAGTCTCATTAAGTCAATAAAA 1663 1664 TCCTTGTTTTCGTAGCCCAAAAGTTGGGCCAAATTTTTACCATAGTCAGCATTAGGATCG 1723 1724 GTTGAAGTAATTTTACCATCCTTGAACACATTACGATAAATTTTGGAAGCAATAACAGGT 1783 1844 ACACCTIGAGCATAIGCTIIGGCAAACIIAGACICGCIIICIAAAGCAGICACGGCAAIA 1903 1904 GAAAATTGGGCCATTGGATGTAGATCTTTTGGGAGGCTATCTAAAAGTTGGATAACGTGC 1963 605 AGGGGTATTACTTGTTCTTATACATCCTCCGATAAACATAAGCTGCAACAACAGGA 546 AATACTCCTAGACCAAATCCAGGTACAACCTTGCCACTGTTTAGTGTCTTCCAAACATAA 906 905 TCTTTCAACTGCTCTGTGGAGATGTTCTCTCCACATTCATCAACAACTGATTAATCCAC 846 785 GCAAATGACAAATAAGGATCTGAAAGTGGACTACCCACCAAATGGCCAGTGTGTGCACTA 726 725 ACATITICCACCCICATGATCACIGIGAATIGIGACATAAAGGCGCATCAGCTCAAGCATC 666 485 ATCCCTTTCTCATATGCCTTCTGAAATTCGCTTCGAGTCTGTAAGGCCATAACACCAGTG 426 425 CAAAACTGAGTCATTGGATGAGCCGTAATAGGTAGAGCATCAATTGTTTTTTTACACATGG 366 Gaps 1085 TCTAATAGAATAGGAGGCACCACTTCATACAACTTTGACAACCAATTGAAAAAATGGGTCA 545 ACTIGAGCATCAACTAAGGCAGTCCTCATATGTTGGCTCCCAAAACTTTGACTTATGG Score 215; DB 27; Length 4391; Pred. No. 2.56e-85; 0; Mismatches 462; Indels 0; Query Match 13.9%; Best Local Similarity 59.4%; Matches 677; Conservative 965 1244 1025 1364 1184 1544 1604 1304 1424 a Cp q Cp qq  $^{\text{Cp}}$ qq Cp qq  $^{\rm Cp}$ qq Cp Q Cp qq  $^{\rm Cp}$ qq ζb qq Cp Ωp Cp ΩD  $^{\rm Cp}$ qq Sp g Сp

Search completed: Sat Oct 23 18:29:06 1999 Job time : 2834 secs.



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n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch\_nn Sat Oct 23 19:14:04 1999; MasPar time 351.57 Seconds 945.291 Million cell updates/sec Run on.

Tabular output not generated.

>US-08-702-718-3 (1-1551) from US08702718.seq 1551 Title:

1 TCCTCTAACCTTGACCTTCG... Description: Perfect Score: N.A. Sequence:

.....AAAAAAAAAAAAAAAAA 1551 AGGAGATTGGAACTGGAAGC

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 Nmatch STD 271905 segs, 107135622 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

| j.part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part29 20:part20 21:part21 22:part22 22:part23 24:part24 25:part25 26:part26 27:part27 28:part23 29:part29 30:part36 30:part36 37:part37 38:part38 39:part39 40:part40 41:part41 42:part42 43:part48 44:part44 45:part45 46:part46 47:part47 48:part48 49:part46 50:part56 51:part51 52:part52 53:part53 54:part59 60:part56 65:part56 67:part57 58:part58 n-geneseq35

Mean 9.510; Variance 7.769; scale 1.224 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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tesult		Query					
NO NO	Score	Match	e Match Length DB ID	DB	ID	Description	Pred. No.
	1551	100.0	1551	16	T04200	Sugar beet citrate sv	0.306+00
7	726	46.8	1747 16	16	T04201	Tobacco citrate synth	0.00e+00
m	664	42.8		17	T03410	Potato citrate syntha	0.00+00
4	664	42.8		16	T04199	Potato citrate syntha	0.00e+00
Ŋ	4.2	2.7		П	N81164	Base substituted E.co	3.09e-06
9	42	2.7		П	N81164	Base substituted E.co	3.09e-06
7	39	2.5		9	051746	Oligonucleotide probe	5.63e-05
<b>6</b> 0	38	2.5		6	051746	Oligonucleotide probe	1.46e-04
6	35	2.3	1077 4	46	V39085	Human tumour necrosis	2.46e-03

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## ALIGNMENTS

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DNA encoding plant citrate synthase - used to regulate flower formation, to improve storage of tubers, etc. and to reduce sprouting claim 6; Page 57-60; Brpp. English.

Claim 6; Page 57-60; Brpp. English.

To identify a cDNA from sugar bet which codes for citrate synthase, a cDNA bank of leaf tissue from sugar beet was prepd. Plaques of this cDNA bank were screened using radioactive DNA probes which comprise a mixture of Solanum tuberosum citrate synthase cDNA (T04199) and Nicotian tabacum citrate synthase cDNA (see T04201). One of the clones was sequenced. The nt. sequence is given in T04200.
                                                                                                                                                                               14-SEP-1995.
07-WAR-1995. E00859.
09-WAR-1994. DE-408629.
22-SEP-1994; DE-438366.
19-OCT-1994; DE-438831.
6AGED ) HOECHST-SCHERING AGREVO GMBH.
La Cognata U, Landschutze V, Muller-rober B, Landschuetze V; Mueller-roeber B;
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                                          25-JAN-1996 (first entry)
Sugar beet citrate synthase CDNA.
Citrate synthase; flower formation; ss.
Beta vulgaris strain Zuchtlinie 5S 0026
Key
Location/Qualifiers
cds
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                 T04200 standard; cDNA to mRNA; 1551 BP
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                                                                                                      1 teetetaaeeettgaeettegtteagagttaeaagaaetgatteetgaaeaagaaega 50
                                                                                                                                                    1 TCCICTAACCTIGACCTTCGTTCAGAGTTACAAGAACTGATTCCTGAACAACAGGAACGA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                181 GAAGAGGTATCCGGTTCAGGGGTTTTTCTATACCTGAATGCCAGAAACTTTTACCCGCT
Score 1551; DB 16; Length 1551;
Pred. No. 0.00e+00;
0; Mismatches 0; Indels 0;
  Ouery Match 100.0%;
Best Local Similarity 100.0%;
Matches 1551; Conservative
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used to regulate flower formation,
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                                                        1081 ttagagcttggaaaggtaaagaatccatggcctaatgttgatgctcatagtggagttttg 1140
                                                                                               1081 ITAGAGCITGGAAAGGTAAAGAATCCATGGCCTAATGTTGATGCTCATAGTGGAGTTTTG 1140
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                                                                                                                                                                                                                                                                                               ccaaagagtgtcactatggaatggcttgaaagttttgtaaaagaagagataacataacattga 1320
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Landschutze V, Muller-rober B, Landschuetze V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding plant citrate synthase - used to regulate flower f to improve storage of tubers, etc. and to reduce sprouting Claim ?. Page 60-63; BPpp. English:

To identify a cDNA from tobacco which codes for citrate synthase, a cDNA bank were screened using a radioactive DNA place of this cDNA bank were screened using a radioactive DNA probe which comprises Solamum tuberosum citrate synthase CDNA (T04199). One of the clones was sequenced. The nt. sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1747,
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46.8%, Score 726; DB 16,
Best Local Similarity 78.5%; Pred. No. 0.00e+00;
Matches 1021; Conservative 0; Mismatches 277
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T04201 standard; cDNA to mRNA; 1747 BP.
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Citrate synthase; flower formation; ss.
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19-OCT-1994; DE-438821.
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07-MAR-1995; E00859.
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                    1 TCCTCTAACCTTGACCTTCGTTCAGAGTTACAAGAACTGATTCCTGAACAACAGGAACGA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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P-PSDB; R86383.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potato citrate synthase gene.
Citrate synthase: inhibitor; increased storage capacity: potato;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 42.8%; Score 664; DB 17; Length 1891; Best Local Similarity 78.5%; Pred. No. 0.00e+00; Matches 997; Conservative 0; Mismatches 261; Indels 12;
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(AGRE ) HOECHST-SCHERING AGREVO GMBH.
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T03410 standard; cDNA; 1891 BP.
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443 aaggtettetetggettettttaacaggaaaggtgecatcaaaagagcaagtgaatteaa 502
                                          269 AAGGICTITITIGGCTICITITAACCGGAAAGGTICCIAGCAAAGAGCAAGIAGAIGGIC 328
                                                                                                                               329 TATCAGCAG-ATTTACGAAAACGTGCTTC-TATCCCAGACCATG-TGTACAAAACAATTG 385
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                                                                                       503 ttgtctcaggaattgcagagtcgggcatcatatccctgatcatcatgtatacaactattg
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DNA encoding plant citrate synthase - used to regulate flower formation, to improve storage of tubers, etc. and to reduce sprouting to improve storage of tubers, etc. and to reduce sprouting to improve storage of tubers, etc. and to reduce sprouting of an expensive spring in a cDNA from potato which codes for citrate synthase, a cDNA fragment of citrate synthase from Arabidopsis thaliana was firstly amplified using A.thaliana cDNA and oligos T04.02 and T04.03 which are complementary to the 5 or 3 'end of the coding region of A. thaliana cDNA for citrate synthase. The oligos additionally introduce BamHI cleavage sites at both ends of the amplified cDNA fragment. a cDNA library was prepd. from potato leaves and screened with A. thaliana citrate synthase cDNA. Positive clones were purified and sequenced. The nt sequence is given in T04199. Sequence 1891 BP; 512 A; 370 C; 425 G; 584 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 664; DB 16; Length 1891;
Pred. No. 0.00e+00;
                                                                                                         Potato citrate synthase cDNA.
Citrate synthase; flower formation; tuber storage;
Solanum tuberosum.
                                                                                                                                                                                                                                                                                                                                                                               La Cognata U, Landschutze V, Muller-rober B, Mueller-roeber B;
                                                                                                                                                                                                                                                                               07-WAR-1995; E00859.
09-WAR-1994; DE-408629.
22-EEP-1994; DE-435366.
19-CCT-1994; DE-438821.
(AGRE ) HOECHST-SCHERING AGREVO GMBH.
LT 4
104199 standard; cDNA to mRNA; 1891
104199;
                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.8%;
Local Similarity 78.5%;
hes 997; Conservative
                                                                                  25-JAN-1996 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 95-328278/42.
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                                                                                                                                                                                                                                                                 14-SEP-1995.
07-MAR-1995;
                                                                                                                                                                                                                                          W09524487-A
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1043 tagaagaatgtgggggagaacatttccaaagagcagttgaaagactatgtttggaaaacat 1102
                                                                                                                                                                                                                                                                                                                                                                                         1103 tgaacagtggcaaggttgtccctggttttggacatggagttctgcgaaagactgtaccaa 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1163 gatatacatgccagagagttcgctatgaagcatttgcctgaagatccactgtttcaac 1222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1223 tggtttcaaaaactctacgaagtttt-cctcctgttcttacagaacttggcaaagttaa-a 1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1281 a-cettggccaaatgttgatgcccacagtggtgtgttgttgaactattatggtttaactg 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1340 aagcaagatattatacggtcctctttggcgtatcaagagctcttggcatttgctctcagc 1399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               983 GATACACATGCCAAAGAGAATTTGCGTTGAAGCACTTGCCTGATGACCCATTTTTCAAT 1042
                                                                                       803 gtgcaaattttgctcacatgcttggtttcagtagctctgaaatgcatgaacttcttatga 862
                                                                                                     863 ITGATGAATGTGGAGAGACATCTCGACAGAGCAGTTGAAAGATTATGTTTGGAAGACAC 922
                                                                                                                                                                                                                                                                                                                                                                                                                     923 TAAACAGTGGCAAGGTTGTACCTGGATTTGGTCTAGGAGTATTGCGGAAGACAGATCCAA 982
                             743 tttatcgcaggatgtacaagaatggtgacactatacctaaggatgaatccctggattatg 802
                                             ggototatgtaacaatacacagtgatcatgaaggtggtaatgtcagtgotcacaccggtc 922
                                                                                                                                                                             923 acttggttgctagtgctttgtctgatccttacctctcctttgctgctgctttgaatggtt 982
506 AGCCAACATATGAGGACTGCCTTAGTTTGATTGCTCAAGTTCCTGTTGTTGCAGCTTATG 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-Nov-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
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187..204
/*tag= b
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-APR-1987; US-034819.
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30-MAR-1988; 105163.
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Random point mutations were introduced into the alpha fragment of Random point mutations were introduced into the alpha fragment of E.coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The reverse transcriptase. Nucleotides are unsincorporated by the transcriptase and the molecules are completed to forms that can be manifited and then expressed in a suitable host-vector system.

The sequence covers all 176 difft base substitutions, most of which cocurred singularly in any given mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 ycdchygccgymrttthhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddh 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 778 ICATITGCAGCAGCAITA-AAIGGIITGGCIGGGCCACTCCAIGGAITAGCCAACCAGGA 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lehtovaara P, Knowles J, Kolvula A, BamIoru J, Kellingling L. 188-279927/40.
Introducing random point mutations into nucleic acods by prepn of single stranded template, annealing a primer, elongation, misincorporation, completion of molecules and screening.
                                          Introducing random point mutations into nucleic acods - by prepn of single stranded template, annealing a primer, elongation, misincorporation, completion of molecules and screening.
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Random point mutations were introduced into the alpha fragment of E.coli beta galactosidase. The wild type sequence was obtained as a Single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are mishncorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system.

The sequence covers all 176 difft base substitutions, most of which
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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08-NoV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
                                                                                                                                                                                                                                                                                                                                                                    11 T; 108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 yvybbbvynvhnhnnenecebnnhvehnvhbnnhrnwayvrhdarrddvheeveh 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               837 AGTCCTGCTGTGCATTAAATCAGTTGTTGATGAATGTGGAGAACATCTCGACA 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen WPI; 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 1; Length 204; Pred. No. 3.09e-06;
                                                                                                                                                                                                                                                                                                                                                                                                          Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  60; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 C; 17 G; 11 T;
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//function=multiple cloning site
187.204
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                    Score 42; DB 1; L
Pred. No. 3.09e-06;
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See also P80575.
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                                                                                                                                                                                                                                                                                                                                                                      47 C;
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N81164 standard; DNA; 204 BP
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10.1%;
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.7%;
Best Local Similarity 12.2%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                  204 BP; 21 A;
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30-MAR-1988, 105163.
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Best Local Similarity
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Matches

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Synthetic.

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samples

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Gaps

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Thuman tumour necrosis factor receptors 6-alpha and 6-beta - used in the diagnosis of immune system-related disorder(s)

Disclosure; Fig 1; 91pp; English.

The diagnosis of immune system related disorder(s)

Disclosure; Fig 1; 91pp; English.

The invention also provides

The present sequence represents the human tumour necrosis factor

receptor-6 alpha (TNRR-6 alpha) cDNA. The invention also provides

for the TNRR-6 beta cDNA (V39086). TNRR-6 alpha and TNRR-6 beta are

members of the tumour necrosis factor receptor (TNRR) family. TNRRs

are expressed in endothelial cells, keratinocytes, normal prostate and

particularly of the immune system, substantially altered (whether increased or decreased) levels of TNRR-6 alpha and/or TNRR-6 beta gene expression can be detected, therefore the TNRR-6 alpha and TNRR-6 beta collapsed in the diagnosis of such disorders. Mutations of the TNRR-6 alpha and TNRR-6 beta genes can also be detected. The TNRR polypeptides are claimed to be useful for identifying ligands which may be useful in the treatment of apoptosis related disorders.
                                                                                                                                                                                                                                                                  Human tumour necrosis factor receptor-6 alpha cDNA.

Human tumour necrosis factor receptor-6 alpha; TNFR-6 beta;

Human tumour necrosis factor receptor-6 alpha; TNFR-6 beta;

Endothalial cells; keratinocytes; normal prostate; apoptosis;

Prostate tumour tissue; ss.

Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V07654,

02-DEC-1998 (first entry)

Nucleotide sequence of tumour necrosis related receptor (TR4).

Human: tumour necrosis related receptor; TR4; agonist; antagonist;

inhibition; chronic; acute; inflammation; arthritis; septicaemia;

autoimmune disease; transplant rejection; stroke; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.3%; Score 35; DB 46; Length 1077; Best Local Similarity 94.9%; Pred. No. 2.46e-03; Matches 37; Conservative 0; Mismatches 2; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 T;
                        Indels
                                                                                                                   268 CAGGCAATGGCTCTGCACCAGCACTTGCAGCGGGTAAAAGTTTCTGGC 221
                                                                       13 vhsyyvvhvvshhhsvhhvvhhvhvsvvvhhvvhvvhhvhyhvyvsv 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       326 G;
  Pred. No. 1.46e-04;
43; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/product= "INFR-6 alpha protein"
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111..1013
                                                                                                                                                                                      T 9
V39085 standard; cDNA; 1077 BP.
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Ebner R, Feng P, Gentz RL, Ni
WPI; 98-399142/34.
Best Local Similarity 0.0%;
Matches 0; Conservative
                                                                                                                                                                                                                                                             (first entry)
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115..924
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13-JAN-1998; UO0153.
14-JAN-1997; US-0354
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                                                                                                                                                                                                                                                             26-0CT-1998
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                                              92 hhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynvhnhnnc 151
                                                                                      843 CAGGACTICCIGGIIGGCIAAICCAIGGAGIGGCCCAGCCAAACCAIIIAAIGCIGCIGC 784
1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonuclectide probe MK14-A consists of nucleotides 5-95 of MK14 (Q51735). It hybridized to all spp. of mycobacteria tested, but cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Sequence 91 BP: 5 A: 17 C: 15 G: 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14 (Q51735). It hybridized to all spp. of mycobacteria tested, but cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New oligo:nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New oligo:nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in
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                                                                                                                                                                                                                                                                                                                           31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
56; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
2.5%; Score 39; DB 9; Length 91;
Best Local Similarity 0.0%; Pred. No. 5.63e-05;
Matches 0; Conservative 41; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286 CITITAACCGGAAAGGIICCIAGCAAAGAGCAAGIAGAIGCIC 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 vhsyyvvhvvshhhsvhhvvhhvhhvshvvhhvvhhvhyh 55
                                                                                                                                          152 ncccbnnhvchnvhbnnhrnwayvrhdarrddvhccvch 190
                                                                                                                                                                                      783 AAAIGACAAAIAAGGAICIGAA-AGIGGACIACCCACCA 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 14; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                          Q51746 standard; cDNA; 91 BP. Q51746;
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 14; 23pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAY-1992; US-889651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP-571911-A.
01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spears PA;
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WPI; 93-378844/48.
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24-MAY-1993; 108325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shank DD, Spears
WPI; 93-378844/48.
10;
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Gaps

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Synthetic.

SS.

051746;

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Query Match

samples

ID DE PAC DE PAC

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identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain bisclosure; page 35: 255pp; Brailsh.

Disclosure; page 35: 255pp; Brailsh.

O70468 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)11/TGC)(NNB)6Z(NNB)7(TGC)(NNB)10Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68.

Other specific peptides generated by these generic sequences are shown in R65151-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions — a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or blologically active.They may further comprise a linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                        and prevent e.g. inflammation, arthritis, septicaemia, autoimmune diseases, transplant rejection, infection, stroke, ischaemia, ARDS, restenosis, AIDS, bone disorders and cancer.

Claim 3: Fig 1: 21pp: English.

This is the nucleotide sequence of the human tumour necrosis related receptor (TR4), used in the method of the invention. The TR4 protein or its agonist can be used to treat a subject in need of enhanced TR4 polypeptide activity. The antagonist is used to inhibit TR4 polypeptide activity. The active agents can be used for the treatment and prevention of diseases such as chronic and acute inflammation, arthritis, septicaemia, autoimmune diseases, transplant rejection, stroke, cancer, Alzheimer's disease.

Sequence 1164 BP: 206 A; 396 C; 355 G; 207 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                         New DNA encoding tumour necrosis related receptor - used to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/note= "this sequence represents 'Z'; Z can be a
sequence of 6, 9 or 12 nucleotides (see
comments)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 2.3%; Score 35; DB 49; Length 1164;
Local Similarity 94.9%; Pred. No. 2.46e-03;
Nes 37; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1116 ataaagctttttcataaaaaaaaaaaaaaaaaaaaa 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1513 ATAAAGAGTTTTCATAAAAAAAAAAAAAAAAAAAAAA 1551
                 /product= "human TR4"
                                                                                                                                           Emery J, Tan KB, Truneh A, Young PR; WPI; 98-508248/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                   04-FEB-1997; US-794796.
(SMIK ) SMITHKLINE BEECHAM CORP.
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Q70468 standard; DNA; 114 BP.
Q70468;
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31-JAN-1994; US-189331.
(UINC-) UNIV NORTH CAROLINA.
FOWLKES DM. KAY BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-1995 (first entry)
                                              20-JAN-1998, 20-JAN-1998, 20-JAN-1998, IS-794796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994; U00977.
01-FEB-1993; US-013416.
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                                                                                                                                                               WPI; 98-508248,
P-PSDB; W66102.
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resols notifying proteins or peptide(s) which bind a ligand - by
remaining a recombinant vector library expressing fusion proteins
comprising a bluding domain and an effector domain
bisclosure; Page 35; 255pp; English.

070465 is a generic DNA sequence used to generate random TSAR (Totally
Synthetic Affinity Respents) peptides. This generic formula can also be
represented as follows: X(NNB)6(TGC)(NNB)12(NNB)14(TGC)(NNB)3Y. X
and Y are flanking restriction sites (X is not the same as Y) that are
not specified further. Other generic sequences are shown in R5151-54. TSARs are concatenated by these generic sequences are shown in
R65151-54. TSARs are concatenated heterofunctional proteins or peptides,
comprising at least two functional regions - a binding domain with
R65151-54 and a second effector peptide portion that is
chemically or biologically active. They may further comprise a linker
peptide between the 2 domains. The oligonuclectides are also designed so
that the expressed peptide contains 2 or 4 cysteine residues positioned
in, or flanking, the unpredicted or variant residues positioned
in, or flanking, the unpredicted or variant residues. These residues
confer some degree of conformational rigidity to the peptides. The TSARs
or comprising a TSAR binding domain can be used in vivo to
deliver a chemically or biologically active moiety, eg. metal ion,
radioisctope, peptide, toxin or enzyme, to the specific target or on the
                  that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compsns. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.
                                                                                                                                                                                                                                                                                                                                                                                                 0
peptide between the 2 domains. The oligonucleotides are also designed so
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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/note= "this sequence represents '2'; 2 can be
sequence of 6, 9 or 12 nucleotides (see
comments)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 bnnbnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnbnnb 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              352 CACGITITCGIAAAICIGCIGAIAGAGCAICIACTIGCICITIGCIAGGAAC 301
                                                                                                                                                                                                                                                                                                                                                2.1%; Score 32; DB 12; Length 114; 3.6%; Pred. No. 3.84e-02;
                                                                                                                                                                                                                                                                                                                                                                                            76; Indels
                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 3.84e-02;
32; Mismatches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
55..60
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Q70465 standard; DNA; 114 BP.
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNO-) UNIV NORTH CAROLINA.
FOWLKES DM, KAY BK;
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P-PSDB; R65150 and R65151.
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                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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P-PSDB; W01604.
Nucleic acids encoding STZ and STO polypeptide(s) which confer salt tolerance - useful for producing transgenic plants or other organisms, e.g. yeast, able to grow under saline conditions Claim 1; Page 22; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-220.,
Arabidopsis STZ polypeptide cDNA.
STZ; STO; salt tolerance; transgenic plant; yeast; ss.
Arabidopsis thallana.
Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAY-1996; U08095.
06-JUN-1995; US-471717.
(REGC) UNIV CALIFORNIA.
GASSER CS, Lippuner V;
WPI; 97-042725/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Citalm 3.7 Fage //: Supple Lugitary in the method of the nucleotide sequence of the clone CH377], used in the method of the invention involving secreted proteins from human cells potentially useful as immuno-modulators, anti-tumour agents, itssue growth promoters, haemostatic and thrombolytic agents. It was isolated from an adult human testes cDNA library. They may be used to express the recombinant protein, as tissue/molecular weight markers, for chromosome identification, to identify possible genetic disorders and isolate new related DNA, as sources of primers for PCR, to generate anti-protein or anti-DNA antibodies, or in interaction trap assays to identify sequences that encode interacting proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSRs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
                                                                                                                                                                                                                                                                                                                                                12-0c1-1998 (first entry)
Nucleotide sequence of the CH377_1 clone.
Clone CH377_1; secreted protein; human cell; immuno-modulator; PCR;
anti-tumour agent; tissue growth promoter; haemostatic agent; primer;
thrombolytic agent; molecular weight marker; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 ttctcctagtcaatatctttagtgatyttytttaataaacatgraagcaagraaaaaaa 480
                                                                                                                                                                                          148 CAGTCATTCCTCTCATTCCGCCCAATACCATGTCAACATTGATATTCCCCAGCTGGAAAC 89
                                                                                                                                                                     3 bunbanbanbanbanbtgcanbanbanbanbanbanbanbanbanbanbanbanana 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 46; Length 525;
Pred. No. 1.55e-02;
4; Mismatches 25; Indels 0; Gaps
                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding secreted protein from human cells -potentially useful, e.g. as immuno-modulators, anti-tumour agents, promoters of tissue growth, haemostatic and thrombolytic agents claim 37; page 77; 98pp; English.
                                                                                                                                                                                                                                88 ITCCAAATICTTTCTTTATCTTCAGTCGTTCCTGTTGTTCAGGAATCAG 37
                                                                                                           Length 114;
                                                                                                                       Pred. No. 3.84e-02;
32; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D, Racie LA, Spaulding V, Treacy M; WPI: 98-297936/26.
                                                                                                            DB 12;
                                                                                                            Score 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1529 AAAAAAAAAAAAAAAAAAA 1551
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                                                                                                                                                                                                                                                                                                                     V41453 standard; cDNA; 525 BP.
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                                                                                                         2.1%;
Similarity 3.6%;
4; Conservative
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Local Similarity 65.1%;
Les 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-NOV-1997; U20740.
13-NOV-1997; US-969515.
15-NOV-1996; US-749745.
02-JUN-1997; US-867678.
                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9821332-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                            antibody; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAY-1998.
                                                                                                            Query Match
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New nucleic acid encoding gamma subunits of human G protein - used to detect mutation(s) in, or altered levels of, the subunits and to screen for agonists and antagonists of G protein interaction Claim 1; Page 29; 40pp; Enclish.

Claim 1; Page 29; 40pp; Enclish.

CDNA clones (T47669-75) respectively code for human G protein agamma-2, gamma-3, gamma-4, gamma-5, gamma-7, gamma-11 and gamma-11 subunits (W09412-18). Several human CDNA libraries were partially sequenced to identify expressed sequence tags (EST). By matching sequences of EST to genes of known structure, the 7 new subunit sequences were laolated. The cDNA clone for gamma-11 has been deposited as ATCC 97139. The isolated cDNA clones can be used to produce recombinant gamma subunits in prokaryotic or eukaryotic and the constant of the propertic and diagnostic and account of the constant of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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19-WAY-1997 (first entry)
Human G protein gamma-11 subunit cDNA.
G protein; signal transduction; agonist; antagonist; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 2.1%; Score 32; DB 29; Length 654; Best Local Similarity 76.7%; Pred. No. 3.84e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 T;
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                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
(SMIK ) SMITHKLINE BEECHAM CORP.
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330..654
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607..612
/*tag= d
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108..329
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22-MAY-1995; WO-U064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; W09418
                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                             therapy; ss.
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US-08-702-718-3.rng

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CC (W01604) and TSB281 and TSB282) respectively code for the STZ (W01604) and STO (W01605) polypeptides of Arabidopsis thaliana. CC They were isolated by using clones of an A. thaliana cDNA library CC to transform yeast strains that lacked active calcineurin proteins (i.e. they were more sensitive to growth inhibition by CC salt than wild-type strains). Clones that complemented the salt cC salt the ability to confer salt tolerance analysis. STZ and CT have the ability to confer salt tolerance to plants, yeast, CC fungi and other organisms. Recombinant expression cassettes incorporating the STZ or STO sequence can be used to produce CC transgenic plants able to grow under saline conditions.
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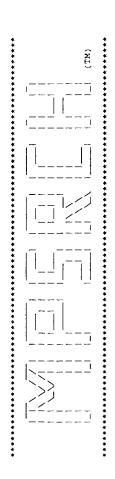
Ouery Match 2.1%; Score 32; DB 28; Length 940; Best Local Similarity 69.0%; Pred. No. 3.84e-12; Matches 58: Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Db 911 aaaaaaaaaaaaaaaaaaaa 934

Qy 1528 AAAAAAAAAAAAAAAAAAAAAAA 1551

Search completed: Sat Oct 23 19:20:04 1999 Job time : 360 secs.

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n.a. - n.a. database search, using Smith-Waterman algorithm

MPsrch\_nn

Sat Oct 23 19:20:21 1999; MasPar time 112.95 Seconds 1187.596 Million cell updates/sec

Run on:

Tabular output not generated.

>US-08-702-718-3 (1-1551) from US08702718.seq 1551 Description: Perfect Score: N.A. Sequence:

1 TCCTCTAACCTTGG.......AAAAAAAAAAAAAAAA 1551 AGGAGATTGGAACTGGAAGC......TITTTTTTTTTTTTTTTTTT

TABLE default Gap 6 Scoring table:

165359 seqs, 43243793 bases x 2 Dbase 0; Query 0 .. Nmatch STD Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

n-issued 1:5A\_COMB 2:5B\_COMB 3:5C\_COMB 4:PCT9\_COMB 5:backfiles1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 8.940; Variance 5.499; scale 1.626

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
c 1	48	3.1	7218	7	US-08-232-	Sequence 14, Applicati	8.27e-14
C1	35	5.3	215	7	US-08-238-	S,	1.88e-05
m	32	2.1	654	4	PCT-US95-0	11	7.54e-05
7	32	2.1	940	m	US-08-471-	Sequence 1, Applicatio	7.54e-05
5	32	2.1	965	٣	US-08-388-	Sequence 22, Applicati	7.54e-05
9	31	2.0	208	7	US-08-686-	Sequence 37, Applicati	2.52e-04
7	31	2.0	1046	Н	US-08-361-	4, A	7
œ	31	2.0	1046	٣	US-08-484-	4	2.52e-04
6	31	0.0	1137	٣	US-08-706-	Sequence 2, Applicatio	2.52e-04
10	31	0.3	1856	٣	us-08-106-	Sequence 1, Applicatio	2.52e-04
11	31	2.0	2589	4	PCT-US96-1	Sequence 1, Applicatio	ci
15	31	0.2	5173	7	US-08-242-	Sequence 1, Applicatio	2.52e-04
13	30	1.9	41	Н	US-08-113-	39,	8.31e-04
14	30	1.9	44	٦	US-08-113-	Sequence 40, Applicati	8.31e-04
15	30	1.9	55	-	US-08-113-	41,	8.31e-04
16	29	1.9	92	-	US-08-120-	94,	2.70e-03
17	29	1.9	92	m	US-08-478-	Sequence 94, Applicati	2.70e-03
18	29	1.9	97	m	US-08-478-	Sequence 87, Applicati	2.70e-03
19	29	1.9	97	F-4	US-08-120-	Sequence 87, Applicati	2.70e-03
2.0	C.	6	140	_	US-08-628-	Sequence 5. Applicatio	2.70e-03

2.70e-03 2.70e-03 2.70e-03 3.1e-04 2.70e-03 2.70e-03 2.70e-03 8.66e-03 8.66e-03 8.66e-03 8.66e-03 8.66e-03 8.66e-03 8.66e-03	8.66e-03 8.66e-03
Sequence 6, Application Sequence 13, Application Sequence 17, Application Sequence 17, Application Patent No. 5194739.  Patent No. 5194739.  Sequence 22, Application Sequence 6, Application Sequence 2, Application Sequence 2, Application Sequence 2, Application Sequence 2, Application Sequence 13, Application Sequence 14, Application Sequence 13, Application Sequence 14, Application Sequence 3, Applic	Sequence 3, Applicatio Sequence 21, Applicati
US-08-628- US-08-686- US-08-554- US-08-226- 5219739-16 5219759-16 US-08-238- US-08-238- US-08-238- US-08-238- US-08-238- US-08-238- US-08-238- US-08-338- US-08-347- US-08-178-	US-08-445- US-08-036-
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	1.8
88888888888888888888888888888888888888	28 28
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	44

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COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                            Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINNER, F.
APPLICANT: FALKNER, F.
APPLICANT: FALKNER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLDOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTAATION NUMBER: 29,768
PREFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
LUDRESSEE: Foley & Lardner STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
                           XXXXXX
RESULT
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REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                 SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS: ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM 486
                                                                                unknown
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                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
NUMBER OF SEQUENCES: 24
NUMBER OF SEQUENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                    1248 CAAGCCAAGAGCTCGGTTGTATAAGCTGTGAGCATATTCCAAGACTCCTTGATACCGC 1189
                                                                                                                                   1368 CTATATTATTGTAGATTCGACAAGAACAAGAGTGAGTTGATATGTCATCAATGTTATGC 1309
                                                                                                                                                                                                                          1308 TCTTCTTTTACAAAACTTTTCAAGCCATTCCATAGTGACACTCTTTGGCCTCTCTAGGGG 1249
                                                                                                                                                                                                                                                                      1188 AAACAAAACCGTATAGTATCTTGCTTCTGTCAAACCATAGTGGTTCAGCAAAACTCCACT 1129
                                                                                                              Gaps
                                                      CLONE: pT29pt-FIS
SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
                                                                                        DB 2; Length 7218;
8.27e-14;
                                                                                        3.1%; Score 48; DB 2; Length 7218
Similarity 0.6%; Pred. No. 8.27e-14;
2; Conservative 195; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                           1128 ATGAGCATCAACATTAGGCCATGGATTCTTTACCTTTCCAAGCTCT 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILING DATE: OS-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                  .T 2
US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
Patent No. 5569830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: BENNETT, Alan
APPLICANT: LABAVITCH, JOHN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
  7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: POWELL, Ann
APPLICANT: STOTZ, Henrik
             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              California
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                                             IMMEDIATE SOURCE:
                                                                                         Query Match
Best Local Similarity
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                                    TOPOLOGY:
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    LENGTH:
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68 YGGNNVGAAKTHYYTHTNVSGADSKTVTDSYNASGTSSSNGGTDGNRSGADSYGSSKTAM 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          566 ITTATCGGAGGATGTATAAGAATGGACAAGTAATACCGCTGGATG-ACTCCCTTGATTAT 624
                                                                                                                                                                                                                                                                                                                                                8 SSSVVSRIASCNDKAKKDGNTISSWIIDCCNRIWGVCDIDIIYRVNNDSGHNKYSSANYN 67
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application PC/TUS9506406A
Sequence 11, Application PC/TUS9506406A
Sequence 11, Application PC/TUS9506406A
GENERAL INFORMATION:
APPLICANT: Janet D. Robishaw, Charles Kunsch
TITLE OF INVENTION: CDNA Clones Encoding Human G Protein
TITLE OF INVENTION: Subunits
NUMBER OF SEQUENCES: 23
NAME/KEY: misc_feature
LOCATION: 1..215
OTHER INFORMATION: Standard_name= "Deduced amino acid
OTHER INFORMATION: sequence of PGIP from bean."
                                                                                                                                                                                                  Match 2.3%; Score 35; DB 1; Length 215; Local Similarity 15.9%; Pred. No 1.88e-06; es 25; Conservative 67; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                  OTHER INFORMATION: Sequence of PGIP from bean." SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: WINDOWS FOR WORKGROUPS SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        625 GGTGGAAATTTCGCACACATGTTGGGATTTGATAGCC 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 TSRNRTGKTANNAVDSRNMGDASVGSDKNTKKHAKNS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 3
PCT-US95-06406A-11 STANDARD; DNA; UNC; 654 BP
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Query Match 2.1%; Score 32; DB 4; Length 654;
Best Local Similarity 76.7%; Pred. No. 7.54e-05;
Matches 46; Conservative 0; Mismatches 14; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                      APPLICANT: Gasser, Charles S.
APPLICANT: Lippuner, Veronica
IIILE OF INVENTION: GENES CONFERRING SALT TOLERANCE AND
ITILE OF INVENTION: THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32; DB 3; Length 940;
Pred. No. 7.54e-05;
0; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 55..738
SEQUENCE 940 BP; 289 A; 235 C; 186 G; 230 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,717 FILING DATE: 06-JUN-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                   SEQUENCE 654 BP; 231 A; 116 C; 142 G; 165 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
                                                                                                                                                                                                   JT 4
US-08-471-717-1 STANDARD; DNA; UNC; 940 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 2307E-606
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                  Sequence 1, Application US/08471717
Sequence 1, Application US/08471717
Patent No. 5859337
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34,774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 940 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.1%;
Best Local Similarity 69.0%;
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
NTI-SENSE: No
                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                   STREET: One Market P
CITY: San Francisco
STATE: California
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94105-1492
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MOLECULE TYPE: CI
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                        ANTI-SENSE:
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1153 GGTTTGACAGAAGCAAGATACTATACGGTTTTGTTTGGGGTATCAAGGAGTCTTGGAATA 1212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                               Sequence 22, Application US/08388672A
Sequence 22, Application US/08388672A
Datent No. 595961
GENERAL INFORMATION:
APPLICANT: Wallace, T. Paul
APPLICANT: Garr, Frank J.
APPLICANT: Old, Lloyd J.
APPLICANT: Welt, Sydney
APPLICANT: Welt, Sydney
TILE OF INVENTION: Recombinant Human Anti-Lewis B
TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32; DB 3; Length 965;
Pred. No. 7.54e-05;
44; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
SEQUENCE 965 BP; 192 A; 170 C; 226 G; 200 T; 177 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : :::: || :| :| :: ::: || :| :100 | | ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: ||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.30
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US-08-686-878A-37 STANDARD; DNA; UNC; 208 BP.
                                                                                                          r 5
US-08-388-672A-22 STANDARD; DNA; UNC; 965 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/388,672A FILING DATE: 14-FEB-1995 CLASSIFICATION: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Hanson, No. 5795961man D.
REGISTRATION NUMBER: 30,946
REPRENCE/DOCKET NUMBER: LUD 5409
TELECOMMUNICATION INFORMATION:
TELEPAN: 212-688-9200
ILEFRA: 212-688-9200
INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 37, Application US/08686878A Sequence 37, Application US/08686878A Patent No. 5708157
                       1528 AAAAAAAAAAAAAAAAAAAAAAA 1551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Felfe and Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              805 Third Avenue
LENGTH: 965 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.1%;
Best Local Similarity 21.4%;
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 000
TTY: New York
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                                                                                                                                                                      XXXXXX
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ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET P P Box 1404 CITY: Alexandria
                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          992 AAAAAAAAAAAAAAAAA 1014
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                                                                             COUNTRY: United States
ZIP: 22313-1404
                                                                                                                       COMPUTER READABLE FORM:
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MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
                                                                Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 GTAANTTTGTCNGNNGATAAATTGAANATAACNGNGATTAANGNNTNATGNTAAAAAAAA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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C Patent No. 563341
C APPLICANT: De Greef, Willy
APPLICANT: Use De Souza, Maria-Helena
C APPLICANT: De Oliveria, Dulce E.
APPLICANT: De Souza, Maria-Helena
APPLICANT: DE SOUZA, Maria-Helena
APPLICANT: DE SOUZA, MARIA-HELEN
C TITLE OF INVENTION: PLANTS WITH MODIFIED FLOWERS, SEEDS OR TITLE OF INVENTION: EMBRYOS
C TITLE OF INVENTION: EMBRYOS
C NUMBER OF SEQUENCES: 13
C CORRESPONDENCE ADDRESS.
                                                                                       APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Evans, Cheryl
APPLICANT: Evans, Cheryl
ITILE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
NUMBER OF SEQUENCES: 71
CURRESPUNDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patenth Pelease #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/686,878A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
SEQUENCE 208 BP; 109 A; 12 C; 23 G; 43 T; 21 OTHER.
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US-08-361-467B-4 STANDARD; DNA; UNC; 1046 BP.
                                                                                                                                                                                                                                                              ADDRESSEE Genetics Institute, Inc
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: BEOWN. SCOLE A:
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEFAM: (617) 498-8224
INFORMATION FOR SEQ. ID NO: 37.
SEQUENCE CHARACTERISTICS:
                                    McCoy, John
LaVallie, Edward
Racie, Lisa
                     Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 208 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.0%;
Local Similarity 61.8%;
les 47; Conservative
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02140
                     Jacobs.
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    SENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                             APPLICANT:
APPLICANT:
                                      APPLICANT:
                                                              APPLICANT:
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US AX
AD DE XX
DT XX
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1469 TTCACTTGTAAATATATTGTATGGTTTCTTGATCAAAACATGAGATAAAGAGTTTTCATA 1528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/0848433C
Sequence 4, Application US/0848433C
Patent No. 5767374
GENERAL INFORMATION:
APPLICANT: De Greef, Willy
APPLICANT: Un Emmelo, John
APPLICANT: De Oliveria, Dulce E.
APPLICANT: De Souza, Maria-Helena
APPLICANT: Van Montagu, Marc
TITLE OF INVENTION: PLANTS WITH MODIFIED FLOWERS, SEEDS OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

2.0%; Score 31; DB 1; Length 1046;
Best Local Similarity 60.8%; Pred. No. 2.52e-04;
Matches 87; Conservative 0; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 1046 BP; 360 A; 254 C; 166 G; 266 T; 0 OTHER
SOFTWARE: Patentin Release #1.0, Version #1.30 CUPPENT APPLICATION DATA: APPLICATION NUMBER: US/08/361,467B FILING DATE: 2-DEC-1994 CLASSIFICATION: 800
                                                                                                            CLASSIFICATION: 800
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: US 07/681,492
FILING DATE: 04-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP90/01275
FILING DATE: 01-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 89 402 224.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .T 8
US-08-484-332C-4 STANDARD; DNA; UNC; 1046 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 31.196
REFERENCE/DOCKET NUMBER: 010830-027
TELECOMMUNICATION INFORMATION:
TELEPAN: (703) 836-620
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1046 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: EP 89 402 224.3 FILING DATE: 04-A0(3-198)
ATTORNEY/AGENT INFORMATION:
NAME: Schulman, Robert M
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Gaps

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ANTI-SENSE: NO FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             872 AAGCAAAGAGAAAGAACGTAGTTTTCTTGTTTTTCCTATTTTGTTTTCTCTCTATCAAAAC 931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA to mRNA IMMEDIATE SOURCE: CLONE: 3C9 SEQUENCE 1046 BP; 360 A; 254 C; 166 G; 266 T; 0 OTHER.
                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,332C
FILING DATE: 7-JUNE-1995
CLASSIFICATION: 800
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/361,467
FILING DATE: 22-DEC-1994
PRIOR APPLICATION DATA:
                                                  ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STRETT: P.O. BOX 1404
SITKE Alexandria
SIATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 04-APR-1991
PRIOR APPLICATION NUMBER: 05.7681,492
FILING DATE: 04-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP90/01275
FILING DATE: 01-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 89 402 224.3
FILING DATE: 04-AUG-1989
ATTORNEY/ABENT INFORMATION:
NAME: SCHULMAN, ROBERT M.
RECISTRATION NUMBER: 31,196
REFERENCE/DOCKET NUMBER: 31,196
REFERENC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-706-214-2 STANDARD; DNA; UNC; 1137 BP.
                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08706214 Sequence 2, Application US/08706214 Patent No. 5770720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1529 AAAAAAAAAAAAAAAAAAAAA 1551
TITLE OF INVENTION: EMBRYOS NUMBER OF SEQUENCES: 13 CORPESPONDENCE ADDRESS:
                                                                                                     STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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Gaps
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Sequence 1, Application US/08706214
Patent No. 5770720
GENERAL INFORMATION:
APPLICANT: Deul, Thomas F.
APPLICANT: Shenk, Thomas E.
APPLICANT: TITLE OF INVENTION: UBIQUITIN CONJUCATING ENZYMES HAVING TITLE OF INVENTION: TANNSCRIPTIONAL REPRESSOR ACTIVITY NUMBER OF SEQUENCES: 4
APPLICANT: Deul, Thomas F.

APPLICANT: Wang, Zhoa-Yi
APPLICANT: Shenk, Thomas E.

IIILE OF INVENTION: UBJOUTIN CONJUCATING ENZYMES HAVING
TITLE OF INVENTION: TRANSCRIPTIONAL REPRESSOR ACTIVITY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Paul A. Stone, Esq.
STREET: One Metropolitan Square, 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 88..564
SEQUENCE 1137 BP; 294 A; 285 C; 275 G; 283 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/706,214
FILING DATE: 30-AUG-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 31; DB 3; Le
Pred. No. 2.52e-04;
0; Mismatches 4;
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US-08-706-214-1 STANDARD; DNA; UNC; 1856 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/018,040
FILING DATE: 21.WAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,995
FILING DATE: 30.AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Stone, Paul A.
REGISTRATION NUMBER: 38,628
REFERENCE/DOCKET NUMBER: JWH 10033
TELECHMUNICATION INFORMATION:
TELEPHONE: (314) 231-440
TELEFX: (5502697583 MCI
INFORMATION: FOR ESQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1137 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.0%;
Best Local Similarity 89.7%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 63102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                     Abbara
STREET: One ...
CITY: St. Louis
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                Length 1856;
                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 807..1283
SEQUENCE 1856 BP: 401 A; 499 C; 518 G; 438 T; 0 OTHER.
                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,214
FILING DATE: 30 AUG-1996
COPPESPONDENCE ADDRESS - ADDRESSEE: Paul A. Stone, Esq. STREET: One Metropolitan Square, 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                   1809 ATAAACTGTTTATAAAAAAAAAAAAAAAAAAAAAAA 1847
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application PC/TUS9612860
Sequence 1, Application PC/TUS9612860
Sequence 1, Application PC/TUS9612860
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORPESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 2.0%; Score 31; DB 3; Lø
Best Local Similarity 89.7%; Pred. No. 2.52e-04;
Matches 35; Conservative 0; Mismatches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .T 11
PCT-US96-12860-1 STANDARD; DNA; UNC; 2589 BP
                                                                                                                                                                                                         NAME: Stone, Paul A.
REGISTRATION NUMBER: 38,628
REFRENCE/DOCKET NUMBER: JWH 10033
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 231-5400
TELERAX: (314) 231-4342
TELEX: 6502697583 MCI
INFORMATION FOR SEQ. ID NO: 1.
SEQUENCE CHARACTERISTICS:
                                                                                                                         FILING DATE: 30-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/018,040
FILING DATE: 21-MAY-1996
PRIOR APPLICATION NUMBER: US 60/002,995
FILING DATE: 30-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                     LENGTH: 1856 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                          St. Louis
Missouri
                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO FEATURE:
                                                    63102
                                            COUNTRY:
                                  STATE:
                             CITY:
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Sequence 1, Application US/08242677
GENERAL INFORMATION:
APPLICANT: Wu, Foon W.
APPLICANT: Wu, Foon W.
TITLE OF INVENTION: Cellular Nucleic Acid Binding Protein
TITLE OF INVENTION: Treatment of AIDS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE S. 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
O
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                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.0%; Score 31; DB 4; Length 2589
Best Local Similarity 89.7%; Pred. No. 2.52e-04;
Matches 35; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: cDNA
SEQUENCE 2589 BP; 844 A; 436 C; 522 G; 787 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,677
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Brezzer, David J.

REGISTRATION NUMBER: 24,774

REGISTRATION NUMBER: A-62464/DJB

RELECOMMUNICATION INFORMATION:

TELEFONE: (415)781-1989

TELEFAN: (415)389-3249

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2589 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JT 12
US-08-242-677-1 STANDARD; DNA; UNC; 5173 BP.
                                                                       APPLICATION NUMBER: PCT/US96/12860
FILING DATE: 06 AUG 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSD:401
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-789-1400
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                    FILING DATE: 0 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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5047 CACTITITIGITAAATIGIATICITICCTITAATAAAATAITITAAGCAATIGICCAATAAA 5105
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                                                                                                                                                                          0; Gaps
                                                                                                                                             Length 5173;
                                                                                                                                             Score 31; DB 2; Length 5173; Pred. No. 2.52e-04; 0; Mismatches 25; Indels
                                                                                                   LOCATION: 1..4863
SEQUENCE 5173 BP; 1348 A; 1116 C; 1309 G; 1400 T; 0 OTHER
                                                                                                                                                                                                                                                                                                                                                                               Sequence 39, Application US/08113646A
Sequence 39, Application US/08113646A
Patent No. 5578468
GENERAL INFORMATION:
APPLICANT: PICKUP, David J.
APPLICANT: PICKUP, Davalkumar
APPLICANT: PATEL, Dhavalkumar
APPLICANT: ANTCZAK, James B.
TILLE OF INVENTION: SITE-SPECIFIC RNA CLEAVAGE
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NOWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/113,646A
FILING DATE: 31-AUG-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/084,406
FILING DATE: 10-AUG-1987
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: RNA (genomic)
SEQUENCE 41 BP; 33 A; 2 C; 1 G; 0 T; 5 OTHER.
                                                                                                                                                                                                                                                                                                                                    J. 13
US-08-113-646A-39 STANDARD; DNA; UNC; 41 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEFAX: 20077 NIXN UR
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: ARLINGTON
STATE: VIRGINIA
COUNTY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                              5107 AAAAAAAAAAAAAAAA 5127
                                                                                                                                                                                                                                                                                         1531 AAAAAAAAAAAAAAAAAA 1551
LENGTH: 5173 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                             Match 2.0%;
Local Similarity 69.1%;
les 56; Conservative
                                                      MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                             linear
                                                                                      NAME/KEY: CDS
                                                                                                                                                Query Match
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Length 41;

DB 1;

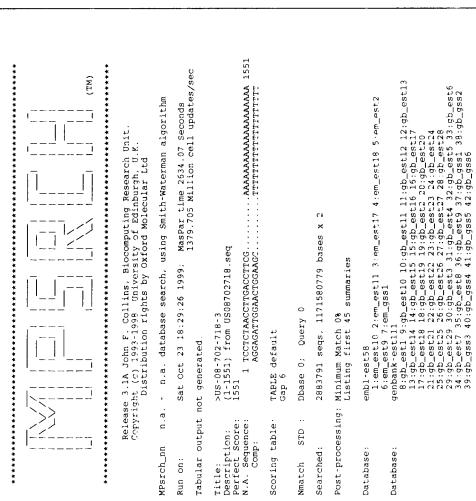
1.9%; Score 30;

Query Match

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              Gaps
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              Indels
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                                                                                                                                                     Sequence 40, Application US/08113646A
Sequence 40, Application US/08113646A
Patent No. 5578468
GENERAL INFORMATION:
APPLICANT: PICKUP, David J.
APPLICANT: PATEL, Dhavalkumar
APPLICANT: ANTCZAK, James B.
TILLE OF INVENTION: SITE-SPECIFIC RNA CLEAVAGE
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/113,646A
Best Local Similarity 80.6%; Pred. No. 8.31e-04;
Matches 29; Conservative 4; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30; DB 1; L
Pred. No. 8.31e-04;
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                                                     1516 AAGAGTTTTCATAAAAAAAAAAAAAAAAAAAAAA 1551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: RNA (genomic) SEQUENCE 44 BP; 36 A; 2 C; 1 G; 0 T; 5 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 AAAAGAUUUUAUAAAAAAAAAAAAAAAAAAAAAAAAA 39
                                       JT 15
US-08-113-646A-41 STANDARD; DNA; UNC; 55 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                        T 14
US-08-113-646A-40 STANDARD; DNA; UNC; 44 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/113,646A
FILING DATE: 31-AUG-1993
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/084,406
FILING DATE: 10-AUG-1987
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
                                                                                                                                                                                                                                                                                                                           STAIE: VINGAL...
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
--WOTTER: IBM PC COMPATIBLE
--TEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                            3: NIXON & VANDERHYE P.C. 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 1579-20 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 41, Application US/08113646A Sequence 41, Application US/08113646A Patent No. 5578468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELES: 200797 NIXN UR
INFORMATION FOR SO ID NO: 40:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.9%;
Best Local Similarity 80.6%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                       CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    xxxxxx
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CC GENERAL INCOMATION:
CC APPLICANT: PATEL. DAVID AUGUST
CC AUGUST
CC AUGUST
CC APPLICANT AUGUST
CC AUGU
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Search completed: Sat Oct 23 19:22:19 1999 Job time : 118 secs.



Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 12.169; Variance 6.306; scale 1.930

Statistics:

## SUMMARIES

		œ					
Result		Query					
No.	Score		Match Length DB	DB	ID	Description	Pred. No.
	281	18.1	471	20	AA896953	L30-386T3 Ice plant La 1.08e-189	1.08e-189
C1	223	14.4	502	17	T44185	7448 Lambda-PFL2 Arabi	2 470-143
m	C+	14.2	478	31	R90544	16899 Lambda-PRL2 Arab	9.57e-142
4	201	13.0	676	23	A1176862	EST220465 Normalized r	6.50e-126
S	191	12.3	657	15	AA606966	vm94h09.rl Knowles Sol	5.06e-118
9	188	12.1	417	24	C96653	C96653 Rice callus Ory	
7	183	11.8	527	31	R90561	16916 Lambda-PRL2 Arab	9.83e-112
α	178	11.5	620	56	AU002699	AU002699 Bombyx mori p	æ
σ	164	10.6	501	11	AA313713	EST185581 Colon carcin	-
10	156	10.1	522	10	AA237580	mx11d01.rl Soares mous	1.17e-90

row: H column: 6

FORWARD: T7 BACKWARD: T3 Plate: L30-4 rc Seq primer. T3

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/note="vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not: Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots: 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA cliserts were directionally cloned with Sal-Not arms using //db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION 16899 Lambda-PRL2 Arabidopsis thaliana cDNA clone 189D15T7, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 GGTCACCTGGTTGGTAGTGCACTTTCAGACCCATATCTGTCATTTGCAGCTGCATTAAAT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTTTAGCTGGGCCACTCCATGGTTTGGCTAATCAGGAAGTTTTGCTTTGGATCAAATCA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       859 GTIGTIGAIGAAIGIGGAGAAACAICTCGACAGAGCAGTIGAAAGAITAIGIITGGAAG 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310 ACATTAAACAGTGGCAAGGTTATTCCGGGGTATGGTCACGGTGTTCTNCGCAATACTTGA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    919 ACACTAAACAGIGGCAAGGIIGIACCIGGAIIIGGICIAGGAGIAIIGGGGAAGACA-GA 977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          370 TCCCCGAINTIGITIGCCAAAGAGGAATTTTCCNINGNAGNANCTTCCCINANGGCCCCC 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                619 GATTATGGTGGAAATTTCGCACACACATGTTGGATTGATAGCCCTCAGATGCTTGAGCTG 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 ATGAGGCTTTACATCACCATCCACAGTGATCATGAAGGTGGAAATGTTAGTGCTCACACACT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               799 GGTTTGGCTGGGCCACTCCATGGATTAGCCAACCAGGAAGTCCTGCTGTGGATTAAATCA 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250 GTCGTAGAGGAATGTGGAGAAGATATATCAAAAGAACAGTTGAAAGAATATGTTTGGGAA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 GAITATGGTGCAAATTTTTCCCACATGTTGGGATTTGATGATGAAAAGGTGAAAGGGCTC 69
                                                                                                                                 MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
On Jan 7, 1998 this sequence version replaced qi:948518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 14.4%; Score 223; DB 17; L
Best Local Similarity 78.2%; Pred. No. 2.47e-143;
Matches 333; Conservative 0; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                        /organism="Arabidopsis thaliana"
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90 c 118 g 149
                                                                          MSU-DOE Plant Research Laboratory Michigan State University
                                                                                                                                                                                                                                                                                                                                                                                     /strain="var columbia"
                                                                                                                                                                                       Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 9
                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="123C9T7"
                                                Contact: Thomas Newman
                                                                                                                                                                                    17-353-0854
                                                                                                                                                              Lansing, Mi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1034 TITTIC 1039
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COMMENT
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                                                                       /organism-"Mesembryanthemum crystallinum"
/note-"Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 980 CAAGATACACATGCCAAAGAGAATTTGCGTTGAAGCACTTGCCTGATGACCATTTTTTC 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1100 AGAATCCATGGCCTAATGTTGATGCTCATAGTGGA-GTTTTGCTGAACCACTATGGTTTG 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 CATTAAAAAGTGGCAAGGTTGTACCTGGATATGGCCATGGAGTTCTGCGCAAGACGGATC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 CAAGATACTCTTGCCAGAGGGACTTTGCCCTTAAGCACTTACCTAATGATCCACTATTTC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 AACTGGTTTCGAAGCTGTATGAA-TGGTGCCTCCAATTCTGACAGAGGTTGGGAAGGTAA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 AGAA-CCATGGCCGAATGTTGATGCCCACAGTGGGTGTATTGCTGAACTACTATGGTTTG 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       744185 502 bp mRNA EST 07-JAN-1998
7448 Lambda-PRL2 Arabidopsis thaliana cDNA clone 123C9T7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GGTTGGCTGGCCCACTTCATGGATTAGCCAATCAGGAAGTGTTGCTGTGGATCAAGTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TTGTGGATGAATGTGGAAAAACATCAGCACGGAGCAGCTAAAAGATTATGTCTGGAAGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            860 TIGITGATGAATGIGGAGAACAICTCGACAGAGCAGIIGAAAGAITAIGIIIGGAAGA 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   920 CACTAAACAGTGGCAAGGTTGTACCTGGATTTGGTCTAGGAGTATTGCGGAAGACAGATC 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          740 GCCATTTGGTGGTAGTCCACTTTCAGATCCTTATTTGTCATTTGCAGCAGCATTAAATG 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCCATTTGGTGGGTAGCGCACTTTCAGATCCTTACCTTTCATTTGCAGCTGCACTGAATG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gabs
                                                                                                                                                     /db_xref="taxon:3544"
/clone="L30-386"
/clone_lib="lce plant Lambda Uni-Zap XR expression library, 30 hours NaCl treatment"
/tissue_type="Leaf, 30 h 0.4M NaCl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                      Score 281; DB 20; Length 471; Pred. No. 1.08e-189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                         /dev_stage="Six week old"
95 c 122 g 127
High quality sequence stop: 320.
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                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         419 ACAAGAAAGCAAGATACTACACTGTT 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thale cress.
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 18.1%;
Best Local Similarity 84.3%;
Matches 376; Conservative
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                      FEATURES
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AI176862 676 bp mRNA EST 20-JAN-1999
EST220465 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
NOVERSO 3' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 676)
1 Lee, N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J., Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
1060 GAAGIGGIGCCICC-TATICIATIAGAGCIT-GGAAA-GGIAAAGAAICCAIGGCCIAAT 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1266 CTTTGGCCTCTCTAGCGGCAAGCCAAGAGTCGGTCCCATATAAGCTGTGAGCATATTCC 1207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1206 AAGACTCCTTGATACCCCAAACAAAACCGTATAGTATCTTGCTTCTGTCAAACCATAGTG 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1146 GTTCAGCAAAACTCCACTATGAGCATCAACATTAGGCCATGGATTCTTTACCTTTCCAAG 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1086 CICTAATAGAATAGGAGGACCACTTCATACAACITTGACAACCAAITGAAAAATGGGTC 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 CAGIGCCCTCGACACTCCGAACAGGACTGTGTAGTAATTCATCTCCGTCATGCCATAGTA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 CTGGAGCAGCACCCACTGTGAGCATCTACGTTGGGCCAGGGGTTCTTAGCCTTTCCTTG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303 CTCTAAGAGGATATTGGGCACAATCTTGTACAGCTGAGCAACCAGCTTAAACATGGGATC 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 CTTGGGCCTTTCTAGAGGGAAGCCTAGGGCTCTGCTCCAGATAAGCTGGGCCAACACACC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363 CTTGGGCAGATGTTTCAGAGCAAACTCTCGCTGACAGGAATATCGTGGATCAGTCTTCCT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423 TAGGACTGCATGACCATATCCTGGGACAACCCGTCCCGAGTTGAGTGTTCCAGATGTA 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Organ: ovary; Vector: pT7T3Pac; Site_1: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Jan 19, 1998 this sequence version replaced gi:2152042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Normalized rat ovary, Bento Soares"
188 c 150 g 181 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA Tel: (301)-838-5529 Fax: (301)-838-0208 Email: nhlee@tigr.org Seq primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 201; DB 23; Length 676; Pred. No. 6.60e-126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 177; Indels
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/db_xref"*ATC (inhost):2031570"
/db_xref"*taxon:10118"
/clone="ROVBX80"
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                                                                                                                                                                                                                   Newman, T., deBruin, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohirogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, G. and Ingerscale gartial sequencing of anonymous Arabidopsis cDNA clones ps148729
On Apr 14, 1993 this sequence version replaced gi:693655.
                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, euphyllophytes, Spermatophyta, Magnollophyta; eudicotyledons; Rosidae, Capparales; Brassicaceae, Arabidopsis.
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/strain="var columbia"
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90 c 113 q 13
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Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
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Location/Qualifiers
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/note="Organ: embryo: Vector: pSPORT: Site_1: Not1:
Site_2: Sall: Cloned unidirectionally from mRNA prepared
from 800 blastocysts. Primer: Sall(dT):
5'-CGGTCGACCGTCGACCGTTTTTTTTTTTT-3'. cDNAs were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA606966 657 bp mrNA EST 30-SEP-1997 wm94Nb9.r1 Knowles Solter mouse blastocyst B1 Mus musculus CDNA clone IMAGE:1005953 5' similar to SW:CISY_PIG P00889 CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR ;, mRNA sequence.
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                                                                        543 GACAAGCAGCTGCTGGTTTGGTAGTGCATGCAAGGGCCTGCCAGGCCATTCATAGCTGC 602
                                                                                                                                                                                                                                                                                                                                                              906 ATCTITCAACTGCTCTGTCGAGATGTTCTCTCCACATTCATCAACAACTGATTTAATCCA 847
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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On Sep 12, 1996 this sequence version replaced gi:1328460
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
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/db_xref="taxon:10090"
/clone="IMAGE:1005953"
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
euphyllophytes, Spermatophyta, Magnoliophyta, Liliopsida, Poales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           960 AGTATTGCGGAAGACAGATCCAAGATACACATGCCAAAGAGAATTTGCGTTGAAGCACTT 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1138 TIGCTGAACCACTAIGGITIGACAGAAGCAAGAIACIAIACGGITITIGITIGGGGTAICA 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1020 GCCTGATG-ACCCATTTTTCAAT-TGGTGTCAAAGTTGTATGAAGTGGTGCTCCTATT 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             484 CIGCICCAGIACTAIGGCAIGACGGAGAIGAACTACIACACAGICCIGIIIGGAGIGICI 543
                                                                                                                                                                                                                                                                        900 GAAAGAITAIGIIIIGGAAGACACIAAACAGIGGCAAGGIIGIACCIGGAIIIIGGICIAGG 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 AGTACTGAGGAAGACTGACCCTCGCTATTCCTGTCAGCGAGAGTTTGCTCTGAAACATCT 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 GCCTAAGGGATTCCCATGTTCAAGCTGGTGGCTCAGCTGTACAAGATTGTGCCCAATATC 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             424 CICITAGAGCAAGGGAAGGCIAAGAACCCITGGCCCAACGIAGACGCICACAGIGGGGIG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                544 CGGGCACTGGGTGTGCTAGCCCAGCTCATCTGGAGCAGAGCCCTAGGCTTCCCCCTGGAA 603
                                                                                                                                                                                 660 CCCTCAGATGCTTGAGCTGATGCGCCTTTATGTCACAATTCACAGTGATCATGAGGGTGG 719
                                                                                                                                                                                                                                            66 TAATGTAAGTGCCCACACACACCATTTGGTGGGCAGCGCA-TTTCAGACCCTTACCTGTC 124
                                                                                                                                                                                                                                                                                                                                                            125 CTTTGCAGCAGCCATGAATGGGCTGGCGGGCT-CTACATGGACTAGCAAATCAGGAGGT 183
                                                                                                                                                                                                                                                                                                                                                                                                                     780 ATTIGCAGCAGCATIAAAIGGITIGGCIGGGCCACICCAIGGAITAGCCAACCAGGAAGT 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 GCTTGTCTGGCTGACACGTACAGAAGGAAGTTGGCAAAGACGTGTCAGATGAGAAGTT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 ACGAGACTACATCTGGAACACACTCAATTCAGGACGGGTGGTCCCAGGATACGGTCATGC 303
                                                                                                                      6 CCCTCAGIICACCGAGCICAIGCGIIIGIACCICACCAIACIGACCAIGAGGGIGG 65
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                                                              Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCUS C96653 417 bp mRNA EST 19-UCT-15 DEFINITION C96653 Rice callus Oryza sativa cDNA clone C10531_5A, mRNA
   Length 657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       National Institute of Agrobiological Resources Rice Genome Research Program 2-1-2 Kannondai,Tsukuba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Aug 21, 1998 this sequence version replaced
Score 191; DB 15; L
Pred. No. 5.06e-118;
0; Mismatches 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sasaki, T. and Minobe, Y. Rice cDNA from callus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Takuji Sasaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93758954
C96653.1 GI:3758954
Query Match 12.3%;
Best Local Similarity 67.3%;
Matches 410; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1258 AGGCCAAAG 1266
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95148729
On Apr 14, 1993 this sequence version replaced gi:693674
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                                                                            MSU-DOE Plant Research Laboratory
Michigan State University
                                                                                                                   MSU-Lu-
Lansing, Mi
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7 dye primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Lambda-PRL2"
106 c 122 q 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 TTATCCGAAGGGATGTATAANAAT 386
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                                                         Contact: Thomas Newman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AU002699.1 GI:4159092
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77.6%;
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Matches 298; Conservative
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94159092
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Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H.,
McIntosh, L., Ohlragge, J., Raikhel, N., Somerville, S., Thomashow, M.,
Retzel, E. and Somerville, C.
Genes galore: a summary of methods for accessing results from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, euphyllophytes, Spermatophyta, Magnoliophyta; eudicotyledons;
                                                                                                                                                  /strain="cultivar Nipponbare, sub_species Japonica"
/note="Vector: pBluescript IS St+; Site_1: Site_2:
Not1: CDNA prepared from rice callus mRNAs by using
oligo(dT) as a primer and ligating to the SelI-NotI site
of pBluescript II SK+ phagemid. "
/db.xref="taxon:4530"
/map="ll" taxon:4530"
/clone="closi_5A"
/clone="los1_5A"
a 76 c 108 g 118 t
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16916 Lambda-PRL2 Arabidopsis thaliana cDNA clone 189H3T7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              562 TATGTTTATCGGAGGATGTATAAGAATGGACAAGTAATACCGCTGGATGACTCCCTTGAT 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 TAIGCAGCAAACTTTTCACACATGCTTGGGTTTGATGATCCCAAAATGCTCGAGTTGATG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         622 TATGGTGGAAATITCGCACACATGTTGGATTTGATAGCCCTCAGATGCTTGAGCTGATG 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 CGACTATATGTGACAATCCACACTGATCATGAAGGTGGAAATGTCAGTGCTCATACTGGA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATCTGGTTGGAAGTGCTCTGTCAGATCCTTATCTTTTTGCAGCTGCACTGAATGGT 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           862 GITGAIGAAIGIGGAGAAGAACAICICGACAGAGCAGITGAAAGAITAIGITIGGAAGACA 921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         742 CATTIGGIGGGIAGICCACTITCAGAICCTTAITTGICATTIGCAGCAGCATTAAAIGGI
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                                                                                                                                                                                                                                                                                                                                                                                              Length 417;
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                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 73.1%; Pred. No. 1.16e-115; Matches 305; Conservative 0; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                            Score 188; DB 24;
                                                                                                                                  /organism="Oryza sativa"
          Tel: 0298-38-7441
Fax: 0298-38-7468
Email: tsasaki@abr.affrc.go.jp
                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
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                                                                        PROJECT = 'RGP'
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Strain—"var columbia"

/strain—"var columbia"

/note—"vercor: lambda zip-Lox: Site_1: Sal; Site_2: Not;

Lambda PRL2 is a cDNA library derived from equal

quantities of 4 pools of mRNA. The mRNA sources were 1) 7

quantities of 4 pools of mRNA. The mRNA sources were 1) 7

quy germinated etiolated seedlings: 2) tissue culture

grown roots; 3) staged plants half with 24 hour light

cycle, half on 16 hr light, 8 hour dark-rosettes: 4)

same plants as 3 but aerial tissue (stems, flowers and

sliques. The vector is BRL's lambda Zip-Lox. The cDNA

inserts were directionally cloned with Sal-Not arms using

oligo dr primed cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AU002699 620 bp mRNA EST 15-JAN-1999
AU002699 Bombyx mori p50(Daizo) Bombyx mori cDNA clone n0357, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 ATACCIGAAIGCCAGAAACITITACCCGCIGCAAGIGCIGGIGCAGAGCCAIIGCCIGAA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTCTTTTGTGGCCTTCTCTTAACTGGAAAGGTACCTAGCAAAGAGGAAGTTGAAGCACTG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 TCGAAAGACTTGGCGAACCGTGCTGCTGTGCCAGATTATGTGTACAATGCCATCGATGCT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 CIGCCIICCACAGCICAICCAAIGACICAAITIGCIAGCGGTGIIAIGGCCCICCAGGIG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 CAAAGTGAGTTTCAAAAGGCATATGAGAATGGAATTCATAAGTCAAAGTTCTGGGAGCCA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 ACATATGAGGATTGCCTCAACCTGATTTGCTCGTGTTNCCTGTTGTAGNCTGCATAATGT 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 ATTCCTGAGTGCCAGAAAGTATTACCTACTGCCCAGTCTGGAGCTGAACCATTACCGGAG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 9.83e-112;
0; Mismatches 80;
                                                                                                                                                                                                                             1. .527
/organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /map="873F09; 1q21.3-1q23.2; 9" /clone="189H3T7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    946 GGATTTGGTCTAGGAGTATTGCGGAAGACAGATCCAAGATACACATGCCAAAGAGAATTT 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1126 CATAGTGGAGTTTTGCTGAACCACTATGGTTTGACAGAAGCAAGATACTATACGGTTTTG 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GCTAATCAAGAGGTTCTGGTATGGCTCGAGAACTGCGCAAACAAGTTGGTGATAATTTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 ACAGAAGAGCAACTCAAAGAATTCATCTGGAAAACACTTAAATCTGGTCAGGTTGTACCT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       886 TCGACAGAGCAGTTGAAAGATTATGTTTGGAAGACACTAAACAGTGGCAAGGTTGTACCT 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 GGTTACGGTCATGCAGTACTTAGAAAAACTGATCCAAGATATACTTGCCAGCGTGAGTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 GCTCTTAAGCACTTACCCAATGACCCATTATTCAAGCTGGTCGCTGCTGTTACAAGGTT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 GTTCCGCCGATCCTCACCGAACTTGGCAAAGTCAAGAAGCCATGGCCTAATGTAGACTCC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 CATTCGGGAGTTCTTTTGCAGTATTATGGTCTGAAGGAGATGAACTACTATACAGTAATG 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        481 TTTGGAGTGTCCCGAGCGTTGGGTGTTCTCGCTCAGTTGATTTGGTCCCGTGCGCTCGGA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GATCCTTACTTATCTTTCGCGGCTGGACTCAATGGTCTTGCTGGACCACTTCACGGCCTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         706 GATCATGAGGGTGGAAATGTTAGTGCACACAGTGGCCATTTGGTGGGTAGTCCACTTTCA 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 766 GATCCTTATTTGTCATTTGCAGCAGCATTAAATGGTTTGGCTGGGCCACTCCATGGATTA 825
                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Lepidoptera; Bombycoidea; Bombycidae; Bombyx.
1 (bases 1 to 620)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GACCACGAGGGTGGAAACGTTTCTGCGCACACTACGCATTTAGTGGGTTCTGCTCTTAGT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 178; DB 26; Length 620;
Pred. No. 8.20e-108;
0; Mismatches 202; Indels 0;
                                                                                                                                    Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S. Establishment of cDNA database of Bombyx mori
                                                                                                                                                                                   Unpublished (1999)
On Sep 1, 1995 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib-"Bombyx mori p50(Daizo)"
141 c 146 g 171 t
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                                                                                                                                                                                                                                                  Contact: Mita K
Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmita@uexs64.nirs.go.jp
PROJECT = CREST Project by JST'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Bombyx mori"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="p50(Daizo)"
/db_xref="taxon:7091"
/clone="n0357"
                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 65.3%;
Matches 380; Conservative
                      domestic silkworm.
                                               Bombyx mori
                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                            ORGANISM
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RESULT

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1 (bases 1 to 50)

S Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man Wai, C.,

White, O., Sutton, G., Blake, J.A., Erandon, R.C., Man Wai, C.,

Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,

Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,

Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.

Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,

Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,

Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Pullion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
                       EST185581 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to similar to citrate synthase, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fraser, C.M. and Venter, J.C. Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.iigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   843 GCTGTGGATTAAATCAGTTGTTGATGAATGTGGAGAACATCTCGACAGAGCAGTTGAA 902
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EcoRI; Site_2: XhoI"
/db_xref="ATCC (inhost):109839"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TGCAGCAGCCATGAACGGGCTGGCAGGCCTCTCCATGGACTGGCAAATCAGGAAGTGCT 60
19-APR-1997
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Apr 14, 1993 this sequence version replaced gi:693326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="KM12C"
/cell_line="KM12C(HCC)-parental human colon
carcinoma;Dukes B2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 10.6%; Score 164; DB 11; Length 501; Best Local Similarity 66.9%; Pred. No. 7.09e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 160; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref-"taxon:9606"
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mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kerlavage, AR
                                                                                                                                                       AA313713.1 GI:1966042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Other_ESTs: THC171646
501 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bioinformatics
                                                                                                                                                                                                                                                   Homo sapiens
AA313713
                                                                                                                   91966042
                                                                                                                                                                                                                        human.
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COMMENT
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
(Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1070 CTCCTATTCTATTAGAGCTTGGAAAGGTAAAGAATCCATGGCCTAATGTTGATGTTGATGTTATA 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           950 TIGGICIAGGAGIATIGCGGAAGACAGATCCAAGATACACAIGCCAAAGAGAATITGCGI 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1130 GIGGAGITITICCIGAACCACIAIGGITIGACAGAAGCAAGAIACIATACGGITITIGITIG 1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 TGAAACATCTGCCTAAGGATCCCATGTTCAAGCTGGTGGCTCAGCTGTACAAGATTGTGC 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 CCAATATCCTCTTAGAGGAAGGGAAGGCTAAGAACCCTTGGCCCAACGTAGACGCTCACA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       418 GTGGGGTGCTGCTCCAGTACTATGGCATGACGAGATGAACTACTACACAGTCCTGTTTG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        890 CAGAGCAGTTGAAAGATTATGTTTGGAAGACACTAAAACAGTGGCAAGGTTGTACCTGGAT 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 ACGGTCATGCAGTACTGAGGAAGACTGACCCTCGCTATTCCTGTCAGCGAGAGTTTGCTC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        710 ATGAGGGTGGAAATGTTAGTGCACACACTGGCCATTTGGTGGGTAGTCCACTTTCAGATC 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 CTTACCTGTCCTTTGCAGCAGCCATGAATGGGCTGGCGGGGCT-CTACATGGACTAGCAA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 770 CTTATTTGTCATTTGCAGCAGCATTAAATGGTTTGGCTGGGCCACTCCATGGATTAGCCA 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGAGGGTGGTAATGTAAGTGCCCACACACACATTTGGTGGG-AGCGCTGTT-CAGACC 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                 3; Caps
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VanDeynze,A.E., Sorrells,M.E., Park,W.D., Ayres,N.M., Fu,H.,
Cartinhour,S.W. and McCouch,S.R.
Anchor Probes for Comparative Mapping of Grass Genera
Unpublished (1997)
On Nov 29, 1993 this sequence version replaced gi:634857.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA231705 307 bp mRNA EST 27-FEB-199
27-FEB-199
200534.R cDNA from oat Avena sativa cDNA clone CDO534, mRNA
sequence.
AA231705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 ATGAGAAGTTACGAGACTACATCTGGAACACACTCAATTCAGGACGGGTGGTCCCAGGAT
                                                                                                                                                                                                                                                                                                                                                        Length 522;
                                                                                                                                                                                                                                                                                                                                                      Score 156; DB 10; Length 522
Pred. No. 1.17e-90;
0; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1190 GGGTATCAAGGAGTCTTGGAATATGCTCACAGGTTATATGG 1230
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                                                                                                                                                            /clone="IMAGE:679873"
/clone_lib="Soares mouse NML"
/tissue_type="Liver"
/lab_host="DH108"
/ 125 c 150 g 118 t
                                                                                                            /db_xref-"taxon:10090"
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AA231705.1 GI:1854091
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.4%;
Matches 346; Conservative
                                                                                     Bonaldo.
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Laro,M., Lew,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA237580 522 bp mPNA EST 03-MAP-1997 mx11d01.rl Scares mouse NML Mus musculus cDNA clone IMAGE:679873 5' similar to SW:CISY_PIG P00889 CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                        | 1143 GAACCACTATGSTITGACAGAAGCAAGAIACTAIACGGITITGTITGTITGGGTAICAAGGAG 1202
                                                                                                                                                                                                                                                                                                        1023 TGATGACCCATTTTTTCAATTGGTGTCAAAGTTGTATGAAGTGGTGCCTCCTATTCTATT 1082
                                                                                                                                                                                                                                                  241 TAATGACCCCATGTTTAAGTTGGTTGCTCAGCTGTACAAGATTGTGCCCAATGTCCTCTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 CCAGTATTATGGCATGACGGAGATGAATTACTACACGGTCTGTTTGGGGTGTCACGAGC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 ATTGGGTGTACTGGCACAGCTCATCTGGAGCCGAGCCTTAGGGGTTCCCTCTAGAAAGGGC 480
                                  121 AGACTACATCTGGAACACACTCAACTCAGGACGGGTTGTTCCAGGCTATGGCCATGCAGT 180
                                                                                                                                        181 ACTAAGGAAGACTGATCCGCGATATACCTGTCAGCGAGAGTTTGCTCTGAAACACCTGCC 240
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                                                                                                                                                                        903 AGATTATGTTTGGAAGACACTAAAACAGTGGCAAGGTTGTACCTGGATTTGGTCTAGGAGT
                                                                                                                                                                                                                                                                                                                                                        301 AGAGCAGGGTAAAGCCAAGAATCCTTGGCCCAATGTAGATGCTCACAGTGGGGTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1392879
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louls, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-HHMI Mouse EST Project
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                       /note="Vector: Uni-ZAP XR/pBluescript; Site_1: EcoRI; Site_2: XhoI: A Uni-ZAP XR cDNA library was constructed from etiolated leaf mRNA from the oat cultivar 'Brooks' and converted to pBluescript (amp resistant) as described in Heun et al. (1991) Genome 34:437-447. For insert amplification, use M13 forward and reverse primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clones from this library are designated with the prefix 'CDO'. *Note: Clone CDO1081 was recloned into the TA cloning vector and carries kanamycin resistance." /db_xref="kaxon:4498"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA112941 466 bp mRNA EST 01-AUG-1997 2n59b06s.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562451 5' similar to SW:CISY_PIG P00889 CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR; mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 CGTAATACAGATCCACGATACTCGTGCCAAAGGGAGTTTGCACTTAAGTATTTACCCCGAG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TGGATCAAATCTGTGATGGAAGAAACCGGGAGTAACATTACAACTGATCAGCTTAAAGAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          907 TATGTTTGGAAGACACTAAACAGTGGCAAGGTTGTACCTGGATTTGGTCTAGGAGTATTG 966
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1 (bases 1 to 466)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hollman,M., Hultman,M., Klucaba,T., Lew,, Lennon,G., Marra,M., Parsons,J., Rikkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                  Email: srm4@cornell.edu
cDNA from oat (Avena sativa); reverse sequence of RFLP probe
CDO534. Sequence determined by Nicola M. Ayres.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 GACCCACTITICCAACTGGTCTCCAAGTIGTACGAAGTTGTGCCTCCTATCCT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 75.8%; Pred. No. 8.76e-87; 22; Conservative 0; Mismatches 71: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="CDO534"
/clone_lib="cDNA from oat"
                                                                                                                                                                                                                                                                                          /organism="Avena sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="etiolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 9
                                                                                                                                                                                                                                                                                                                 /cultivar="Brooks"
                                               Cornell University Ithaca, NY 14853-1901, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA112941.1 GT:1664291
                        Dept Plant Breeding
Contact: McCouch SR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 C
                                                                                              Tel: 607 255 0420
Fax: 607 255 6683
                                                                                                                                                                                                                                                                 307
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/note="Organ: skeletal muscle; Vector: pBluescript SK-; Ste_1: BooRi, Site_2: Xhol; Cloned unidirectionally. Primer: Oligo dT. Skeletal muscle from patient with malignant hyperthermia. Average insert size: 1 0 kb; mir_APA xR Vector; -5' adaptor sequence: 5' GAATTGGGAGGG 3' -3' adaptor sequence: 5' CTGGAGTTTTTTTTTTTTTTTT 3'" /db_xref="GDB:4595741"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vh38q11.rl Barstead mouse pooled organs MPLR84 Mus musculus CDNA clone IMAGE:889316 5' similar to SW:CISY_PIG P00889 CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR; mRNA sequence.
                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2292 std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 AATTICACCAACAIGITAGGCIATACIGAICAICAGTICACIGAGCTCACGCGCCTGIAC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 CTCACCATCCACAGGGACCATGAGGGTGGCAATGTAAGTGCCCATACCAGCCATTGGTG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 GGCAGTGCGTNTTCCGACCCGTTACCTGTCCTTTGCAGCAGCCATGAACGGGCTGGCAGG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 GCT-CTCCATGGACTGGCAAATCAGGAAGTGCTTGTCTGGCTAACACACAGGTGCAGAAGGA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      810 GCCACTCCATGGATTAGCCAACCAGGAAGTCCTGCTGTGGATTAAATCAGTTGTTGATGA 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTTGGCAAAGATGTGTCAGATGAGAAGTTACGAGACTACATCTGGAACACACTCAACTC 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      631 AATTTCGCACACGTGTTGGGATTTGATAGCCCTCAGATGCTTGAGCTGATGCGTTTAT 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            870 ATGTGGAGAGAACATCTCGACAGAGCAGTTGAAAGATTATGTTTGGAAGACACTAAACAG 929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                   Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:693136
                                                                                                                                                                                            Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 127; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Stratagene muscle 937209"
/tissue_type="muscle"
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                                                                                                                                                         Washington University School of Medicine
                                                                                                                                                                                      4444 Forest Park Parkway, Box 8501, St. 7
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 143; DB 36;
Pred, No. 1.31e-80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 423.
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WashU-Merck EST Project
Unpublished (1995)
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Best Local Similarity 68.8%;
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                                                                                                                               Contact: Wilson RK
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                                   JOURNAL
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LOCUS 217455 213 bp mRNA EST 10-NOV-1992 DEFINITION ATTS0029 AC16H Arabidopsis thaliana CDNA clone TAT2B1 5' similar to CITRATE SYNTHASE, MITOCHONDFIAL PPECURSOP. Swiss-Prot entry P00889,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Bardet C., Axelos M., Tremousaygue D., Lebas M., Lagravere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Arabidopsis thaliana"
/strain="ecotype Columbia"
/note="Vector: Lambda ZAPII; tissue=cell suspension
culture of ecotype columbia; clone_library=Acli6H; Cloning
vector: Lambda ZAPII; Physiological condition: cycling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
Rosidae; Capparales; Brassicaceae; Arabidopsis.
1 (bases 1 to 213)
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                                                                     1020 GCCTGATGACCCATTTTTCAATTGGTGTCAAAGTTGTATGAAGTGGTGCCTCCTATTCT 1079
                                                                                                                                          381 GCCTAAAGATCCCATGTTCAAGCTGGTGGCTCAGCTGTACAAGATTGTGCCCCAATATCCT 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 AGIACTGAGGAAGACTGACCCTCGCTATTCCTGTCAGCGAGAGTTTGCTCTGAAACATCT 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 GTAGIGCACITICAGACCCATAICIGICATITIGCAGCIGCATIAAAIGGITTAGCIGGGC 124
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900 GAAAGATTATGTTTGGAAGACACTAAAACAGTGGCAAGGTTGTACCTGGATTTGGTCTAGG 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 TCACCATCCACAGTGATCATGAAGGTGGAAATGTTAGTGCTCACACACTGGTCACCTGGTTG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 135; DB 8; Length 213; Pred. No. 1.83e-74;
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BP 27,31338 Castanet-Tolosan cedex, France
Email: lescuredtoulouse.inra.fr.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                       1080 ATTAGAGCTTGGAAAGGTAAAGAATCCATGGCC 1112
                                                                                                                                                                                                                                         441 CTIAGAGCACGGGAAGCCIAAGAACCCIIGGCC 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:3702"
/clone="TAT2B1"
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40 c 52 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
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Matches 178; Conservative
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UMR05 CNRS/INRA
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217455
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                                                                                                                                  Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 473)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 TAATGTAAGTGC-CACACACAAGCCATTTGGTGGGCAGCGC-CTTTCAGACCCTTACCTGTC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             780 ATTIGCAGCAGCATTAAAIGGTTIGGCTGGGCCACTCCAIGGAITAGCCAACCAGGAAGT 839
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                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 GCTIGTCTGGCTGACACACTACAGAAGGAAGTIGGCAAAGACGTGTCAGATGAGAAGTT
                                                                                                                                                                                                                                                                                                           The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1402331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Barstead mouse pooled organs MPLRB4" /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                 Washu'HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 9.2%; Score 143; DB 14; Length 473; Best Local Similarity 68.0%; Pred. No. 1.31e-80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="pooled organs"
/dev_stage="7 day"
/lab_host="DHIOB"
/lab_host="DHIOB"
                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/Mouse EST Project
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/organism="Mus musculus"
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               4A498291.1 GI:2233314
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                                                                     house mouse.
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2; Gaps

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/organism-"Arabidopsis thaliana"
/organism-"Arabidopsis thaliana"
/strain-"var columbia"
/note-"Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note-"Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1)
day germinated etiolated seedlings: 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark-rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques. The vector is BL's lambda Zip-Lox. The obnA
inserts were directionally cloned with Sal-Not arms using
                                                                                                                                                                                                                                                                                                                                                                             Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C. Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones 95148729
                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis.
1 (bases 1 to 252)
                       AA720224 252 bp mRNA EST 30-DEC-1997 33417 Lambda-PRL2 Arabidopsis thaliana cDNA clone 158x12T7, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Michigan State University
MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.
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/clone_lib="Lambda-PRL2"
54 c 64 g 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSU-DOE Plant Research Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oligo dT primed cDNA./db_xref-"taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Thomas Newman
                                                                                                                                                               AA720224.1 GI:2733834
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Arabidopsis thaliana
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1247 IGCCGCIAGAGAGGCCAAAGAG 1268
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Search completed: Sat Oct 23 19:13:43 1999
Job time: 2657 secs.

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	(WE)
Release Copyrig	1A John F. Collins, Biocomputing Research Unit. (c) 1993-1998 University of Edinburgh, U.K. stribution rights by Oxford Molecular Ltd
MPsrch_pp protein -	in - protein database search, using Smith-Waterman algorithm
Run on: Tabular output not	<pre>Fri Oct 22 15:45:02 1999; MasPar time 17.45 Seconds 532.612 Million cell updates/sec t generated.</pre>
Title: Description: Perfect Score: Sequence:	>US-08-702-718-4 (1-437) from US08702718.pep 3243 I SSNLDLFSELQELIPEQQEPLERPKSVTMEWLEKFCKFFA 437
Scoring table:	PAM 150 Gap 11
Searched:	170751 seqs, 21266608 residues
Post-processing:	Minimum Match 0% Listing first 45 summaries
Database:	a-geneseq35 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part4 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part2 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 40:part30 31:part31 32:part37 38:part38 39:part39

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Variance 154.962; scale 0.230 Mean 35,586; Statistics:

### SUMMARIES

	Pred. No.	3.53e-302	1.87e-258	2.20e-242	2.20e-242	4.10e-17	1.28e+01	1.77e+01	2.45e+01	2.08e+01	6.36e+01	5.44e+01	6.36e + 01	6.36e + 01	4.64e+01	4.64e+01	5.44e+01
	Description	Sugar beet citrate sy	Tobacco citrate synth	Potato citrate syntha	Potato citrate syntha	Citrate synthase enco	Methionyl-tRNA synthe	Methyl tetrahydropter	An antitumour protein	New DNA sequence isol	AFT-1 interacting pro	H. pylori cell envelo	Equine herpesvirus (E	Equine herpesvirus US	H. pylori ORF 06ep302	ORF	H. pylori cell envelo
	ID	R82839	R82840	R86383	R82838	R14357	W20051	W38570	W87531	W56163	R89749	W20183	R84104	R52668	W55574	W55330	W21009
	DB	14	14	15	14	m	53	34	39	31	17	21	15	σ	29	д. С1	C1
	Query Match Length DB	437	469	471	471	436	657	456	266	738	219	237	324	324	329	329	461
æ	Query	100.0	86.3	81.3	81.3	9.6	e.	3.1	3.1	3.1	5.9	2.9	2.9	5.9	2.9	ص (1	9.5
	Score	3243	2800	2637	2637	312	103	101	66	100	93	94	93	93	95	95	94
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Partial sequence of b 6.36e+01 Omega-cyclohexane fat 6.36e+01 Cellulose synthase op 6.36e+01 Human secreted protei 1.02e+02 Rat CC chemokine rece 1.02e+02 Staphylococcus aureus 7.44e+01 Class II EPSPS used 7.44e+01 Class II EPSPS ynthas 7.44e+01 Cystathionine gamma s 1.02e+02 Tyrosine phenollyase 1.19e+02 Tyrosine phenollyase 1.19e+02 Tyrosine phenollyase 1.19e+02 Sequence transcribed 1.61e+02 Sequence blankollyase 1.19e+02 Pmell7 encoded by CDN 1.19e+02 Pmell7 encoded by CDN 1.19e+02	Carboxydothermus hydr CF-5 pathogen resista CF-5 pathogen resista CF-5 pathogen resista T.thermophilus nitrat Virulence gene cluste	on. 5S 0026 GMBH. Muller-rober B, Landschuetze V;	- used to reduce 1sh.  Which codes 2st from sugar energy and the codes 2st from sugar solution tube 2st from sequenced.	.53e-3 ches
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88888888888888888888888888888888888888	an ac ac ac ac	R82839 standard; R82839 standard; R82839 standard; 25-JAN.1996 (fii Sugar beet citral citrate synthase Citrate synthase Heta vulgaris st. W9524487-4 14-SEP-1995; E0.0 07-MAR-1994; DE-12-CEP-1994; DE-12-CEP-1994; DE-13-CEP-1994; DE-13-CEP-1994; DE-12-CEP-1994; DE-12-CEP-1994; DE-12-CEP-1994; DE-12-CEP-1994; DE-12-CEP-1994; DE-12-CEP-1994; DE-12-CEP-1994; DE-13-CEP-1994; DE-13-CEP-	N-PSDB, T042 DNA encoding to improve s Disclosure; To identify synthase, a synthase, a probes which synthase cDN (see T04201) given in T04 Sequence 4 ery, Match	Local hes 4
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DNA encoding plant citrate synthase - used to regulate flower formation,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35 ssgldlrselqelipeqqdrlkklksehgkvqlgnitvdmvlggmrgmtgllwetslldp 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : Gaps
                                                                                                                                                                                                                  141 NVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQL
                                  121 pdhvyktidalpitahpmtqfctgvmalqtrsefqkayekgihkskfweptyedclslia
                                                                                                                181 qvpvvaayvyrrmykngqviplddsldyggnfahmlgfdspqmlelmrlyvtihsdhegg
                                                                                                                                                                                                                                                                       kdyvwktinsgkvvpgfglgvlrktdprytcgrefalkhipddpffglvsklyevvppil
                                                                                                                                                                                                                                                                                                         301 KDYVWKTLNSGKVVPGFGLGVI,RKTDPRYTCQREFALKHLPDDPFFQLVSKLYFVVPPTI,
                                                                                                                                                                                                                                                                                                                                                                                         361 LELGKVKNPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRALGLPLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to improve storage of tubers, etc. and to reduce sprouting Disclosure; Page 60-63: 87pp; English.

To identify a cDNA from tobacco which codes for citrate synthase, a cDNA bank of leaf tissue from tobacco was prepd. Plaques of this cDNA bank were screened using a radioactive DNA probe which comprises Solanum tuberosum citrate synthase cDNA (T04199). One of the clones was sequenced. The nt. sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Landschuetze
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.3%; Score 2800; DB 14; Length 459;
larity 85.7%; Pred. No. 1.87e-258;
Conservative 34; Mismatches 27; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Landschutze V, Muller-rober B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AGRE ) HOECHST-SCHERING AGREVO GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tobacco citrate synthase.
Citrate synthase; flower formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R82840 standard; Protein; 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              pksvtmewlekfckrra 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 PKSVTMEWLEKFCKRRA 437
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22-SEP-1994; DE-435366.
19-OCT-1994; DE-438821.
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es 373; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 95-328278/42.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mueller-roeber B
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Inhibiting citrate synthase (CS) activity in plants - to inhibit of lower formation and improve storage capacity, e.g. in potatoes, also new CS sense and anti-sense DNA sequences.

Talso new CS sense and anti-sense DNA sequences.

Claim 5; Page 15-19; 35pp; German.

The potato citrate synthase (CS) gene or CDNA sequence encoding CS The potato citrate synthase (CS) gene or CDNA sequences. CS DNA sequences are useful for altering CS activity in plants. Antisense CS sequences are be used to inhibit CS activity in plants. Antisense CS sequences can be used to inhibit CS expression in plants and has the effect of inhibiting flower formation and by doing so improves the plant's storage capacity. This is partic. useful in crop plants of any kind but esp. useful in potatoes. In addition to altering CS activity the DNA sequences can also be used to identify similar sequences in the genomes of other plants and in the production of transgenic plants with altered CS activity. This sequence is represented the amino acid sequence of potato citrate synthase.
                                                                                                                                                                                                                                                  241 NVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQL 300
                                                                                                                                                             335 kdyawktlksgkvvpgfghgvlrktdprytcqrefalkhlpedplfqlvaklyevflqfl 394
                                                                                                                                                                                                        301 KDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYEVVPPIL 360
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                                                                   nvsahtghlvasalsdpylsfaaalnglagplhglangevllwiksvveecgeniskegl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Citrate synthase; inhibitor; increased storage capacity; potato;
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81.3%; Pred. No. 2.20e-242;
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Matches 356; Conservative
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                                                                                                                                                                                                                                                                                                                                                454 pksvtmewlenhckk 468
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22-SEP-1994; DE-435366.
19-OCT-1994; DE-438821.
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334 eqlkdyvwktlnsgkvvpgfghgvlrktvprytcqrefamkhlpedplfqlvsklyevfl 393
   238 EGGNVSAHTGHLVGSFLSDFYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENIST 297
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R14357 standard; Protein; 436 AA.
                                                                                                                                                                                                                                                                    23-JAN-1992 (first entry)
Citrate synthase encoded by aarA.
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W20051 standard; Protein; 657
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Best Local Similarity 31.1%;
Matches 102; Conservative
                                                                                                                                                 453 lerpksvtmewlengckk 470
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                                                                                                                                                                                                                                                                                                                                                                                                       (NAKA-) NAKANO SUMISE KK.
WPI; 91-329112/45.
                                                                                                                                                                                                                                                                                                     Acetic acid resistance.
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05-FEB-1990; JP-024395.
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05-FEB-1990; 024395.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding plant citrate synthase - used to regulate flower formation, to improve storage of tubers, etc. and to reduce sprouting Disclosure; Page 53-56, B7pp; English.

To identify a cDNA from potto which codes for citrate synthase, a CDNA fragment of citrate synthase from Arabidopsis thaliana was firstly amplified using A. thaliana cDNA and oligos T04202 and T04203 which are complementary to the 5' or 3' end of the coding region of A. thaliana cDNA for citrate synthase. The oligos additionally introduce BamHI cleavage sites at both ends of the amplified cDNA fragment. a cDNA library was prepd. from potato leaves and screened with A. thaliana citrate synthase cDNA. Positive clones were purified and sequenced. The nt sequence is given in T04199.
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                             274 eggnvsahtghlvasalsdpylsfaaalnglagplhglangevllwiksvveecgenisk 333
                                                                                         eqlkdyvwktlnsgkvvpgfghgvlrktvprytcgrefamkhlpedplfglvsklyevfl 393
                                                                                                                                                                 94 pdegirfrglsipecqkvlpaakpggeplpegllwllltgkvpskeqvnsivsgiaesgi 153
179 IAQVPVVAAYVYRPMYKNGQVIPLDDSLDYGGNFAHMLGFDSPQMLEL-MRLYVTIHSDH 237
                                                                                                                   298 EQLKDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYEVVP 357
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Mueller-roeber B;
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R82838 standard; Protein; 471
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22-SEP-1994; DE-435366.
19-OCT-1994; DE-438821.
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N-PSDB; T04199.
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Score 312; DB 3; Length 436;
Pred. No. 4.10e-17;
85; Mismatches 108; Indels 33; Gaps 29;
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91 eeviylllngelpnkaqydtftntltnhtllheqirnffngfrrdahpmailcgtvgals 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 a-f-ypdandiaip-an-rdla--a-mrliakiptiaawayk--ytqqeafiyprnd-ln 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 yaenflsmmfarmsepykvnpvlaramnrililhadheg-naststvrlagstganpfac 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 iaagiaalwgpahgganeavlk-mlarigk-kenipa-fiag-v-kdknsgvklmgfghr 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321 VLRKTDPRYTC-QRE-FA-LKHLP--DDPFFQLVSKLYEVVPPILLELGKVKNPWPNVDA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The aarA gene encodes the citrate synthase and is part of an acetic acid resistance operon comprising aarA, aarB and aarC. The DNA can be used to prepare an acetic acid resistant strain of bacteria for use in acetic acid fermentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acetic acid resistant gene with in plasmid and transformed acetobacter - improves yield of acetic acid fermentation. Disclosure; Fig 5; 12pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  373 ysgiilkamgiptsmf-tvlfavarttg 399
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding methionyl-tRNA synthetase from Staphylococcus aureus world 29 - useful for protection against bacterial infections of claim it Pages 19-20; Bnglish.

WCUH 29 - useful for protection against bacterial infections claim it Pages 19-20; Jupp: English.

The present sequence is a novel methionyl tRNA synthetase protein from Staphylococcus aureus strain WCUH29 (NCIMB 40771), which is related by amino acid sequence homology to Bacillus subtilis tRNA synthetase encoded by the mets gene. The enzyme catalyses the aminoacylation of tRNA-Met, by a two step mechanism. The first step involves formation of a stable enzyme:methionyl adenylate complex resulting from the specific binding and reaction of ATP and L-methionine. Subsequently, the 3' terminal adenosine of anzyme-bound tRNA-Met reacts with the aminoacyl adenylate, leading to to the esterification of the tRNA and release of AMP. Vectors comprising the DNA (or polynucleotides having at least 70 % identity to it) can be used for the recombinant production of the anzyme or tryme. The enzyme or its related DNA (through gene therapy) is used to induce an immunological response in a manmal to generate antibodies to protect against disease. The antibodies protect against disease. The antibodies protect against disease. The antibodies or by mechanical, chemical or thermal damage or by mechanical, chemical or thermal damage or by morphysics or wounds in the mucous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Methyl tetrahydropteroyltriglutamate-homocysteine methyltransferase. Streptococcus pneumoniae protein; genetic immunisation; antagonist; immunological response; inoculation; antibody production; inhibitor; T cell immune response; antimicrobial compound; bacterial adhesion; extracellular matrix protein; protein-mediated cell invasion; wound; pathogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel Streptococcus pneumoniae proteins and related DNA - useful for diagnosing anti-microbial agents for treatment of bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Methionyl-tRNA synthetase from Staph. aureus. tRNA synthetase; Bacillus subtilis; metS; immunological response; antibody; bacterial infection; adherence; damaged tissue; wound healing; skin; protection; vaccine. Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Mismatches 10; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 23; Length 657;
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(SMIK ) SMITHKLINE BEECHAM PLC.
Black MT, Hodgson JE, Knowles DJC, Nicholas RO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 ilmkdgkmskskgnv-vdpnilidrygldatryy 334
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Pred. No. 1
                                                                                                                                                                                                                          23-JUL-1997,
17-JAN-1997, 300317.
19-JAN-1996, GB-001095,
27-JUL-1996, GB-015845.
(SMIK ) SMITHKLINE BEECHAM PLC.
Hodgson JE, Lawlor EJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W38570 standard; Protein; 456 AA.
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Local Similarity 38.2%;
les 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                        Hodgson JE, Lawlor EJ;
WPI; 97-365943/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-017670.
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14-MAY-1996; US-0176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; T71309
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This sequence represents a Streptococcus pneumoniae protein that, based on homology with an E. coll protein, is a methyl tetrahydropteroyltri glutamate-homocysteine methyltransferase, and is encoded by a DNA of the invention. The DNA sequences were isolated from S. pneumoniae strain closops (NCIMB 40794). The Streptococcus pneumoniae proteins of the invention can be used to identify compounds which interact with and inhibit or activate the activity of the proteins. Antagonists can be used to treat diseases caused by S. pneumoniae proteins, through genetic immunisation. They can also be used to induce an immunological response in a mammal by inoculation with the S. pneumoniae proteins or delivery of the encoding nucleic acids in a vector adequate to produce antibody and/or recal immune responses to protect the animal from disease. The proteins can also be used to identify antimicrobial compounds which are capable of inhibiting their bioactivity. In particular the proteins of the invention can be used to prevent adhesion of bacteria to mammalian extracellular matrix proteins on in-dwelling devices or in wounds, to block protein-mediated mammalian cell invasion, and to block the normal implantation of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or other surgical techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               249 vyadlvnlpvdaigl-dfvegkktlelvkggfpadktlyvgivngkniwrnnyekslavl 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308 eqipa-enivltsscsllhv-pfttaneefepallnhfaf-avekldeirdldairnqqq 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 dqyddsirqivvketlqqtldasrgvttlplgverrtdnpiyvtwtgadtvlgdvpkspr 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transformed by vector containing base coding sequence
Claim 1; Page 7-8; 15pp; Japanese.
The present sequence encodes an antitumour protein, and is isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 101; DB 34; Length 456; Pred. No. 1.77e+01;
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15; Mismatches 26; Indels
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Tricholoma matsutake.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 99;
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(NORQ ) NORINSUISANSHO SHOKUHIN SOGO.
WPI; 99-074153/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W87531 standard; Protein; 566 AA
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Local Similarity 32.38;
Les 21; Conservative
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Best Local Similarity 19.6%;
Matches 30; Conservative
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Sequence 566 AA;
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13-FEB-1997; JP-029275.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; V83626.
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                                                                                                                                                                                                                                                 New CDNA and e.g. vector, host cell and polypeptide - used to produce polypeptide in high yields, which is used in cosmetics claim 9; pages 9-11. 15pp: Japanese. The present sequence represents protein encoded by a new DNA sequence isolated from Pinctada fucata. The protein be used as an ingredient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transduction events involved in plant defence responses to pathogens such as fungi, nematodes, bacteria and viruses.
Sequence 219 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant transcriptional activator AFT-1 - isolated from Arabidopsis and useful for modifying gene expression and modulating plant defence responses to pathogens.

Plant defence responses to pathogens.

R89749 is a partial Arabidopsis proteasome, a plant defence-related protein PDRPS were isolated using a protein tresidues 33-194 fusion protein, i.e. AFTI (Arabidopsis 14-3-31) protein residues 33-194 fused to Lexa, a DNA binding protein, in an interaction trap assay. AFTI is a transcriptional activator protein and may be used to enhance, control or modify plant gene expression, e.g. in the regulation of plant storage components (esp. napin, legumin or phaseolin). AFTI can also be used to modulate signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-5EP-1996 (first entry)
AFT-1 interacting protein (partial proteasome).
Arabidopsis fourteen-three-three 1; AFT1; Cruciferae; regulation;
transcription activator; gene expression modulator; crucifer;
signal transduction; defence response; gene therapy; transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                   3.1%; Score 100; DB 31; Length 738; 34.4%; Pred. No. 2.08e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 93; DB 17; Length 219;
Pred. No. 6.36e+01;
8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Mismatches 11; Indels
                                                28-JUL-1998 (first entry)
New DNA sequence isolated from Pinctada fucata.
Pinctada fucata; protein; cosmetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 VIPLDDSLDYGGNFAHMLGFDSPQMLELMRLY 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 rltllkkhffsyq-ghvsaalvlggv-ditg 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 lvgfssalsfgcnyrpvlgfnsgymlgglrlf 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 RLKKIKKEFGSFOLGNINVDMVLGGMRGMTG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JAN-1996.
22-JUN-1995; 109669.
23-JUN-1994; US-266451.
(GEHO ) GEN HOSPITAL CORP.
(MASS-) MASSACHUSEITS GEN HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R89749 standard; Protein; 219 AA.
               W56163 standard; Protein; 738 AA
                                                                                                                                                          28-MAY-1997; 138461.
15-JUL-1996; JP-184459.
(MIKI-) MIKIMOTO SEIYAKU KK.
WPI; 98-254410/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.9%;
Local Similarity 45.2%;
Les 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 34.4%;
nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goodman HM, Zhang H; WPI; 96-078601/09.
                                                                                                                                                                                                                                                                                                                                                                  738 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis sp.
                                                                                                                                                                                                                                     N-PSDB; V22683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP-693554-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; T11341
                                                                                                                                                                                                                                                                                                                                               cosmetics
                                                                                                                                            31-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                  W56163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R89749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
RESULT
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08-JUL-1997 (first entry)

1. pylori cell envelope transporter protein, 179677.aa.

Cytoplasmic; vaccine; prevention; treatment; infection; identification;

Cytoplasmic; vaccine; prevention; iffe cycle; activator; bacteria, inhibitor;

duodenal ulcer disease; chronic gastritis; diagnosis; envelope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a Helicobacter pylori cell envelope transporter protein. The protein may be used in a vaccine to prevent or treat H. Pylori infection or to identify H. Pylori polypeptide binding compounds, useful as potential H. Pylori life cycle activators or inhibitors. The genomic sequence of H. Pylori life cycle activators or determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. Pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 VVAAYVYRRMYKNGQVIPLD-DSLDYGGNFAHMLGFDSPQMLELMRLY--VTIHSDHEGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85 viptfalalmptfndlvgfgvdsmgltpknahylgyiapvflvlvricqgvavggelpga 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAR-1996 (first entry)
Equine herpesvirus (EHV4) unique short (US2) gene prod..
Equine herpesvirus 4; EHV4; unique short; US2; recombinant; vaccine; attenuated virus; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori nucleic acid sequences and related bolypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter claim 56; Pages 401; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "EHV-1, EHV-4, HSV-1, PRV, HSV-2, MDV, and IBR consereved US2 region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 NVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHG-LANQEV-LLWIKSVVDE 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 wvfvh-ehapqgq-kntyigflta-svvsgillgslvyigiymvfdkpvved 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.9%; Score 94; DB 21; Length 237;
24.1%; Pred. No. 5.44e+01;
Ative 33; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                     /note= "encoded by cocon GTR"
                                                                                                                                                                                                                                           'note= "encoded by codon TIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith D, Mellgaerd BL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R84104 standard; Protein; 324 AA.
R84104;
T 11
W20183 standard; protein; 237 AA.
                                                                                                                                                             cell envelope; transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 24.1%;
nes 27; Conservative
                                                                                                                                                                                                                                                                                                                                             06-JUN-1996; U09122.
07-JUN-1995; US-487032.
01-APR-1996; US-630405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Equine herpesvirus 4
                                                                                                                                                                                   Helicobacter pylori.
                                                                                                                                                                                                                      misc_difference 126
                                                                                                                                                                                                                                                               misc_difference 127
                                                                                                                                                                                                                                                                                                                                                                                                                               Berglindh OT, Smit
WPI; 97-052306/05.
N-PSDB; T67415.
                                                                                                                                                                                                                                                                                                                                                                                                              (ASTR ) ASTRA AB.
                                                                                                                                                                                                                                                                                                        WO9640893-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09522607-A1
                                                                                                                                                                                                                                                                                                                                19-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qγ
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                         .
9
                                                                                                                                                                                                                                                       T00532 encodes R84104 the equine herpesvirus 4 (EHV) unique short 2 (US2) gene prod. A recombinant attenuated EHV can be produced by deleting the above US2 gene (a region not essential for replication) from the viral DNA. The attenuated virus can be used as a foetal safe vaccine to protect an equine against EHV, or in a test to determine if an equine has been vaccinated against or is infected with EHV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 nkswqpsfv-cgklfetiplttv-dykhllkq-kvlpgqdhpesarsllqhkssfvsppp 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nkswqpsfv-cgklfetiplttv-dykhllkq-kvlpgqdhpesarsllqhkssfvsppp 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 SKFWEPTYEDCLSLIAQVPVVAAYVYRRMYKNGQVIPLDDSLDYGGNF-AHMLGFDSPQM 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant equine herpesvirus (EHV) have a foreign DNA sequence inserted into their genomes. The inserted sequence is a piece of foreign, double stranded DNA which encodes an RNA molecule which does not naturally occur in the animal into which the EHV is introduced. The foreign DNA sequence is introduced into the EHV is a homology vector. The cocombinant EHV's are used to prepare vaccines to protect horses from infectious EHV. Recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Equine herpesvirus US2 gene product.
Equine herpesvirus, US2; vaccine; antigen; protection; prophylaxis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Equine herpesvirus (Strain: Dutta; Individual isolate: S-4EHV-000).
                                                                                                                                                      Recombinant equine herpes viruses pref. contg. a deletion in a region not essential for replication - used in vaccines to protect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant equine herpes viruses - used to prepare vaccines to protect horses from infectious equine herpes virus Example 1; Paye 84-86; 153pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 93; DB 15; Length 324;
Pred. No. 6.36e+01;
24; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                attenuated EHV's can be produced by removing the US2 gene. Sequence 324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match
Local Similarity 24.7%; Pred. No. 6.36e+01;
ies 18; Conservative 24; Mismatches 25
                                                                                                                                                                                                          horses from infection
Example 13; Pages 89-90; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R52668 standard; Protein; 324 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.9%;
Best Local Similarity 24.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-AUG-1993; U07424.
07-AUG-1992; US-926784.
                      17-FEB-1994; US-198094.
                                                                           Cochran MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 -nfkrliyavvdp 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224 LELMRL-YVTIHS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 LELMRL-YVTIHS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 -nfkrliyavvdp 224
                                               (SYTR ) SYNTRO CORP. Chiang CH, Cochran N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SYTP ) SYNTRO CORP.
16-FEB-1995; U02087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 94-065715/08.
                                                                                              95-302714/39.
                                                                                                                                                                                                                                                                                                                                                                                                                        324 AA;
                                                                                                                               N-PSDB; T00532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; Q56617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09403628-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cochran MD;
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
RE
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No rection and for diagnosis of H. pylori infection

Polypeptide(s) - useful in vaccines to treat or prevent H. pylori

Infection and for diagnosis of H. pylori infection

Infection and for diagnosis of H. pylori infection

Catalms 14,96; Page 779-779; 1145pp: English.

Catalms 14,96; 114pp: English.

Catalms 14,96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interest, particular regions can be isolated from H. pylorí by PCR amplification for recombinant polypeptide production, e.g. in E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-1998 (first entry)
H. pylori ORF hp3ell024orf49 protein.
H. pylori ORF hp3ell024orf49 protein.
H. pylori onscine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
Helicobacter pylori.
99737044A1.
99-007-1997.
                                                                    24-JUN-1998 (first entry)
H. pylori ORF O6ep30223_23557202_c2_130 cytoplasmic protein.
H. pylori orF of the prevention; treatment; infection; envelope: identification; binding compound bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 95; DB 29; Length 329;
Pred. No. 4.64e+01;
16; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 veempliasvifnrl-kkgmplqmdgalnyq-efsh 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 IAQVPVVAAYVYRRMYKNGQVIPLDDSLDYGGNFAH 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W55330 standard; Protein; 329 AA.
W55574 standard; Protein; 329 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.9%;
Best Local Similarity 27.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Conservative
                                                                                                                                                                                                                                                                                                                                     09-OCT-1997.

05-DEC-1997.

06-DEC-1996; US-761318.

29-MAR-1996; US-625811.

20-APR-1996; US-58731.

25-OCT-1996; US-738859.

28-OCT-1996; US-738859.

ALM RA, SMIKED D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-736905.
US-738859.
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                                                                                                                                                                                                                                                                Helicobacter pylori.
WO9737044-Al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; V24983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-DEC-1996;
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28-OCT-1996;
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                                    W55574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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AMERRA ASTRA AB.

PI ALM RAY, SMITH D.

BY WPI: 97-50312246.

BR WPI: 97-50312246.

BR WPI: 97-50312246.

BR Hollochacter pylori nucleic acid sequences and encoded probacter pylori nucleic acid sequences to treat or prevent H. pylori protein and tor diagnosis of H. pylori infection and for diagnosis of H. pylori infection

BY Claim 14; Pages 556-557; 1145pp; Engilsh.

CC This sequence is a H. pylori protein of unspecified function.

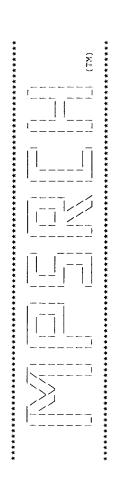
CC This sequences or inhibitors. The compounds of the pylori in a sample and the diagnosis of H. pylori infection or to identify H. pylori polypeptide binding compounds.

CC useful as potential H. pylori life cycle activators or inhibitors. The cut sequences complementary to the DNA and somblibitors. The cut sequences or complementary to the DNA and somblibitors and acid sequences or immibitors. The cut sequences or complementary to the DNA and somblibitors and distribution of H. pylori infection of H. pylori infection. Nucleic addistribution of H. pylori-specific antigens. The genomic sequences and distribution of H. pylori-specific antigens. The genomic sequences or addistribution of H. pylori-specific antigens. The genomic sequences or addistribution of H. pylori-specific antigens. The genomic sequences or core. For ore or or ore the actions to the bacterial DNA. The sequences or and version of H. pylori-specific antigens for or or ore feet least 180 nucleotides, and the predicted fooling regions conting education for significant and active from versions can be isolated from H. pylori by PCR companies, particular regions can be isolated from H. pylori by PCR consisting the particular sequences of interest, particular regions can be isolated from H. pylori by PCR consist Abach and active Now 1664e+01; Matches 10; Conservative 16; Mismatches 8; Indels 2; Gaps 2; Babst Local Similarity 27.8%; Pacer 951.
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Search completed: Fri Oct 22 16:48:53 1999 Job time: 231 secs.

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Fri Oct 22 16:32:52 1999; MasPar time 29.50 Seconds 871.352 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-702-718-2 (1-471) from US08702718.pep 3466 1 MVFYRSVSLLSKLRSRAVQQ......PLERPKSVTWEWLENQCKKA 471 Title:

Description: Perfect Score:

Sednence:

PAM 150 Gap 11 Scoring table:

179066 seqs, 54579741 residues Searched: Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptremb19
1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle
9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified
13:sp\_vertebrate 14:sp\_virus

Mean 49.897; Variance 94.480; scale 0.528 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES		
Result	Score	Query	Query Match Length	ä	II	Description	NO POST
	2 1 1 2 2 1 1		5000			reset therein	
7	3466	100.0	471	10	043175	ETHANOLAMINE AMMONIA-L	0.00e+00
2	3098	89.4	469	10	024135	CITRATE SYNTHASE (EC 4	0.00e+00
٣	2892	83.4	472	10	080433	CITRATE SYNTHASE (EC 4	0.00e+00
4	2820	81.4	474	10	C64869	CITRATE SYNTHASE (EC 4	0.00e+00
Ŋ	2637	76.1	437	10	096544	CITRATE (SI)-SYNTHASE	0.000+00
9	2058	۲. س	339	10	024259	CITRATE (SI)-SYNTHASE	0.00e+00
7	1897	54.7	466	4	075390	CITRATE SYNTHASE (EC 4	0.00e+00
00	270		411	7	053115	CITRATE SYNTHASE (FRAG	2.160-28
σ	264	7.6	411	C1	059777	CITRATE SYNTHASE (EC 4	2.91e-27
10	263	7.6	411	7	P77936	CITRATE SYNTHASE (EC 4	4.490-27
11	261	•	356	C a	054382	CITRATE SYNTHASE (EC 4	1.07e-26
12	251	7.5	372		028929	CITRATE SYNTHASE (CITE	1.070-26
13	260	7.5	411	C1	060047	CITRATE SYNTHASE (EC 4	1.64e-26
14	259	7.5	411	7	059469	CITRATE SYNTHASE (EC 4	2.53e-26
15	258	7.4	411	~	059779	CITRATE SYNTHASE (EC 4	3.89e-26
16	256		411	C3	059775	CITRATE SYNTHASE (EC 4	9.20e-26
17	246	7.1	379	c į	034002	CITRATE SYNTHASE.	6.64e-24
18	243	7.0	410	C1	697650	CITRATE SYNTHASE (EC 4	2.38e-23
19	229	9.9	379	~	032705	CITRATE SYNTHASE (EC 4	8.73e-21
20	229	9.9	429	C 3	033915	CITRATE SYNTHASE (EC 4	8.73e-21

1.07e-19 5.60e-19 4.40e-18	.31e .17e	4 - 1 - 1 - 1	.63e- .80e- .30e-	2.00e-01 6.63e-01 2.70e-01 2.70e-01 3.65e-01	3.65e-01 3.65e-01 8.91e-01 1.19e+00 1.60e+00
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068883 P94325 033066	923	7 8 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	00000	Q57513 O67104 O14969 Q53751 O47153	082180 016103 059641 047160 062977
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223	200 193 189	181 181 181	180 153 128 113	100 100 100 100 100	1004 1004 1004 1003 1003
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## ALIGNMENTS

		PHYTA; ;		expression			; 0; Gaps	LKKIK 60		 KPGGE 120	FATGV 180        FATGV 180
		GURANDOTA, VIPIDIPLANTE: STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; EUFHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; AGTERIDAE; SOLANANAE; SOLANALES; SOLANACEAE; SOLANUM.			+ NH(3).		Length 471; Indels 0	WVFYRSVSLLSKLRSRAVQSNVSNSVRMLQVQTSSGLDLFSELVQELTPEQQDPLKKIK 	SDWKGSIGNITVDMVLGGMPGHTGLLWKPHYLDPDEGIRFFGLSIPETQKVLPAAKPGGE	SDMKGSIGNITVDMVLGGMRGMTGLLMRPHYLDPDEGIRFRGLSIFECQKVLPAAKPGGE	PLPEGLLMLLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATGV 
:	PDATE)   UPDATE)	VERDOUM (TOTALO). VERDOUPLANTA: EMBPYOPHYTA: TES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOT SOLANANAE; SOLANALES; SOLANACEAE; SOLANDM.		LANDSCHUTZE V., WILLMITZER L., MUELLER-FREBER R; "Mitochondria" citrate synthase from potato: predominant in mature leaves and young flower buds.";	- ACETALDEHYDE	32;	10; +00; 0;	DLRSELVQI	P.F.F.GL.SIP	RERGLSIF	MYTTIDALI           MYTTIDALI
471 AA	SEQUENCE UPDATE) ANNOTATION UPDATE) 3.1.7).	IYTA; EMB VOLIOPHYT )LANACEAE		MLER-ROE om potato ouds.";		00. BC96A65C CRC32	3466, DB 10; No (00e+00; Mismatches 0	QVQTSSGL 	TEDPDEGI	YLDPDEGI	SGIISTII
PRT;	CREAT LAST LAST (EC 4.	STREPTOPH KTA; MAGN NALES; SC		R L., MUE thase fro flower b	ETHANOLAMINE	mn15200. MW; BC96	Score 3466; Pred No O O; Mismato	NVSNSVPWI 	MTGLLWKPF	MIGLEWKP	NSIVSGIAE
PRELIMINARY;	04-1/3; 01-NOV-1996 (TREMBLREL. 01, 01-NOV-1996 (TREMBLREL. 01, 01-JAN-1999 (TREMBLREL. 09, 01-JAN-1MINE AMMONIA-IYASE	SOLANOM TUBEROSOM (FOTATO) EUKAPYOTA; VIRIDIPLANTAE; 6 EUPHYLLOPHYTES; SPERMATOPH; ASTERIDAE; SOLANANAE; SOLA!		LANDSCHUETZE V. WILLMITZER L., MUELLER-PA "Mitochondria" citrate synthase from pota in mature leaves and young flower buds.";	ACTIVITY: ETI COBALAMIN. G483510;	52612	Query Match 100.0%; Rest Local Similarity 100.0%; Matches 471; Conservative	PSPAVQQSI          RSPAVOOSI	MVLG3MPG		KVPSKEQVI           KVPSKEQVI
PRELIM	(TREMBLREL. (TREMBLREL. (TREMBLREL.	VIRIDIP VIRIDIP TES; SP SOLANAN	OM N.A. DESIREE	E V., W iai cit	/56-/64 IC ACTI R: COBA 12; G483		nilarity Conse	VSLLSKL 	IGNITVD	SIGNITAD	LWLLLTG
1 043175	04.51/3; 01-NOV-1996 01-NOV-1996 01-JAN-1999 ETHANOLAMIN	SOLANDM TUB EUKARYOTA; EUPHYLLOPHY ASTERIDAE;	SEQUENCE FROM N.A. STRAIN-CV. DESIREE;	DSCHUETZ tochondr	PLANTA 196: 555-764(1995)!- CATALYTIC ACTIVITY: E!- COFACTOR: COBALAMIN. EMBL; X75082; G483510;	MENDEL; 152 LYASE. SEQUENCE	Match ocal Sim s 471;	1 MVFYPS			
RESULT ID Q431			RP SEQUENCE STRUCTURY		KL PLANIA CC -!- CA CC -!- CO DR EMBL;		Query 1 Rest L/ Matches	40 %	25 Db 61	Qy 61	Db 121 Qy 121

0

181 MALQVQSEFQKAYEKGIHKSKYWEFTYEDSMNLIAQVPLVAAYVYRRMYKNGDTIFKDES 240

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240
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                                                         241 LDYGANFAHMLGFSSSEMHELLMRLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFAAA 300
                                                                                              241 LDYGANFAHMLGFSSSEMHELLMRLYVIIHSDHEGGNVSAHTGHLVASALSDPYLSFAAA 300
                                                                                                                                   301 LNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYVWKTLNSGKVVPGFGHGVLRK 360
                                                                                                                                                                                                               361 TVPRYTCQREFAMKHLPEDPLFQLVSKLYEVFLLFLQNLAKLKFWPNVDAHSGVLLNYYG 420
                                                                                                                                                                                                                                                    361 TVPRYTCQREFAMKHLPEDPLFQLVSKLYEVFLLFLQNLAKLKPWPNVDAHSGVLINYYG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEHGKVQLGNITVDMVLGGMRGMTGLLWETSLLDPDEGIRFRGLSIYECQKVLPAAKPGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SDM-KGSIGNITVDMVLGGMRGMTGLLWKFHYLDFDEGIRFRGLSIFECQKVLFAAKFGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 EPLPEGLLWLLLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 VMALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLIAQVPLVAAYVYRRMYKNGNTIPKDD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 VMALQVQSEFQKAYEKGIHKSKYWEPTYEDSMNLIAQVPLVAAYVYRRMYKNGDTIPKDE 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLDYGANFAHMLGFSSSDMHEL-MKLYVIIHSDHEGGNVSAHTGHLVASALSDPYLSFAA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MVFYRGVSLLSKLRSRAVQQTNLSNSVRWLQVQTSSGLDLRSEL-QELIPEQQDRLKKLK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEDPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
ASTERIDAE; SOLANANAE; SOLANALES; SOLANACEAE; NICOTIANA.
                181 MALQVQSEFQKAYEKGIHKSKYWEPTYEDSMNLIAQVPLVAAYVYRRMYKNGDTIPKDES
                                                                                                                                                         120 EPLPEGLLWLLITGKVPSKEQVDSLSQELRSRATVPDHV-YKTIDALPVTAHPMTQFATG
.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV. SNN;
LA COGNATA U. LANDSCHUETZE V., WILLMITZER L., MUELLER-POEREP
PLANT CELL PHYSIOL. 0:0-0(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF
OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                           421 LTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENQCKKA 471
                                                                                                                                                                                                                                                                                                             Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
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Pred. No. 0.00e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                            469 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -! - SIMILARITY: TO OTHER CITRATE SYNTHASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; A04220; E13'432; T.
PROSITE; PSOUBOB; CITRATE_SYNTHASE; 1.
PFAM; PF00285; Citrate_synt; 1.
LYASE; TRICARBOXYLIC ACID CYCLE.
SEQUENCE 469 AA; 52492 MW; 6BE3C32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TREMBLREL. 05, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NICOTIANA TABACUM (COMMON TOBACCO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITRATE SYNTHASE (EC 4 1 3 7)
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                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X84226; E137432;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423;
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024135
024135;
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                                                                                                           358 RNTDPRYICQREFALKHLPDDPLFQLVSNLFEVVPPILTELGKVKNPWPNVDAHSGVLLN 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 RKTVPRYTCQREFAMKHLPEDPLFQLVSKLYEVFLLFLQNLAKLK-PWPNVDAHSGVLLN 417
298 ALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYAWKTLKSGKVVPGFGHGVLR 357
                                          300 ALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYVWKTLNSGKVVPGFGHGVLR 359
                                                                                358 KIDPRYTCQREFALKHLPEDPLFQLVAKLYEVFLQFLQNLAKLNPWPNVDAHSGVLLNYY 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 KAEHGKVQLGNITVDMVLGGMRGMTGLLWETSLLDPEEGIRFRGLSIPECQKLLPGAKPG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 GEPLPEGLLWLLLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQFAT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 GVMALQVQSEFQKAYEKGIHKTKYWEPTYEDSITLIAQLPVVAAYIYRRMYKNGQSISTD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 ESLDYGANFAHMLGFSSSEMHELLMRLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 AALNGLAGPLHGLANQEVLLWIKSVVSECGENVTKEQLKDYIWKTLNSGKVVPGYGHGVL 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MVFFRSVSLLNKLRSRAVQQSNLSNTVRWFQVQTSASDLDLRSQL-KELIPEQQERIKKL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              DAUCUS CAROTA (CARROT).
URADIDE VIRDIDELANTAE: STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
ASTERIDAE: ARALIALES; APIACEAE; DAUCUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 DSLDYGANFAHMLGYDSPSMQEL-MRLYVIIHTDHEGGNVSAHTGHLVASALSDPYLSFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MVFYRSVSLLSKLRSRAVQQSNVSNSVRWLQVQTS-SGLDLRSELVQELIPEQQDRLKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 GEPLPEGLLWLLLTGKVPTKEQVDALSAELRSRAAVPEHV-YKTIDALPVTAHPMTQFAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                     418 GLTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENHCKKA 469
                                                                                                                                                                                         420 GLTEARYYTVLFGVSRALGICSQLIMDRALGLPLERPKSVTMEWLENGCKKA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)O OXALOACETATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 0.00e+00;
55; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAID—CV. MS YONSUN;

TAKITA E., FOXAMA H., SHIRANO Y., SHIBATA D., HARA T.;

"CDMA encoding carrot mitochondrial citrate synthase.";

SUBMITTED (AUG-1998) TO EMEL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                     01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITAATE SYNTHASE (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 2892; DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: TO OTHER CITRATE SYNTHASES.
EMBL: AB017159: D1033521; --
PROSITE: PS00480: CITRATE_SYNTHASE; 1.
PTASE: TRICARBOXYLIC ACID CYCLE.
SEQUENCE 472 AA; 52656 WW; D46C38CC CRC32;
                                                                                                                                                                                                                                                                                                  472 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PATHWAY: TRICARBOXYLIC ACID CYCLE
                                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TREMBLREL. 08, CREATED)
                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.48;
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Matches 383; Conservative
                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                      080433;
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EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 AEPLPEGILMILLIGKVPSKEQVEALSKDLANRAAVPDYV-YNAIDALPSTAHPMTGFAS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 GVMALQVQSEFQKAYEKGIHKSKYWEPTYEDSMNLIAQVPLVAAYVYRRMYKNGDTIPKD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 ESLDYGANFAHMLGFSSSEMHELLMRLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299 AALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYVWKTLNSGKVV?GFGHGVL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 KSEHGKVQLGNITVDMVIGGMRGMTGLLWETSLLDPEEGIRFRGLSIPEC2KVLPTAQSG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 GVMALQVQSEFQKAYENGIHKSKFWEPTYEDCLNLIARVPVVAAYVYRRMYKNGDSIPSD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 RNIDPRYVCQREFALKHLPDDPLFQLVSKLYEVVPPVLTELGKVKNPWPNVDAHSGVLLN 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MVFFRSVSAFTRLRSRVQGQGSSLSNSVRWIQMQSSTDLDLKSQL-QELIPEQQDRLKKL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MVFYRSVSLLSKLRSRA-VQQSNVSNSVRWLQVQTSSGLDLRSELVQELIPEQQDRLKKI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55; Mismatches 38; Indels 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 KSLDYGANFSHMLGFDDEKVKEL-MRLYITIHSDHEGGNVSAHTGHLVGSALSDPYLSFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 AALNGLAGPLHGLANQEVLLMIKSVVEECGEDISKEQLKEYVWKTLNSGKVIPGYGHGVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               418 YYGLTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENQCKKA 471
                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CV. COLUMBIA;
ROUNGLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.P., ADAMS M.D.,
SOMERVILLE C.R., VENTER J.C.;
SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        418 HYGLTEARYYTVLFGVSRSLGICSQLIWDRALGLALERPKSVTMDWLEAHCKXA 471
  418 HYGLTEARYYTVLFGVSRAIGICSQLVWDRALGLPLERPKSVTMEWLENHCKKS 471
                      418 YYGLTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENQCKKA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY CITPATE + COA = ACETYL-COA + H(2)9
                                                                                                                                                                        (TREMBLREL. 07, LAST SEQUENCE UPDATE)
(TREMBLREL. 07, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2820; DB 10;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i-STMILARITY TO OTHER CITRATE SYNTHASES.
EMBL; ACO04521; G3120180; --
PROSITE; PSO0460; CITRATE_SYNTHASE; 1.
SEQUENCE 474 AA; 52782 MW; 64FF2AC6 CRC32;
                                                                                                                  474 AA
                                                                                                                                                                                                                                                       ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)
                                                                                                                                                                                                                                                                                                                   CAPPARALES; BRASSICACEAE; ARABIDOPSIS
                                                                                                                                                       01-AUG-1998 (TREMBLREL. 07, CREATED)
                                                                                                                    PPT;
                                                                                                                                                                                                                 CITRATE SYNTHASE (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 81.4%;
Best Local Similarity 79.1%;
Matches 375; Conservative
                                                                                                                  PRELIMINARY;
                                                                                                                                                                                           01-AUG-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                         SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OXALOACETATE
                                                                                                                                                                            01-AUG-1998
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064869
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                                          01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-TEB-1999 (TREMBLREL. 09, LAST SEQUENCE UPDATE)
CITAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
CITAN-1999 (TREMBLREL. 09, LAST) (CONDENSING ENIXME)
(CITRATE (SI)-SYNTHASE (CG. 4.1.3.7) (CONDENSING ENIXME)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 IAQVPLVAAYVYRRMYKNGDTIPKDESLDYGANFAHMLGFSSSEMHELLMRLYVTIHSDH 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 PEEGIRFRGFSIPECQKLLPAASAGAEPLPEGLLWLLLTGKVPSKEQVDALSADLRKRAS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 EQLKDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYEVVP 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 PDEGIRFRGLSIPECOKVLPAAKPGGEPLPEGLLWLLLTGKVPSKEQVNSIVSGIAESGI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 ISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKYWEPTYEDSMNL 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGGNVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENIST 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SSNLDLRSEL-QELIPEQQERLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35 SSGLDLPSELVQELIPEQQDPLKKIKSDMKG-SIGNITVDMVLGGMPGMTGLLWKPHYLD 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TPACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
CARYOPHYLLIDAE; CARYOPHYLLALES; CHENOPODIACEAE; BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 IPDHV-YKTIDALPITAHPMTQFCTGVMALQTRSEFQKAYEKGIHKSKFWEPTYEDCLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 IAQVPVVAAYVYRRMYKNGQVIPLDDSLDYGGNFAHMLGFDSPQMLEL-MRLYVTIHSDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358 PILLELGKVKNPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRALGLP
                                                                                                                                                                                                                                                                                                                                                          ď
                                                                                                                                                                                                                                                                                                                                                     LA COGNATA U., LANDSCHUETZE V., WILLMITZER L., MUELLER-ROEBER
PLANT CELL PHYSIOL. 0:0-0(0).
-i- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41; Mismatches 36; Indels
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024259.
01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE (SI)-SYNTHASE EC 4.1.3.7) (CONDENSING ENZYME)
(CITRATE CONDENSING ENZYME) (CITRAGENASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 2637; DB 10;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  437 AA; 48881 MW; 003588CE CRC32;
    437 AA.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00285; citrate_synt; 1.
MENDEL; 15201; BETvu;2977;mn15201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match
Local Similarity 81.3%;
nes 356; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  418 LERPKSVTMEWLEKFCKR 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              453 LERPKSVTMEWLENGCKK 470
                                                                                                                                                                                                               BETA VULGARIS (SUGAR BEET)
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X84228; E137433; -.
    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                            OXALOACETATE
                                                                                                                                                                   (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                        096544;
096544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
              POPULUS DELIOIDES X POPULUS BALSAMIFERA SUBSP. TRICHOCARPA.
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                  60 KGIHKSKYWEPTYEDSLSLIARVPIVASYIYRRIYKDGKVIPMNDSLVIGGNFSHMLGFD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                    120 SPEMQEL-MRLYVTNHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 EVLLWIKSVVEECGENITTEQLKDYVWKTLNSGKVVPGFGHGVLRKTVPRYTCQREFALK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 HLPDDPLFQLVSKLYEVVPPVLTQLGKVKNPWPNVDAHSGVLLNYYGLTEARYYTVLFGV 298
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                                                                                                                                                                                                                                                                                                                                              1 MPTKEQVGALSKELRDRALVHDYV-FKAIDALPVTAHPMTQFATGVMALQVQSEFQKAYE 59
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LA COGNATA U., LANDSCHUETZE V., WILLMITZER L., MUELLER-ROEBER B.; PLANT CELL PHYSIOL. 0:0-0(0).
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)0 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning and sequence analysis of human citrate synthase cDNA."; SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)0 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
                                                                                                                                                                                                                                                                               Length 339;
                                                                                                                                                                                                                                                                                                              Indels
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01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                         / Match 59.7%; Score 2068; DB 10;
Local Similarity 81.7%; Pred. No. 0.00e+00;
Hes 276; Conservative 35; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 SRSIGICSQLIWDRALGLPLERPKSVTMELLENHCKKA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                434 SRALGICSQLIWDRALGLPLERPKSVTMEWLENQCKKA 471
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                                                                                                                                                                                                                                          339 AA; 37834 MW; B2DA24A9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     466 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OXIDATIVE METABOLISM.
-!- SIMILARITY: TO OTHER CITPATE SYNTHASES
EMBL, AF047042, G3288815, ...
PROSITE: TROROMS: CITRATE_SYNTHASE; 1.
LYASE; TROROMYLIC ACID CYCLE.
SEOUENCE 466 AA; 51706 MW: C0532604 CRC
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                                                                                                                                                                                                  PFAM: PF00285; citrate_synt; 1.
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                                                                   VIOLALES: SALICACEAE; POPULUS.
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                                                                                                                                                                                     E275838;
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                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                         OXALOACETATE
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                                                                                                                                                                                                                                          SEQUENCE
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54.7%; Score 1897; DB 4; Length 466;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 FAHMLGFSSS-EMHEL--LMR--LY-VII-HSDHEGGNVSAHTGHLVASALSDPYLSFAA 299
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                                                                                                                                                                                                                                                                                  86 DPDEGIRFRGFSIPECQKLLPKAKGGEEPLPEGLFWLLVTGCIPTEEQVSWLSKEWAKRA 145
                                                                                                                                                                                                                                                                                                                                153 IISLIIMYTTIDALPVIAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKYWEPTYEDSMN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 LIAQVPLVAAYVYRRMYKNGDTI-PKDESLDYGANFAHMLGFSSSEMHELLMRLYVTIHS 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264 DHEGGNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLVWLTQLQKEVGKDV 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 SDEKLRDYIWNTLNSGRVVPGYGHAVLRKTDPRYTCQREFALKHLPNDPMFKLVAQLYKI 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 LLLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSE 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332 SKEQLKDYVWKTLNSGKVVPGFGHGVLRKTVPRYTCQREFAMKHLPEDPLFQLVSKLYEV 391
                                                                                                                      27 SASSINLK-DILADLIPKEQARIKIFRQQHGKTVVGQITVDMMYGGMRGMKGLVYETSVL 85
                                                                                                                                                                                                 34 ISSGLDLRSELVQELIPEQQDRLKKIKSDM-KGSIGNITVDMVLGGMRGMTGLLWKPHYL 92
                                          6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             146 ALPSHVV-TMLDNFPTNLHPMSQLSAAVTALNSESNFAQAYARGISRTKYWELIYEDSVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 LIAKLPCVAAKIYRNLYWEGSGIGAIDSNLDWSHNFTNMLGYTDHQFTEL-MRLYLTIHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 7.8%; Score 270; DB 2; Length 411; Local Similarity 28.6%; Pred. No. 2.16e-28; nes 92; Conservative 91; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BALAYEVA N.;
                                          84; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-AB BACTERIUM;
RAOULT D., RYDKINA E., ROUX V., EREMEEVA M., BALAYEVA
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
BENBL; U59912; G1390003; -.
PFAM; PF00285; citrate_synt; 1.
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LAST ANNOTATION UPDATE)
Best Local Similarity 59.3%; Pred. No. 0.00e+00;
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01-NOV-1996 (TREMBLREL. 01, LAST SEQI
01-NOV-1998 (TREMBLREL. 08, LAST ANN
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                                          256; Conservative
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Q53115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 FAHML-GFSSSE--MHELLMR-LY-VII-HSDHEGGNVSAHTGHLVASALSDPYLSFAAA 300
                                                                                                                312 LRAAVLKETCKEVLKELGQLDGNPLLQIAIEL-EAIALKDEYFIERKLYPNVDFYSGIIY 370
                                                                                                                                                                       358 LRKTVPRYTCQREF-AMKHLPEDPLFQLVSKLYEVFLLFLQNLAKLKPWPNVDAHSGVLL 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 LLLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 F---YP-DLLNFK--EADYELTAIRMIAKIPTIAAMSYK--YSIGQPFIYPDNSLDFTEN 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 FQKAYEKGIHKSKYWEPTYE-DSMNLIAQVPLVAAYVYRRWYKNGDT-IPKDESLDYGAN 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 FLHMMFATPCTKYTVNPIIKNALNKIFILHADHEQ-NASTSTVRIAGSSGANPFACISTG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 LNGLAGPLHGLANQEVLLWIKSV-VEEC-GENISKEQLKDYVWKTLNSGKVVPGFGHGVL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254 GIASLWGPAHGGANEAVINMLKEIGSSENIPKYIAKAKDKNDPFRLMGFGHRV--YKNYD 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313 RAAVLKETCKEVLKELGQLDNNPLLQIAIEL-EAIALKDEYFIERKLYPNVDFYSGIIYK 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                      300 ALNGLAGPLHGLANQEVLLWIKSV--VEECGENISKEQLKDYVWKTLNSGKVVPGFGHGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 IASLWGPAHGGANEAVINMLKEIGSSEYIPKYIAKAKDKNDPFRLMGFGHRV--YKNYDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.6%; Score 264; DB 2; Length 411; Best Local Similarity 28.0%; Pred. No. 2.91e·27; Matches 90; Conservative 91; Mismatches 112; Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-HA-91;
RADKINA E., RYUX V., EREMEEVA M., BALAYEVA N.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CITRATE SYNHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF
OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)Q +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RICKETTSIALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (EC 4.1.3.7) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  411 AA; 46162 MW; 9921533A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                           411 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- SIMILARITY: TO OTHER CITRATE SYNTHASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RICKETTSIACEAE; RICKETTSIEAE; RICKETTSIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FMBL; U59731; G1390011; --
PROSITE; PSO0480; CITRATE_SYNTHASE; 1.
PFAM; PF00285; Citrate_synt, 1.
LYASE; TRICARBOXYLIC ACID CYCLE.
                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                 371 KAMGIP-SOMFTVLFAIARIVG 391
                                                                                                                                                                                                                                                                                  417 NYYGLTEARYYTVLFGVSRALG 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |: :: :||||::|
418 YYGLTEARYYTVLFGVSRALG 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 AMGIP-SQMFTVLFAIARTVG 391
                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RICKETTSIA SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
                                                                                                                                                                                                                                                                                                                                                                             LT 9
Q59777
                                                                                                                                                                                                                                                                                                                                                                                                                                 059777;
                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                           QC
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88 LLIYGELPSGEQYNNFTKQVAHHSLVNERLHYL-FQTFCSSSHPMAIMLAAVGSL---SA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 LLLIGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 F---YP-DLLNFK--EADYELTAIRMIAKIPTIAAMSYK--YSIGQPFIYPDNSLDFTEN 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 FOKAYEKGIHKSKYWEPTYE-DSMNLIAQVPLVAAYVYRRMYKNGDT-IPKDESLDYGAN 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 FLHMMFATPCTKYKVNPIIKNALNKIFILHADHEQ-NASTSTVRIASSSGANPFACISTG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255 IASLWGPAHGGANEAVINMLKEIGSSEYIPKYIAKAKDKNDPFRLMGFGHRV--YKNYDP 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 LNGLAGPLHGLANQEVLLWIKSV-VEEC-GENISKEQLKDYVWKTLNSGKVVPGFGHGVL 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           359 RKTVPRYTCQREF-AMKHLPEDPLFQLVSKLYEVFLLFLQNLAKLKPWPNVDAHSGVLLN 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 7.6%; Score 263; DB 2; Length 411; Local Similarity 28.0%; Pred. No. 4.49e-27; es 90; Conservative 91; Mismatches 112; Indels 28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-M S\6;
ROUX V, RYDKINA E., EREMEEVA M., RAOULT D.;
SUBMITTED (COT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CITRATE SYNHHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF
OXIDATIVE METABOLISM.
-!- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                       BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RICKETTSIALES;
RICKETTSIACEAE; RICKETTSIEAE; RICKETTSIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; PICKETTSIALES;
RICKETTSIACEAE; RICKETTSIEAE; RICKETTSIA.
                                                                           01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411 AA; 45266 MW; A54EAICF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            356 AA
                           411 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SIMILARITY: TO OTHER CITRATE SYNTHASES. EMBL; U74756; G1658283; -. TRATE_SYNTHASE; 1. PROSITE; PSO0480; CITRATE_SYNTHASE; 1. EYEAM: PFO0285; citrate_synt; 1. LYASE; TRICARBOXYLIC ACID CYCLE.
                                                                                                                                                         CITRATE SYNTHASE (EC 4.1.3.7) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITRATE SYNTHASE (EC 4.1.3.7) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PATHWAY: TRICARBOXYLIC ACID CYCLE
                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  418 YYGLTEARYYTVLFGVSRALG 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372 AMGIP-SQMFTVLFAIARIVG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-PUERTO RICO:
                                                                                                                                                                                                                RICKETISIA MONTANA.
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RICKETISIA SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
LT 10
P77936
P77936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT 11
054382
054382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Match 7.5%; Score 261; DB 2; Length 356; Local Similarity 27.6%; Pred. No. 1.07e-26; es 89; Conservative 92; Mismatches 112; Indels 29; Gaps 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 980404343.
KEDNK H.-P., CLAYTON P. A., TOMR J.-F., WHITE O., NELSON K.E.,
KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
RICHARDSON D. L., KEFLARVAGE A.P., GRANAM D.E., KYRPIDES N.C.,
FLEISCHAANN P.D., OTAATENBUSH J., IEE N.H., SUTTON G.G., GILL S.
KIRKNESS E.F., DOUGHEPTY B.J., MCRENEY K., ADAMS M.D., LOFTUS B.,
KIRKNESS E.F., DOUGHEPTY B.J., MCRENEY K., ADAMS M.D., LOFTUS B.,
COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M.,
SADOW P.M., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
MAGON T.M., OISEN G.I., FPASEP C.M., SMITH H.O., WOESE C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 LLLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTOFATGVMALQVQSE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 F---YP-DLLNF-FKEADYELTAIRMIAKIPTIAAMSYK--YSIGQPFVYPDNSLDFTEN 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 FQKAYEKGIHKSKYWEPTYE-DSMNLIAQVPLVAAYVYRRMYKNGDTIP-KDESLDYGAN 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 FLHMM-FATPCEKYKVNPVVKNALNKIFILHADHEQ-NASTSTVRIAGSSGANPFACVST 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 GIASLWGPAHGGANEAVINMLKDIGSVENIPKYIAKAKDKNDNFRLMGFGHRV--YKNYD 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          358 LRKTVPRYTCQREF-AMKHLPEDPLFQLVSKLYEVFLLFLQNLAKLKPWPNVDAHSGVLL 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 ALNGLAGPLHGLANQEVLLWIKSV--VEECGENISKEQLKDYVWKTLNSGKVVPGFGHGV 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 PRAAVLKETCKEVLKELGQLDNNPLLQIAIEL-EAIALKDEYFIERKLYPNVDFYSGIIY 327
                                                                                                                                                                                                                                                                                                                                                                                                                                            44 LLIYGELPNSKQYNDFTKKVAHHALVNERLHYL-FQTFCSSSHPMAIMLAAVGSL---SA 99
               DAVIS M.J., YING Z., BRUNNER B.R., PANTOJA A., FERWERDA F.H.; "Rickettsial relative associated with papaya bunchy top disease."; CURP. MICPOBIOL, 36:80-84(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247 FAHMLGFSSS-EMHEL--LMR--LY-VTI-HSDHEGGNVSAHTGHLVASALSDPYLSFAA
                                                                           1- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)0 +
                                                                                                                                         -! - CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARCHAEA; EURYARCHAEOTA; ARCHAEOGLOBALES; ARCHAEOGLOBACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The complete genome sequence of the hyperthermophilic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                         356 AA; 40030 MW; 15BF55D0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372 AA
                                                                                                                                                                                      - 1 - SIMILARITY - TO OTHER CITRATE SYNTHASES.
                                                                                                                                                                                                   EMBL; U76908; G2894797; -
PROSITE: PS00480; CITRATE_SYNTHASE; 1.
LYASE: TRICARBOXYLIC ACID CYCLE.
                                                                                                                       " - PATHWAY - TRICARROXYLIC ACID CYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-VC-16 / DSM 4304 / ATCC 49558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQI
01-NOV-1998 (TREMBLREL. 08, LAST ANNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328 KAMGIP-POMFTVLFATARTVG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          417 NYYGLTEARYYTVLFGVSRALG 438
                                                                                                                                                                  OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITRATE SYNTHASE (CITZ).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARCHAEOGLOBUS FULGIDUS
MEDLINE; 98087556.
                                                                                                   OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARCHAEOGLOBUS.
                                                                                                                                                                                                                                                                                         NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                        Query Match
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028929
028929;
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Pred. No. 1.07c-26; 77; Mismatches 114; Indels 22; Caps 16;
                                                                                                                                                                                                                                                                                                                                                    142 RNIIPPALEFSHAANFLYMLHGEEPTKTAERALDMDLILHAEHEL-NASTFAARIAASTL 200
                                                                                                                                                                                                                                                                                                                                                                                               233 -DIIPKDESLDYGANFAHML-GFSSSEMHELLMRLYVTIHSDHEGGNVSAHTGHLVASAL 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 SDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEEGGENISKEÖLKDYVWKTLNSGKVV 350
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                                                                                                                                                                                                                                                               85 LPPYTHPMVVLRTATSYLGSLDKKIA-VRTREETFNKAKDLIAKFPTIVAY-YHRI-RTG 141
                                                                                                                                                                                                                                                                                                           173 MTQFATGVMALQVQSEFQKAYEKGIHKSKYWEPTYEDSMNLIAQVFLVAAYVYRRMYKNG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                          201 ADIYACVVAATGTLMGPLHGGAAQEVM---R-MLREVASP-RRAE--EYVKRKIEAGERI 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 MGFGHRVYRGVMDPRAELLR-YLAKRLAAEG----STKWFEISEAIAKAAYKYKLLPNV 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 PGFGHGVLRKTV-PRYTCQREFAMKHLPEDPLFQLVSKLYEVFLLFLQNLAKLKPW-PNV 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 LLLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSF 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match 7.5%; Score 260; DB 2; Length 411; Local Similarity 27.7%; Pred. No. 1.64e-26; hes 89; Conservative 92; Mismatches 112; Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-NIT-118;
RACULL D., RYDKINA E., ROUX V., EREMEEVA M., BALAYEVA N.,
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)0 +
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RICKETTSIACEAE; RICKETTSIEAE; RICKETTSIA.
                                                                                                                                                                    / Match 7.5%; Score 261; DB 1; Length 372; Local Similarity 26.6%; Pred. No. 1.07e-26; les 77; Conservative 77; Mismatches 114; Indels 3:
sulphate-reducing archaeon Archaeoglobus fulgidus.";
NATURE 390:564-370(1997).
EMBL; AP01011; G2649234; -.
TIGR; AF1340; -. 12645; citrate_synt; 1.
FPRAM; PF00205; citrate_synt; 1.
SEQUENCE 372 AA: 42270 MW; DB9662BC CRC32;
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01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (EC 4.1.3.7) (FRAGMENT).
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-!- SIMILARITY: TO OTHER CITRATE SYNTHASES.
EMBL; U59726; G1390019; -.
PROSITE; PSO0480; CITRATE_SYNTHASE; 1.
PFAM; PFRO0285; citrate_synt; 1.
LYASE; TRICARBOXYLIC ACID CYCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQ
01-NOV-1998 (TREMBLREL. 08, LAST ANN
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                                                                                                                            IASLWGPAHGGANEAVINMLKEIGSSEYIPKYIAKAKDKNDPFRLMGFGHRV--YKNYDP 312
                                                                                                                                                                    301 LNGLAGPLHGLANQEVLLWIKSV-VEEC-GENISKEQLKDYVWKTLNSGKVVPGFGHGVL 358
                                                                                                                                                                                                            313 RAAVLKETCKEVLKELGQLDNNPLLQIAIEL-EAIALKDEYFIERKLYPNVDFYSGIIYK 371
                                                                                                                                                                                                                                       129 LLLIGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSE 188
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                                          196 FLHMMFATPCTKYTVNPIIKNALNKIFILHADHEQ-NASTSTVRIAGSSGANPFACISTG 254
                                                                             247 FAHML-GFSSSE--MHELLMR-LY-VTI-HSDHEGGNVSAHTGHLVASALSDPYLSFAAA 300
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RAOULT D., RYDKINA E., POUX V., EPEMEEVA M., BALAYEVA N.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CITRATE SYMTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE METABOLISM.
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
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RICKETTSIACEAE; RICKETTSIEAE; RICKETTSIA.
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (EC 4.1.3.7.) (FRAGMENT).
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-1- SIMILARITY: TO CTHER CITRATE SYNTHASES.
EMBL: U59727: G1389975; -.
PFROSITE: PS00480; CITRATE_SYNTHASE; 1.
PFAM: PF00285; citrate_synt; 1.
LYASE: TRICARROXYLIC ACID CYCLE.
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88 LLIYGELPSGEQYNNFTKQVAHHSLVNERLHYL-FQTFCSSSHPMAIMLAAVGSL---SA 143
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RAOULT D., RYDKINA E., ROUX V., EREMEEVA M., BALAYEVA N.;
SUBMITTED (UNN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)0 +
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RICKETTSIACEAE; RICKETTSIEAE; RICKETTSIA.
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                                                                                                                      411 AA
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-:- SIMILARITY: TO OTHER CITRATE SYNTHASES.
EMBL; U59735, G1390015; -.
PROSITE: FSO0480; CITRATE_SYNTHASE; 1.
PFAM; PF00285; citrate_synt; 1.
LYASE; TRICARBOXYLIC ACID CYCLE.
                                                                                                                                                                                                                 CITRATE SYNTHASE (EC 4.1.3.7) (FRAGMENT).
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                                                                                                                    PRT;
                                   418 YYGLIEARYYTVLFGVSRALG 438
372 AMGIP-SQMFTVLFVIARIVG 391
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                                                                                                                    PRELIMINARY;
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Q59779
Q59779;
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Oct 22 16:55:04 1999; MasPar time 6.83 Seconds 749.237 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-702-718-4 (1-437) from USO8702718.pep 3243 1 SSNLDLRSELQELIPEQQER......LERPKSVIMEWLEKFCKRRA 437 Title:

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

119857 seqs, 11713122 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-issued 1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1

Mean 33.342; Variance 155.188; scale 0.215 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Pred. No.	2.02e+01	3.74e + 01	3.74e+01	3.74e+01	3.74e + 01	3.74e+01	4.36e+01	4.36e+01	4.36e+01	5.90e+01	4.36e+01	4.36e+01	4.36e+01	1.07e+02	6.85e + 01	1.07e+02	1.07e+02	1.07e+02	9.24e+01	1.07e+02	1.07e+02	1.07e+02	1.07e+02
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Score Match Length DB ID Description Pre-  Match Length DB ID Description Pre-  97 3.0 62.4 US-08-756 Sequence 4, Applicatio 2.9  93 2.9 324 1 US-08-198 Sequence 4, Applicatio 3.2  93 2.9 324 1 US-08-35 Sequence 4, Applicatio 3.2  93 2.9 3031 1 US-07-689 Sequence 2, Applicatio 3.2  94 2.8 430 1 US-08-833 Sequence 4, Applicatio 3.2  95 2.8 430 1 US-08-833 Sequence 4, Applicatio 3.2  96 2.8 430 1 US-08-836 Sequence 4, Applicatio 3.2  97 2.8 430 1 US-08-80 Sequence 4, Applicatio 3.2  98 430 1 US-08-80 Sequence 4, Applicatio 4.2  99 2.8 430 1 US-08-86 Sequence 4, Applicatio 4.2  90 2.8 430 1 US-08-86 Sequence 4, Applicatio 4.2  90 2.8 430 1 US-08-476 Sequence 4, Applicatio 4.2	Score Match Length DB ID Description Pre-  1 97 3.0 1 9.1 3.2 1 9.1 3.2 1 9.2 3.2 1 9.3 2.9 3.2 1 9.3 2.9 3.2 1 9.3 2.9 3.2 1 9.3 2.9 3.2 1 1 05-08-198- Sequence 4, Applicatio 3. 2 9 3.2 1 1 05-08-138- Sequence 4, Applicatio 3. 2 9 3.2 1 1 05-08-33- Sequence 4, Applicatio 3. 3 2.9 3.3 1 1 05-07-689- Sequence 4, Applicatio 3. 3 2.9 43.0 1 05-08-833- Sequence 4, Applicatio 3. 3 2.9 43.0 1 05-08-833- Sequence 4, Applicatio 3. 3 2.9 43.0 1 05-08-834- Sequence 44, Applicatio 3. 3 2.9 43.0 1 05-08-8476- Sequence 44, Applicatio 4. 3 2 2.8 43.0 1 05-08-476- Sequence 44, Applicatio 4. 3 2 2.8 43.0 1 05-08-476- Sequence 44, Applicatio 4. 3 2 2.8 43.0 1 05-08-476- Sequence 44, Applicatio 4. 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Score Match Length DB ID Description Pre-  Match Length DB ID Description  97 3.29 324 3 PCT-US93-0 Sequence 4, Applicatio 3.  93 2.9 324 1 US-08-198- Sequence 4, Applicatio 3.  93 2.9 324 1 US-08-323- Sequence 4, Applicatio 3.  93 2.9 324 1 US-08-323- Sequence 4, Applicatio 3.  92 2.8 430 1 US-08-833- Sequence 4, Applicatio 3.  92 2.8 430 1 US-08-835- Sequence 4, Applicatio 3.  92 2.8 430 1 US-08-835- Sequence 4, Applicatio 4.  92 2.8 430 1 US-08-835- Sequence 4, Applicatio 4.  93 2.9 509 2 US-08-835- Sequence 4, Applicatio 4.  94 2.8 509 2 US-08-476- Sequence 44, Applicatio 4.  95 2.8 430 1 US-08-476- Sequence 47, Applicatio 4.  96 2.8 509 2 US-08-476- Sequence 17, Applicatio 5.  97 2.8 509 2 US-08-476- Sequence 11, Application 5.	Score Match Length DB ID Description Pre-  Match Length DB ID Description  97 3.0 324 3 0.08-756 Sequence 4, Applicatio 2  93 2.9 324 1 05-08-198 Sequence 4, Applicatio 3  93 2.9 324 1 05-08-198 Sequence 4, Applicatio 3  93 2.9 3031 1 05-08-35 Sequence 2, Applicatio 3  92 2.8 430 1 05-08-89 Sequence 2, Applicatio 3  92 2.8 430 1 05-08-36 Sequence 4, Applicatio 3  92 2.8 430 1 05-08-36 Sequence 4, Applicatio 4  92 2.8 430 1 05-08-36 Sequence 4, Applicati 4  92 2.8 430 1 05-08-36 Sequence 4, Applicati 4  93 2.9 3031 05-08-37 Sequence 1, Applicati 4  94 2.8 510 2 05-08-37 Sequence 1, Applicati 4  95 2.8 510 2 05-08-348 Sequence 11, Applicati 4  95 2.8 510 2 05-08-345 Sequence 11, Applicati 4	Score Match Length DB ID Description Pre-  Match Length DB ID Description  97 3.29 324 2 US-08-756- Sequence 4, Applicatio 3.  93 2.9 324 1 US-08-198- Sequence 4, Applicatio 3.  93 2.9 324 1 US-08-198- Sequence 4, Applicatio 3.  93 2.9 324 1 US-08-323- Sequence 4, Applicatio 3.  92 2.8 430 2 US-08-33- Sequence 4, Applicatio 3.  92 2.8 430 1 US-08-833- Sequence 4, Applicatio 3.  92 2.8 430 1 US-08-36- Sequence 44, Applicati 4.  92 2.8 430 1 US-08-36- Sequence 44, Applicati 4.  92 2.8 510 2 US-08-77- Sequence 27, Applicati 4.  93 2.9 US-08-37- Sequence 27, Applicati 4.  94 2.8 510 2 US-08-44- Sequence 11, Applicati 4.  95 2.8 510 2 US-08-345- Sequence 11, Applicati 4.  95 2.8 510 2 US-08-345- Sequence 11, Applicati 4.  96 2.8 510 1 US-08-345- Sequence 11, Applicati 4.	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86 2.7 557 2 US-08-967- Sequence 4, Applicatio 1.07e+02 86 2.7 557 1 US-08-608- Sequence 2, Applicatio 1.07e+02 86 2.7 557 1 US-08-608- Sequence 2, Applicatio 1.07e+02 86 2.7 557 1 US-08-608- Sequence 2, Applicatio 1.07e+02 87 1 US-08-608- Sequence 2, Applicatio 1.07e+02 89 2.7 557 1 US-08-608- Sequence 6, Applicatio 1.07e+02 89 2.7 568 1 US-08-608- Sequence 5, Applicatio 1.07e+02 84 2.6 259 2 US-07-891- Sequence 54, Applicatio 1.24e+02 85 2.6 1005 3 PCT-0857- Sequence 2, Applicatio 1.24e+02 85 2.6 1005 3 PCT-08940- Sequence 3, Applicatio 1.24e+02 85 2.6 1005 3 PCT-08940- Sequence 3, Applicatio 1.24e+02 85 2.6 1005 1 US-08-608- Sequence 3, Applicatio 1.24e+02 85 2.6 1005 1 US-08-089- Sequence 3, Applicatio 1.24e+02 85 2.6 1005 2 US-08-266- Sequence 3, Applicatio 1.24e+02 85 2.6 1005 2 US-08-266- Sequence 3, Applicatio 1.24e+02 85 2.6 1045 3 PCT-0893-0 Sequence 44, Applicatio 1.24e+02 85 2.6 1454 3 PCT-0893-0 Sequence 44, Applicatio 1.24e+02 85 2.6 1454 3 PCT-0893-0 Sequence 12, Applicatio 1.24e+02 85 2.6 1454 3 PCT-0893-0 Sequence 12, Applicatio 1.24e+02 85 2.6 1454 3 PCT-0893-0 Sequence 12, Applicatio 1.24e+02 86 2.6 1454 3 PCT-0893-0 Sequence 12, Applicatio 1.24e+02 87 2.6 1050 0 Sequence 12, Applicatio 1.24e+02 88 2.6 1454 3 PCT-0893-0 Sequence 12, Applicatio 1.24e+02 88 2.6 1454 3 PCT-0893-0 Sequence 12, Applicatio 1.24e+02 89 2.6 1454 3 PCT-0893-0 Sequence 12, Applicatio 1.24e+02 89 2.6 1454 3 PCT-0893-0 Sequence 12, Applicatio 1.24e+02 89 2.6 1454 3 PCT-0893-0 Sequence 12, Applicatio 1.24e+02 89 2.6 1454 3 PCT-0893-0 Sequence 12, Applicatio 1.24e+02 89 2.6 1454 3 PCT-0893-0 Sequence 12, Applicatio 1.24e+02 80 2.6 1454 3 PCT-0893-0 Sequence 12, Applicatio 1.24e+02 81 2.6 1454 3 PCT-0893-0 Sequence 12, Applicatio 1.24e+02 82 2.6 1454 3 PCT-0893-0 Sequence 12, Applicatio 1.24e+02 83 2.6 1454 3 PCT-0893-0 Sequence 12, Applicatio 1.24e+02 84 2.6 1454 3 PCT-0893-0 Sequence 12, Applicatio 1.24e+02 85 2.6 1454 3 PCT-0893-0 Sequence 12, Applicatio 1.24e+02 86 2.6 1454 3 PCT-0893-0 Sequence 12, Applicatio 1.24e+02	ALIGNMENTS  THE SEQUENCE 9, APPLICATION US/08756317  SEPLICANT: Kishor, Timochy A. APPLICANT: Kishor, David M. APPLICANT: Kishor, David M. APPLICANT: Misky Timochy A. APPLICANT: Misky Timochy A. APPLICANT: Misky Timochy A. APPLICANT: Misky Timochy A. APPLICANT: Stark David M. INTILE OF INVENTION: Doly The Hydroxyalkoncate Synthase OCRESPONDENCE ADDRESS:  ADDRESSEE: ANDLO MANIES: ADDRESSEE: ALOLIG, White 6 Durkee STREE TY. COUNTRY: USA  COUNTRY: USA  COMPUTER TRADABLE FORM: MEDIUM TYPE: ThOPPY disk COMPUTER: INN PC Compatible COMPATION TYPE: ThOPPY disk COMPUTER: INN PC COMPATION STARE: DATE: 25-NOY-1996  CURRENT APPLICATION NUMBER: US 60/007,693  FILING DATE: 25-NOY-1995  ATTORNEY APPLICATION NUMBER: US 60/007,693  FILING DATE: 22-NOY-1995  ATTORNEY APPLICATION NUMBER: 30.602  REPERENCYPOCKET NUMBER
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                                                                                 Ouery Match 3.0%; Score 97; DB 2; Length 624;
Best Local Similarity 25.3%; Pred. No. 2.02e+01;
Matches 21; Conservative 21; Mismatches 34; Indels 7; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application PC/TUS9307424
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
AITLE OF INVENTION: Recombinant Equine Herpesvirus
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MA-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07424
FILING DATE: 19930806
CLASSIFICATION:
                                                                                                                                                                                                                                                                                 324 AA.
                                          COGY: linear
624 AA; 69538 MW; 1929028 CN;
                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
SEQUENCE 324 AA; 36456 MW; 559982 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER PEACABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application PC/TUS9307424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: John P. White STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: White, John P
TELECOMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELERA: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                              146 WEAHPFFNFIKROYQINAQALQE 168
                                                                                                                                                                                                                 341 -PDDPFFQLVSKLYEVVPPILLE 362
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amino acid
624 amino acids
                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
             TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                          TOPOLOGY:
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 LENGTH:
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                                                      SEQUENCE
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156 NKSWQPSFV-CGKLFETIPLTIV-DYKHLLKQ-KVLPGQDHPESARSLLQHKSSFVSPPP 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 2.9%; Score 93; DB 1; Length 324; Best Local Similarity 24.7%; Pred. No. 3.74e+01; Matches 18; Conservative 24; Mismatches 25; Indels
                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
TITLE OF INVENTION: Recombinant Equine Herpesvirus
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                   SCETWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/198,094
FILING DATE: February 17, 1994
CLASSIFICATION: 435
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            324 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 324 AA; 36456 MW; 559982 CN;
                                                                                                                                                                                                                                                                                              E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application PC/TUS9502087
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application PC/TUS9502087
                                                                                                              Sequence 4, Application US/08198094 Patent No. 5741696
                                                                                                                                                                                                      ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New YORK
COUNTRY: USA
                                                                                       Sequence 4, Application US/08198094
                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 324 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 324 amino acid.
                                                                                                                                                                                                                                                                  ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy c
                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 LELMRL-YVTIHS 235
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PCT-US95-02087-4
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          US-08-198-094-4
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RESULT
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SEQUENCE
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TITLE OF INVENTION: Recombinant Equine Herpesviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08323531
Patent No. 5731188
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
TITLE OF INFORMEN: Recombinant Equine Herpesvirus
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
                                                                                                                                           ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PattentIn Release #1.0, Version #1.25
CURRAN APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 AA.
         NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
SEQUENCE 324 AA; 36456 MW; 559982 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/198,094
FILING DATE: FEBRUARY 17, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECHONIC (212)278-0400
TELEFAX: (212)391-0525
TELEFAX: 42253
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08323531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 324 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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: New York
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: USA
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                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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APPLICANT: Ben Bassat, Arie
APPLICANT: Calhoon, Roger D
APPLICANT: Calhoon, Roger D
APPLICANT: Fear, Anna L
APPLICANT: Gelfand, David H
APPLICANT: Meade, James H
APPLICANT: Tal, Rony
APPLICANT: Wong, Hing
APPLICANT: Tal, Rony
APPLICANT: Benziman, Moshe
TITLE OF INVENTION: EXPRESSION OF CELLULOSE SYNTHASE OPERON NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: McCutchen, Doyle, Brown & Enersen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 NKSWQPSFV-CGKLFETIPLTTV-DYKHLLKQ-KVLPGQDHPESARSLLQHKSSFVSPPP 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 93; DB 1; Length 324;
Pred. No. 3.74e+01;
24; Mismatches 25; Indels
                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: McCutchen, Doyle, Brown & Enersen
STREET: Three Embarcadero Center
CIIY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3031 AA.
                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/926,784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
JENCE 324 AA; 36456 MW; 559982 CN;
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT,
                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEPAX: (212)664-0525
TELEPAX: 422523
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 324 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/07689008
Patent No. 5268274
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/07689008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.9%;
Best Local Similarity 24.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 -NFKRLIYAVVDP 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
TITLE OF ENURENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                          464 FWSEVYETTMALFLVRVTIITLMFPSKGKFNVTEKGGVLEEEEFFDLGATYPNII-FAGIM 522
                                                                                                                                                                                                                                                                                     Score 93; DB 1; Length 3031;
Pred. No. 3.74e-01;
30; Mismatches 27; Indels 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 61198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      430 AA.
                                                                                                                                                                                                      MOLECULE TYPE: protein
JENCE 3031 AA; 328497 MW; 44365167 CN;
APPLICATION NUMBER: US/07/689,008
FILING DATE: 19910422
CLASSIFICATION: 435
PROOF APPLICATION DATA:
APPLICATION NUMBER: US 337,194
FILING DATE: 12-APPL-1989
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/833,485 FILING DATE: 07-APR-1997 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 44, Application US/08833485
Patent No. 5804425
GENERAL INFORMATION:
                                                                                              NAME: Murphy, Lisabeth Feix
REGISTRATION NUMBER: 31547
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 393-2200
TELEFAX: (415) 393-2286
TELEX: 340817 MACPAG SFO
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3031 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 44, Application US/08833485
                                                                            FILING DATE: 23-MAR-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                523 TLGLLIGLFELTFHFNQLAG 542
                                                                                                                                                                                                                                                                                                                                223 MLELMR-LY-VTIHSDHEGG 240
                                                                                                                                                                                                                                   7.9%;
Local Similarity 20.0%;
nes 16: Conservative
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STREET: 700 C...
CITY: St. Louis
TATE: Missouri
                                                                                                                                                                                      TYPE: AMINO ACID
                                                                                                                                                                                                linear
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                                                                                                                                                                                                                  SEQUENCE
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Sequence 44, Application US/08306063
Patent No. 563435
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Rishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 YKPLLGEDCRRIMDIFRHLGVEIKEDDEKLVVTS-PGYQVNTPHQVLYTGNSGTTTRLLA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 FAHMLGFDSPQMLELMR-LYVIIHSDHEGGNVSAHTGHLVGSPLSDPYLSFAAALNGL-A 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 92; DB 2; Length 430;
Pred. No. 4.36e+01;
15; Mismatches 31; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,063
FILING DATE: 13-SEP-1994
                                                                                                                                                                                                                                                                                                                                                            38-21(15117)A
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
CLASSIFICATION: 435
                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
JENCE 430 AA; 46852 MW; 962324 CN;
                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Heerner Jr., Dennis R.
RECISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)37-6047
INFORMATION FOR SED ID NO: 44:
SEQUENCE CHARATERISTICS:
LENGTH: 430 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 44, Application US/08306063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 430 amino acids
amino acid
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Best Local Similarity 31.9%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 700 Chest
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 GLLSGLGNESVL 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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43 YKPLLGEDCRRIMDIFRHLGVEIKEDDEKLVVTS-PGYQVNTPHQVLYTGNSGTTTRLLA 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27, Application US/08737524B
Patent No. 5912414
GENERAL INFORMATION:
APPLICANT: CARL SAVERIO FALCO
APPLICANT: CARL SAVERIO FALCO
APPLICANT: CARL SAVERIO FALCO
APPLICANT: MARY ELIZABETH HARRETT LOCKE
TITLE OF INVENTION: UNCLEIC ACID FRAGMENTS, CHIMERIC
TITLE OF INVENTION: THE METHIONINE CONTENT OF THE SEEDS
TITLE OF INVENTION: OF PLANTS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                 Score 92; DB 1; Length 430;
Pred. No. 4.36e+01;
15; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USEE: E. I. DU PONT DE NEMOURS AND COMPANY
P: 1007 MARKET STREET
WILLMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARF: MICROSOFT WORD FOR WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,524B
                                                                                                                                                                                                     38-21(10660)A
   APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
PPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: UNITED STATES OF AMERICA 21P: 19998
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETIE, 3.50 INCH
                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
HENCE 430 AA; 46852 MW; 962324 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27, Application US/08737524B
                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: HOETNET Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REPERENCE/DOCKET NUMBER: 38-21
TELEPHONE: (314)537-609
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.8%;
Best Local Similarity 31.9%;
Matches 23; Conservative
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CLASSIFICATION:
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US-08-737-524B-27
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APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 YKPLLGEDCRRTMDIFRHLGVEIKEDDEKLVVTS-PGYQVNTPHQVLYTGNSGTTTRLLA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                15; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,008
FILING DATE: 07-JUN-1995
PRIOR APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                               Score 92; DB 1; Length 430;
Pred. No. 4.36e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                430 AA
                                                                                                                                                                                                  38-21(10660)A
               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28 AUG-1991
CLASSIFICATION: 435
                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPT;
                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
JENCE 430 AA; 46852 MW; 962324 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 44, Application US/08476008
Patent No. 5627061
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 44, Application US/08476008
                                                                                                                                                                                                                             TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
                                                                                                                                                                                  30,914
                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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Best Local Similarity 31.9%;
Matches 23; Conservative
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CLASSIFICATION: 435
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STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 GLLSGLGNESVL 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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RESULT
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                                                                                                                                                                                                           133 ITAHPMTQFCTGVMALQTRSEFQ--KAYEKGIHKSKFWEPTYEDCLSLIAQVPVVAAY 188
                                                                                                                                                     Score 90; DB 2; Length 509; Pred. No. 5.90e+01; 18; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Occhiodoro, Teresa
APPLICANT: Bielicki, Julie
APPLICANT: Bielicki, Julie
APPLICANT: Glements, Peter R
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
TITLE OF INVENTION: IDURONATE 2-SULFATASE
COPPRESPONDENCE: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                  E. Scully, Scott, Murphy & Presser
400 Garden City Plaza
                                                                                                                                                                                                                                               510 AA
     NAME: LYNNE M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
REFERENCE/POCKET NUMBER: BB-1059-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEFAX: 302-773-0164
                                                                                                                         MOLECULE TYPE: protein
ENCE 509 AA; 54816 MW; 1292600 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/484,494
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84162
                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/08484494 Patent No. 5798239 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGIO, FRANK S
REGISTRATION NUMBER: 31,346
REPRENCE/OFCKET NUMBER: 8416;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/08484494
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wilson, Peter J
APPLICANT: Morris, Charles P
APPLICANT: Anson, Donald S
                                                        TELEX: 833420
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 509 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
ATTOPNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                               STANDARD;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9
                                                                                                          single
                                                                                                                                                      / Match 2.8%;
Local Similarity 25.9%;
hes 15; Conservative
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CITY: Garden City
                                                                                                                linear
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OPERATING SYSTEM:
                                                                                                        STRANDEDNESS:
TOPOLOGY: lin
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                                                                                                                                                                                                                                              US-08-484-494-11
                                                                                                                                    SEQUENCE
                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                   27 FFGSFQLGNINVD-M-VLGGMRGMTGLLWETSLLDPEEGIRFRGFSIPECQKLLPAAS 82
                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                    Natch 2.8%; Score 92; DB 2; Length 510; Local Similarity 27.6%; Pred. No. 4.36e+01; les 16; Conservative 16; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/345,212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Anson, Donald S
APPLICANT: Occhhodoro, Teresa
APPLICANT: Glements, Julie
APPLICANT: Glements, Peter R
APPLICANT: Howood, John J
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scully, Scott, Murphy & Presser
400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                       510 AA
                                                                                                                                                                   MOLECULE TYPE: protein
JENCE 510 AA; 57860 MW; 1366158 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER PEADMALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILLING DAIL:
CLASSIFICATION: 435
PPICR APPLICATION DATA
APPLICATION NUMBER: 991.973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGILO, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 41162
TELECOMMUNICATION INFORMATION:
TELECAN: 516-742-4343
TELECAN: 516-742-4343
INFORMATION FOR SED ID NO: 11:
SEDUENCE CHARATERISTICS.
LENGTH: 510 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/08345212
Patent No. 5932211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/08345212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Wilson, Peter J
APPLICANT: Morris, Charles P
               TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO: 11:
                                                          SEQUENCE CHARACTERISTICS.
LENGTH: 510 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
516-742-4366
                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 400 CLTY: Garden City CTTY: Garden City
                                                                                                                                                   linear
                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
  TELEFAX:
                                                                                                                                                                                            SEQUENCE
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                                                                                                      3; Gaps
                                                                                  338 DIAGYDLNKTQMDGMSLLPILRGASNLTWRSDVLVEYQGEG-RNVTDPTCPSLSPGVS 394
                                                                                            COUNTR: USA

COUNTR: USA

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Eloppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,493

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION 1424

PRIOR APPLICATION NUMBER: 991,973
                                            Score 92; DB 2; Length 510;
Pred. No. 4.36e+01;
16; Mismatches 23; Indels
                                                                                                                                                                                                                                                                           APPLICANT: Cachiodoro, Teresa
APPLICANT: Bielicki, Julie
APPLICANT: Clements, Peter R
APPLICANT: Howood, John J
ITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
ITLE OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
                                                                                                                                                                                                                                                                                                                                                      E: Scully, Scott, Murphy & Presser 400 Garden City Plaza
                                                                                                                                           510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 510 AA; 57860 MM; 1366158 CN;
       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 510 AA; 57860 MW; 1366158 CN;
                                                                                                                                           PRT;
                                                                                                                                                                                                                   Sequence 11, Application US/08484493
Patent No. 5728381
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Digiglio, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 84162
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-434
TELEFAX: 516-742-436
TELES X3 301 SANS UR
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                   Sequence 11, Application US/08484493
                                                                                                                                                                                                                                                 APPLICANT: Wilson, Peter J
APPLICANT: Morris, Charles P
APPLICANT: Anson, Donald S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 991,5
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 510 amino acid
TYPE: amino acid
                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
single
                                             Query Match 2.8%;
Best Local Similarity 27.6%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                STREET: 400 Garder
CITY: Garden City
STATE: New York
STRANDEDNESS:
                                                                                                                                           US-08-484-493-11
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                                                                 338 DIAGYDLNKTQMDGMSLLPILRGASNLTWRSDVLVEYQGEG-RNVTDPTCPSLSPGVS 394
                                                                                             27 EFGSFQLGNINVD-M-VLGGMRGMTGLLWETSLLDPEEGIRFRGFSIPECQKLLPAAS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 LKWMGWKNTNTGESTHVEEFKGRVTMSLDTSTNTAYMELSSLRSEDTAVYYCAREY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281 LIMIKSVVDECGENISTEQLKDYVWKTLNSGKVVPGFGLGVLRKTDPR-YTCQREF 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SHIOSAKI, Kouichi
APPLICANT: OSATOMI, Kiyoshi
APPLICANT: TOKIYOSHI, Sachi
TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND
TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
  Pred. No. 4.36e+01;
16; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 86; DB 2; Length 119;
Pred. No. 1.07e+02;
13; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.3C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,845
                                                                                                                                                                                                    119 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Browdy and Neimark
419 Seventh Street N.W. Ste. 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00039
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
SEQUENCE 119 AA; 13166 MW; 84737 CN;
                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08491845
Patent No. 573247
GENERAL INFORMATION:
APPLICANT: MAEDA, Hiroaki
APPLICANT: KIMACHI, Kazuhiko
APPLICANT: EDA, Yasuyuki
                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/08491845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Browdy, Roger L.
REGISTRATION UNDRER: 25.618
REFERENCE/DOCKET UNDRER: MAED.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 119 amino acids amino acids
                                                                                                                                                                                                    STANDARD;
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ilarity 28.6%;
Conservative
Best Local Similarity 27.6%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington
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nes 16; Conserv
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US-08-491-845-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
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DB 1; Length 510;

2.8%; Score 92;

Query Match

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20 LSLSLLLPLLKSGSLGAALLRNGVLMSLTFPILPIIYQQKIMMHIGKDYSWLGLVTGEVI 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.7%; Score 89; DB 2; Length 230;
Best Local Similarity 30.3%; Pred. No. 6.85e+01;
Matches 20; Conservative 16; Mismatches 26; Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC.1995
CLASSIFICATION: 435
230 AA.
                                                                                                 Sequence 457, Application US/08637759B
Patent No. 5876931
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
PRT;
                                                                                                                                                                                          ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPMS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 AA; 25640 MW; 291720 CN;
                                                                                                                                                                                                                                                                                   COMPUTER FEADABLE FORM.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                          Sequence 457, Application US/08637759B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: Fri Oct 22 16:55:47 1999 Job time : 43 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS
TELECOMMUNICATION INFORMATION:
TELEFRAM: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 457:
SEQUENCE CHARACTERISTICS:
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 30309-3450
US-08-637-759B-457
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Oct 22 16:49:12 1999; MasPar time 19.68 Seconds 889.641 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-702-718-4 (1-437) from USO8702718.pep 3243 1 SSNLDLRSELQELIPEQQER......LERPKSVIMEWLEKFCKRRA 437 Title:

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

122810 segs, 40068593 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

1:pirl 2:pir2 3:pir3 4:pir4 pir60 Database:

Mean 49.482; Variance 97.811; scale 0.506 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Score 10. 2834 3 2249 4 4 2096 6 1815 7 1890 6 1815 11 323 124 11 323 11 323 11 323 11 228 11 323 124 125 125 126 20 261 21 266

citrate synthase II ( 1.95e-20 citrate synthase - He 3.23e-19 citrate (si)-synthase II.6e-17 citrate (si)-synthase II.16e-17 citrate (si)-synthase II.16e-14 citrate (si)-synthase II (C B.75e-13 citrate (si)-synthase II (C B.75e-13 citrate (si)-synthase II (C B.75e-13 citrate (si)-synthase III.000 citrate (si)-synthase III.000 probable citrate synt 3.48e-06 probable citrate synt 3.48e-01 conserved hypothetical protein 4.16e+00 hypothetical protein 2.41e+00 probable DNA polymera III.82e+00 probable membrane protei 4.16e+00 DNA topoisomerase (AT 2.41e+00 NNB convertase - rat 4.16e+00 hypothetical protein II.82e+00 hypothetical protein II.82e+00 hypothetical protein II.82e+00	w v	<pre>synthase (EC 4.1.3.7) - Arabidopsis is thaliana #common_name mouse-ear</pre>	revision 05-Mar-1999 #text_change	; Ketchum, K.A.; Crosby, M.L.; , S.M.; Kaul, S.; Mason, T.M.; ims, M.D.; Somerville, C.R.; Venter,	Data Library, May 1998 hromosome II BAC F411 g	islated from GB/EMBL/DDBJ T NID:g3128166; PID:g3128180	3; 97/3; 135/3; 157/1; 184/3; 201/2; ; 313/3; 347/3; 383/3; 400/3; 425/2;	oxo-acid-lyase; tricarboxylic acid cycle ar-weight 52782 #checksum 6960	2834; DB 2; Length 474; No. 0.00e+00; Mismatches 25; Indels 0; Gaps 0;	HGKVQLGNITVDMVIGGMRGMTGLLWETSLLDP 95 	QSGAEPLPEGLLWILLIGKVPSKEQVEALSKDLANRAAV 155 :	DYVYNAIDALPSTAHPMIQFASGVMALQVQSBFQKAYENGTHKSKFWEPTYEDCLNLIA 215 
G69600 D71982 ERAF523 YERECP 140044 S41527 YERYT YERYT YERYT YERYT YERYT YERYT YERYT YERYT YERYT S42047 S42047 S64931 S7663 S71052 G71254 G71254 S71053	ALIGNMENT TPE COMPlet	e (S1) abidop	ednence_	.; Lin, X C.; Sykes A.R.; Ada	EMBL iana	nary; tran: #label ROU :AC004521;	3/3; 75/3 2; 284/3;	lyase; c #molecula	Score; Pred.	IPEQODRLKKLKSEHG 	AQSGAEPLE   :       SAGAEPLE	FASGVMALC
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231 224 225 225 225 225 225 226 227 227 227 227 227 227 227 227 227	н	NTE_NAME SM		SSIONS RENCE authors	missio cripti ession	#Statu #molec #resid #cross		es SC SC	y Match Local S hes 37	36 STDL  ::  1 SSNL	96 EEGI      61 EEGI	156 PDYV      121 PDHV
40000000000000000000000000000000000000	RESULT ENTRY	TITLE ALTERNATE ORGANISM	DATE	ACCESSI REFEREN #aut	#suk #des		GENETIC #map #int	#note KEYWORDS SUMMARY	Query Best Match	Op Oy	do oy	Db 1

418 LERPKSVTMEWLEKFCKP 435

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                                         181 OVPVVAAYVYRRMYKNGQVIPLDDSLDYGGNFAHMLGFDSPQMLELMRLYVIIHSDHEGG 240
                                                                                       276 NVSAHTGHLVGSALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGEDISKEQL 335
                                                                                                                                                                                                                     301 KDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYEVVPPIL 360
                                                                                                                                                                                                                                                                                        94 PDEGIRFRGLSIPECQKVLPAAKPGGEPLPEGLLWLLLTGKVPSKEQVNSIVSGIAESGI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 PEEGIPFRGFSIPECOKLLPAASAGAEPLPEGLLWLLLTGKVPSKEQVDALSADLPKRAS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 ISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKYWEPTYEDSMNL 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 IPDHV-YKTIDALPITAHPMTQFCTGVMALQTRSEFQKAYEKGIHKSKFWEPTYEDCLSL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               274 EGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENISK 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 SSGLDLRSELVQELIPEQQDRLKKIKSDMKG-SIGNITVDMVLGGMRGMTGLLWKPHYLD 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ethanolamine amonia-lyase (EC 4.3.1.7) - potato
#formal_name Solanum tuberosum #common_name potato
08-Sep-1994 #sequence_revision 10-Nov-1995 #text_change
08-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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216 RVPVVAAYVYPRMYKNGDSIPSDKSLDYGANFSHMLGFDDEKVKELMRLYITIHSDHEGG
                                                                                                            336 KEYVWKTLNSGKVIPGYGHGVLRNTDPRYVCQREFALKHLPDDPLFQLVSKLYEVVPPVL
                                                                                                                                                                                                                                                                 396 TELGKVKNPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRALGLALER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238 EGGNVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQLKDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYEVVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394 LFLQNLAKLK-PWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 IAQVPLVAAYVYRRMYKNGDTIPKDESLDYGANFAHMLGFSSSEMHELLMRLYVTIHSDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #checksum 4730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Landschuetze, V.; Willmitzer, L.; Mueller-Roeber, Esubmitted to the EMBL Data Library, September 1993 844316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##CIOSS-references EMBL:X75082; NID:9483509; PID:9483510
FICATION #superfamily citrate (si)-synthase
ammonia-lyase; carbon-nitrogen lyase
#length 471 #molecular-weight 52612 #checks:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 81.3%; Score 2637; DB 2; Best Local Similarity 81.3%; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *type complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           356; Conservative
                                                                                                                                                                                                                                                                                                                                                      456 PKSVIMDWLEAHCKK 470
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S44316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #accession
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TITLE
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**cross-references EMBL:X17528; NID:g11243; PID:e1188578; FID:g2652924
**note the Sequence from Fig. 2 is inconsistent with that from
the Sequence from Fig. 2 is inconsistent with that from
Fig. 1 in having 47-c1y, 125-Trp, 14-Leu, 151-Ser,
185-Asn, 187-Asn, 191-Asn, 348-Leu, an additional Gly
after 89-Trp, an additional Val after 393-Cys and two
additional Arg after 228-Arg, in lacking 114-Leu and
residues 233 to 241
                                                   citrate (si)-synthase (EC 4.1.3.7) precursor, mitochondrial Arabidopsis thaliana
                                                                                                                                                                                                                                                                    #authors Unger, E.A.; Hand, J.M.; Cashmore, A P : Vasconcelos, A C.
#journal plant Mol. Biol. (1989) 13:411 418
#title Isolation of a cDNA encoding mitochondrial citrate synthase
from Arabidopsis thaliana.
#cross-references MUID:91370823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 EEVFALGDCFLPECOKALLPTAQSGGLNHYPRSFVASLNWKGTL-AKSKI,KH-CPKTWNP 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCLTELES-EEPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRELLLA 450
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#active_site His, His, Asp #status predicted
#length 472 #molecular-weight 52941 #checksum 9626
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carbon-carbon lyase; homodimer; mitochondrion;
oxo-acid-lyase; tricarboxylic acid cycle
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                            #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type mRNA
***rocidues 1-472 ##label UNG
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Sun Oct 24 10:10:43 1999

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                                                                                                                                                                                                   ts annotation; X-ray crystallography, 2.7 and 1.7 angstroms Citrate (si)-synthase is found in nearly all cells capable of oxidative metabolism. It catalyzes the condensation of oxaloacetate and acetyl-CoA to form citrate in the tricarboxylic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitochondrion of eukaryote cells. This molecule is a dimer of identical chains. Each dimer binds two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  molecules of acetyl-CoA and two molecules of oxaloacetate at two
                                                                                           citrate (si)-ŝynthase (EC 4.1.3.7) precursor - pig
#formal_name Sus scrofa domestica #common_name domestic pig
15-oct-1982 #sequence_revision 30-Sep-1992 #text_change
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#modified_site N6,N6,N6.trimethyllysine (Lys) #status
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*product citrate (si)-synthase *status experimental *label MAT\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carbon-carbon lyase; homodimer; methylated amino acid;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete amino acid sequence of porcine heart citrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Crystallographic refinement and atomic models of two different forms of citrate synthase at 2.7 and 1.7 angstroms resolution.
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                                                                                                                                                                                                                                                                                                                                                                   ##cross-references EMBL:M21197; NID:g164418; PID:g164419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Remington, S.; Wiegand, G.; Huber, R.
J. Mol. Biol. (1982) 158:111-152
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                                                                           #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-464 ##label BLO
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##residues 28-464 ##label BL2
                                                                                                                                                                         A29966; A01109; A61347
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418 LERPKSVTMEWLEKFCKR 435
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                                                           RESULT
                                                                             ENTRY
                                                                                                                                      DATE
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28 ASSTNLKDILADLIPKEQARIKTFRQQHGNTVVGQITVDMMYGGMRGMKGLVYETSVLDP 87

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S42370 #type complete
citrate (s1)-synthase (EC 4.1.3.7) precursor - Caenorhabditis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 YKTIDALPITAHPMIQFCTGVMALQTRSEFQKAYEKGIHKSKFWEPTYEDCLSLIAQVPV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 VAAIIYRNLYRDGSAVSVIDPKKDWSANFSSMLGYDDPLFAELMRLYLVIHSDHEGGNVS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 RFRGYSIPECQKLLPKAKGGEEPLPEAIWWLLCTGDVPSEAQTAAITKEWNARADLPTHV 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 RFRGFSIPECQKLLPAASAGAEPLPEGLLWLLLTGKVPSKEQVDALSADLRKRASIPDHV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 EEGIRFRGFSIPECQKLLPAASAGAEPLPEGLLWLLLTGKVPSKEQVDALSADLRKRASI 120
                                                                                                                                                                                                                                                             268 GNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLVWLTQLQKEVGKDVSDEK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 GNVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328 LRDYIWNTLNSGRVVPGYGHAVLRKTDPRYTCQREFALKHLPHDPMFKLVAQLYKIVPNV 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 LLEOGKAKNPWPNVDAHSGVLLQYYGMTEMNYTTVLFGVSRALGVLAQLIWSRALGFPLE 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 DEGIRFRGYSIPECQKMLPKAKGGEEPLPEGLFWLLVTGQIPTEEQVSWLSKEWAKRAAL 147
                                                                                                                                                                                                                     148 PSHVVTMLDNFPTNLHPMSQLSAAITALNSESNFARAYAEGIHRTKYWELIYEDCMDLIA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 NLKEVLSKKIPAHNAKVKSFRTEHGSTVVQNVNIDMIYGGMRSMKGMVTETSVLDPEEGI 93
#formal_name Caenorhabditis elegans
07-0ct-1994 #sequence_revision 10-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                  208 KLPCVAAKIYRNLYREGSSIGAIDSKLDWSHNFTNMLGYTDAQFTELMRLYLTIHSDHEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #superfamily citrate (s1)-synthase
carbon-carbon lyase; mitochondrion; oxo-acid-lyase
#length 468 #molecular-weight 51540 #checksum 2659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##cross-references EMBL: Z30423; NID:g458479; PID:g458482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-468 ##label SMI
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EMBO J. (1984) 3:1773-1781
Isolation of the nuclear yeast genes for citrate synthase and
fifteen other mitochondrial proteins by a new screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           citrate (si)-synthase (EC 4.1.3.7) precursor, mitochondrial yeast (Saccharomyces cerevisiae) protein N2019: protein VNR001c #formal name Saccharomyces cerevisiae 25-Feb-1985 *sequence_revision 10-Feb-1995 *text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             545118
Verhasselt, P.; Aert, R.; Voet, M.; Volckaert, G.
Submitted to the EMBL Data Library, January 1994
Twelve open reading frames revealed on the 23.6 kbp segment
flanking the centromere on the Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               **cross-references EMBL:X77395; NID:9496717; PID:9496718
**note
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274 AHTSHLVGSALSDPYLSFSAAMAGLAGPLHGLANQEVLVFLNKIVGEIGFNYTEEQLKEW 333
                                               244 AHTGHLVGSFLSDFYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQLKDY 303
                                                                                                    334 VWKHLKSGQVVPGYGHAVLRKTDPRYECQREFALKHLPNDDLFKLVSTLYKITPGILLEQ 393
                                                                                                                                              304 VWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYEVVPPILLEL 363
                                                                                                                                                                                                   394 GKAKNPWPNVDSHSGVLLQYFGMTEMSFYTVLFGVSRALG-CLSQLIWARGMGLPLERPK 452
                                                                                                                                                                                                                                Aert, R.; Verhasselt, P.; Voet, M.; Volckaert, G. submitted to the Protein Sequence Database, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Verhasselt, P.; Aert, R.; Voet, M.; Volckaert, G. Yeast (1994) 10:1355-1361
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##residues 1-479 ##label VER
##cross-references EMBL X77395; NID:9496717; PID:9496718
:NCE S48338
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835390
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##residues
1-57,'Q',59-77,'E',78-479 ##label S
##cross-references GB:X00782; NID:g3602; PID:g3603
##experimental_source strain D273-10B
SNCE
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*accession A01110
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**cross·references EMBL.271616, NID.91302468, FID.e239778, FID.91302469; MIPS.YNR001c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #domain transit peptide (mitochondrion) #status
predicted #label TNP\
#product citrate (si)-synthase #status predicted #label
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                                                                                                                                                                                                                                                                                                              carbon-carbon lyase; catalyzes condensation of oxaloacetate
and acetyl-CoA to form citrate; oxo-acid-lyase
                                                                                                                                                                                                                                                                                                                                                           tricarboxylic acid cycle
*superfamily citrate (si)-synthase
acetyl-CoA; carbon-carbon lyase; homodimer; mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 PDHVYKTIDALPITAHPMIQFCTGVMALQTRSEFQKAYEKGIHKSKFWEPTYEDCLSLIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 QVPVVAAYVYRRMYKNGQVIPLDDSLDYGGNFAHMLGFDSPQMLELMRLYVTIHSDHEGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      340 EXYLWDTLNAGRVVPGYGHAVLRKTDPRYTAQREFALKHFDYELFKLVSTIYEVAPGVL 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 EEGIRFRGFSIPECQKLLPAASAGAEPLPEGLLWLLLTGKVPSKEQVDALSADLRKRASI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 PEHVIQLLDSLPKDLHPMAQFSIAVTALESESKFAKAYAQGVSKKEYWSYTFEDSLDLLG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220 KLPVIASKIYRNVFKDGKITSTDPNADYGKNLAQLLGYENKDFIDLMKLYLFIHSDHEGG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 NVSAHTTHLVGSALSSPYLSLAAGLNGLAGPLHGRANQEVLEWLFKLREEVKGDYSKETI 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 NVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 KDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYEVVPPIL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       400 TKHGKTKNPWPNVDSHSGVLLQYYGLTEASFYTVLFGVARAIGVLPQLIIDRAVGAPIER 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 EEGIRFRGRTIPEIQRELPKAEGSTEPLPEALFWLLLTGEIPTDAQVKALSADLAARSEI 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 ASEQILKERFAEIIPAKAEEIKKFKKEHGKTVIGEVLLEQAYGGMRGIKGLVWEGSVLDP 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SSNLDLRSELQELIPEQQERLKKIKKEFGSFQLGNINVDMVLGGMKGMTGLLWETSLLUP 60
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citrate (si)-synthase (EC 4.1.3.7), mitochondrial -
Neurospora crassa
#formal_name Neurospora crassa
20.May-1994 #sequence_revision 10-Nov-1995 #text_change
841563
841563
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#length 479 #molecular-weight 53360 #checksum 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                  oxo-acid-lyase; tricarboxylic acid cycle
                                                                                                                                                                                         ##cross-references SGD:S0005284; MIPS:YNR001c
                                                                                                                    ##experimental_source strain S288C
                    **#molecule_type DNA 1-479 **label AER 1-479 **
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                                                                                                                                                                                                                                                                     homodimer
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P.A.; Guarente, L.P.
Mol. Cell. Biol. (1986) 6:4509-4515
Mitochondrial and nonmitochondrial citrate synthases in
Saccharomyces cerevisiae are encoded by distinct homologous
Ferea, T.; Contreras, E.T.; Oung, T.; Bowman, E.J.; Bowman,
                        #journal Mol. Genet. (1994) 242:105-110
#title Characterization of the cit-1 gene from Neurospora crassa encoding the mitochondrial form of citrate synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 FRGFSIPECQKLLPAASAGAEPLPEGLLWLLLTGKVPSKEQVDALSADLRKRASIPDHVY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 ELIDRCPSDLHPMAQLSLAVTALEHTSSFARAYAKGINKKEYWGYTFEDSMDLIAKLPTI 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 HTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQLKDYV 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 LKERFAELLPENIEKIKALRKEHGSKVVDKVTLDQVYGGARGIKCLVWEGSVLDAEEGIR 97
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protein YGR005c; protein YGR016;
#formal_name_Saccharomyces cerevisiae
30-Sep-1992_#sequence_revision 30-Sep-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                #length 469 #molecular-weight 52002 #checksum 490
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*superfamily citrate (si)-synthase
carbon-carbon lyase; mitochondrion; oxo-acid-lyase
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                                                                                                                                                                                                    ##residues 1-469 ##label BOW ##cross-references EMBL:M84187; NID:g168774; PID:g168775
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#accession A25393
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##molecule_type DNA
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##cross-references EMBL:X59720; NID:g1907116; PID:e264468; PID:g1907148:
##cross-references EMBL:X59720; NID:g1907116; PID:e264468; PID:g1907148:
                                                                        *authors Biteau, N.; Fremaux, C.; Hebrard, S.; Menara, A.; Aigle, M.; Crouzet, M. Tecuzet, M. Teast (1992) 8:61-70

*Litle The complete sequence of a 10.8kb fragment to the right of the chromosome III centromere of Saccharomyces cerevisiae. #cross-references MUID:92254505

*accession S26734
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peroxisome; tricarboxylic acid cycle
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#active_site His, His, Asp #status predicted
#length 460 #molecular-weight 51413 #checksum 1279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 QLLDNLPKDLHPMAQFSIAVTALESESKFAKAYAQGISKQDYWSYTFEDSLDLLGKLPVI 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 KTIDALPITAHPMTQFCTGVMALQTRSEFQKAYEKGIHKSKFWEPTYEDCLSLIAQVPVV 185
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Mol. Cell. Biol. (1991) 11:38-46
Intramitochondrial functions regulate nonmitochondrial
                                                                                                                                                                                                                                                                                                                                                                                              Aigle, M.; Biteau, N.; Crouzet, M. submitted to the Protein Sequence Database, March 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    citrate synthase (CIT2) expression in Saccharomyces
##cross-references EMBL:Z11113; NID:q3297; PID:q3299; GB:M14686;
NID:q171226; PID:q171227
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1-460 ##label BIT
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#domain transit peptide (mitochondrion) *status
predicted *label TNP\
*product 14-nm filament protein/citrate synthase *status
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366 VKNPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRALGLPLEPPKSVT 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 EGIRFRGFSIPECOKLLP-A-A-SAG-A--EPLPEGLLWLLLTGKVPSKEOVDALSADLP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 NRGTVNQDCVNFILNLPKDLHSMTMLSMALLYLQKDSKFAKLYDEGKISKKDYWEPFYED 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 SMDLIAKIPRVAAIIYRHKYRDSKLIDSDSKLDWAGNYAHMMGFEQHVVKECIRGYLSIH 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 44.7%; Score 1451; DB 2; Length 462; Local Similarity 48.9%; Pred. No. 2.20e-269; es 215; Conservative 91; Mismatches 124; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 SQINLKKVIAEIIPQKQAELKEVKEKYGDKVVGQYTVKQVIGGMRGMKGLMSDLSRCDPY 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 SNLDLRSELQELIPEQQERLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLDPE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                14-nm filament protein/Citrate synthase (EC 4.1.3.-) -
Tetrahymena thermophila (SGC5)
49K filament-forming protein
#formal_name Tetrahymena thermophila
14-oct-1997_#sequence_revision 07-Nov-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun. (1997) 237:205-210
Direct demonstration of the bifunctional property of
Tetrahymena 14-nm filament protein/citrate synthase
following expression of the gene in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tetrahymena 14-nm filament-forming protein has citrate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 KRASIPDHVYKTIDALPITAHPMTQFCTGVMALQTRSEFQKAYEKG-IHKSKFWEPTYED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #length 462 #molecular-weight 52575 #checksum 9423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chiba, J.; Watanabe, Y.
Biochem. Biophys Res Commun (1991) 174:1028-1034
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oxo-acid-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takeda, T.; Watanabe, Y.; Numata, O.
Biochem. Biophys. Res. Commun. (1997
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##residues 1-462
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CLASSIFICATION #supe
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##molecule_type DNA
##residues 1-486 ##label WAN
##cross-references EMBL:U31900; NID:91276597; PID:9939735; MIPS:YPR001w
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Hall, J.; Storms, K.K.; Vo, D.H.; Winnett, E.
submitted to the EMBL Data Library, July 1995
The sequence of Saccharomyces cerevisiae chromosome XVI rigl
                                                                                                                                                                                                                                                                        382 VIPKKLLTYKKIANPYPNVDCHSGVLLYSLGLTEYQYYTVVFAVSRALG-CMANLIWSRA 440
                                                                                                                                                                                                                                                                                                                       355 VVPPILLELGKVKNPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGIC-SQLIWDRA 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      citrate (si)-synthase (EC 4.1.3.7) - yeast (Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 PEHGIKFQGLTIEECQNRLPNTGIDGDNFLPESMLWLLMTGGVPTFQQAASFPKELAIPG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 PEEGIRFRGFSIPECQKLLPAASAGAEP-LPEGLLWLLLTGKVPSKEOVDALSADI.PKPA 118
175 CLSLIAQVPVVAAYVYRRYKNGQVIPLDDSLDYGGNFAHMLGFDSPQMLELMRLYVIH 234
                                                                        262 CDHEGGNVSAHTTHLVGSALSDPYLSYSAGVNGLAGPLHGLANQEVLKWLLQFIEEKGTK 321
                                                                                                                                                                           322 VSDKDIEDYVDHVISSGRVVPGYGHAVLRDTDPRFHHQVDFSKFHLKDDQMIKLLHQCAD 381
                                                                                                                                                                                                                    295 ISTEQLKDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYE 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SSNLDLRSELQELIPEQQERLKKIKKEFGS-FQLGNINVDMVLGGMRGMTGLLWETSLLD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein LPZIW; protein YP9723.01; protein YPR001w
#formal_name Saccharomyces cerevisiae
19-May-1995 #sequence_revision 01-Sep-1995 #text_change
                                                                                                                       235 SDHEGGNVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.9%; Score 1261; DB 2; Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, April 1995
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NCE S59746
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207; Conservative
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KEYWORDS cark
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Flickinger, M.C.
#journal Appl. Environ. Microbiol. (1992) 58:335-345
#title Cloning and nucleotide sequence of the gene coding for citrate synthase from a thermotolerant Bacillus sp.
#cross-references MUID:92171501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  340 -LP-D-DPFFQLVSKLYEVVPPILLELGKVKNPWPNVDAHSGVLLNHYGLTEARYYTVLF 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 HGGANEAVM----EMLQD-AQTV--EGFKHLLHDKLSKKEKIMGFGHRVYMKKMDPRAAM 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276 MKE-ALKELSAVNGDDLLLQMCEAGEQIMRE--E-KGLFPNLDYYAAPVYWKLGIPIPLY 331
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                                 119 S-IPDHVYKTIDALPITAHPMTQFCTGVMALQTRSEFQKAYEKG-IHKSKFWEPTYEDCL 176
                                                                                                                                               263 LDFINLMRLYTGIHVDHEGGNVSAHTTHLVGSALSDPYLSYSSGIMGLAGPLHGLAAQEV 322
                                                                                                                                                                                                                          323 VFFLIEMNSNIS-SIAREQEIKDYLWKILNSNRVIPGYGHAVLRKPDPRFTAMLEFAQKR 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A43936 #type complete citrate synthase Bacillus sp. #formal_name Bacillus sp. 10.Mar-1993 #sequence_revision 18-Nov-1994 #text_change
                                                                                               203 NLIASLPLLIGRIYSNITNEGHPLGQYSEEVDWCTNICSLLGMTNGTNSSNTCNLTSQQS
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#length 373 #molecular-weight 41970 #checksum 2911
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larity 28.9%; Pred. No. 3.51e-37;
Conservative 82; Mismatches 119; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                            442 GCSRAMGPLTQLVWDRILGLPIERPKSLNLEGLEALTK 479
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K.U.; Sahm, H
Microbiology (1994) 140:1817-1828
Nucleotide sequence, expression and transcriptional analysis
of the Corynebacterium glutamicum gltA gene encoding
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267 GLAGPLHGLANQEVLLWIKSVVDECGENISTEQLKDYVWKTLNSGKVVPGFGLGVLRKTD 326
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                                                                                                                                                                                                             #formal_name Corynebacterium glutamicum
16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change
17-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                          Eikmanns, B.J.; Thum-Schmitz, N.; Eggeling, L.; Luedtke
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#length 437 #molecular-weight 48929 #checksum 2093
                                                                                                                            Query Match 10.0%; Score 324; DB 2; Length 437; Best Local Similarity 28.7%; Pred. No. 2.28e-37; Matches 91; Conservative 94; Mismatches 105; Indels 27;
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tricarboxylic acid cycle
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392 YTVLFGVSRSLGICSQLI 409
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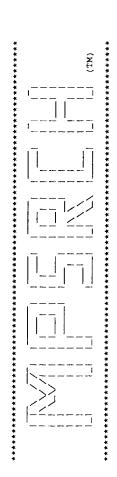
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Donald, L.J.; Molgat, G.F.; Duckworth, H.W.
J. Bacteriol. (1989) 171:5542-5550
Cloning, sequencing, and expression of the gene for
NADH-sensitive citrate synthase of Pseudomonas aeruginosa.
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*formal_mame Pseudomonas aeruginosa
30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change
17-Jul-1998
                                                                                                                                                     Cloning of genes responsible for acetic acid resistance in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 EEVIYLLLNGELPNKVQYDTFTNTLTNHTLLHEQIRNFFNGFRDAHPMAILCGTVGALS 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 A-F-YPDANDIAIP-AN-RDLA--A-MRLIAKIPTIAAWAYK--YTQGEAFIYPRND-LN 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 YAENFLSMMFARMSEPYKVNPVLARAMNRILILHADHEQ-NASTSTVRLAGSTGANPFAC 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261 FAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQLKDYVWKTLNSGKVVPGFGLG 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 YGGNFAHML-G-FDSPQMLE--LMR-LY-VTI-HSDHEGGNVSAHTGHLVGSPLSDPYLS 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 IAAGIAALWGPAHGGANEAVLK-MLARIGK-KENIPA-FIAQ-V-KDKNSGVKLMGFGHR 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315 VYKNFDPRAKIMQQTCHEVLTELGIKDDPLLDLAVEL-EKIA-LSDDYFVQRKLYPNVDF 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 VLRKTDPRYTC-QRE-FA-LKHLP--DDPFFQLVSKLYEVVPPILLELGKVKNPWPNVDA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 309; DB 1; Length 436;
Pred. No. 1.45e-34;
85; Mismatches 108; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *superfamily citrate (si)-synthase allosteric regulation; carbon-carbon lyase; homohexamer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #active_site His #status predicted
#length 436 #molecular-weight 48196 #checksum 9071
                                                                             Fukaya, M.; Takemura, H.; Okumura, H.; Kawamura, Y.;
                                                                                                                                                                                                                                                                                       ##residues 1-436 ##label FUK
##cross-references GB:M34830; NID:q141729; PID:g141730
homohexamer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oxo-acid-lyase; tricarboxylic acid cycle
                                                                                                   Horinouchi, S.; Beppu, T.
J. Bacteriol. (1990) 172:2096-2104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                373 YSGIILKAMGIPTSMF-TVLFAVARTIG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  376 HSGVLLNHYGLTEARYYTVLFGVSRSLG 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *type complete
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                                                                                                                                                                                   Acetobacter aceti.
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                                                                                                                                                                                                            *cross-references MUID:90202732
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Best Local Similarity 31.1%;
Matches 102; Conservative
17-Jul-1998
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                                                                                                                                                                                                                                                                                          ##residues
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                                                                                *authors
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Aloni, G.; Azevedo, V.; Bortero, M.G.; Bessieres, P.;
Alloni, G.; Azevedo, V.; Bortero, M.G.; Bessieres, P.;
Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans,
A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.;
Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, N.J.;
Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghia,
S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.
Guiseppi, G.; Guy, B.J.; Haga, K.; Haiech, J.; Harward,
C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.;
Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.;
Kasahara, Y.; Lagidus, A.; Lardinois, S.; Kunano, M.;
Kurita, K.; Lapidus, A.; Lardinois, S.; Kunano, M.;
Maucel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno,
M.; Moestl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly,
M.; Presecan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.;
A.M.; Presecan, E.; Pujic, P.; Purnelle, B.; Rapoport,
carbon-carbon lyase; oxo-acid-lyase; catalyzes synthesis of citrate from acetyl-CoA and oxaloacetic acid tricarboxylic acid cycle tricarboxylic acid cycle the citrate synthase of gram-negative bacteria is an allosteric enzyme whose activity is inhibited strongly and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 FAHKL-GF--DS-P--QMLE-LM-RLYVTIHSDHEGGNVSAHTGHLVGSPLSDFYLSFAA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89 LLLNGELPTAAQKEQFVGTIKNHTMVHEQL-KTFFNGFRRDAHPMAVMC-GVIGALS-AF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 FLHMMFNTPCETKPISPVLAKAMDRIFI-LHADHEQ-NASTSTVRLAGSSGANPFACIAS 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 GIAALWGPAHGGANEAVL---R-MLDEIGDVSNIDKFVEKAKDKNDPFKLM-GFGHRVYK 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264 ALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQLKDYVWKTLNSGKVVPGFGLGVLR 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 LLLIGKVPSKEQVDALSADLRKRASIPDHVYKII-DALPITAHPMIQFCTGVMALQTRSE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 YHDSLD--ITNPKHREVS-AH--RLIAKMPTIAAMVYK--YSKGEPMMYPRND-LNYAEN 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 FQKAYEKGIHKSKFWEPTYEDCLSLIAQVPVVAAYVYRRMYKNGQ-VI-PLDDSLDYGGN 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   311 NFDPRAKVMKQTCDEVLQELGINDPQLELAMKLEEIAPHDPY-FVE-FNLYPNVDFYSGI 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 KTDPRYTC--QR-EFALKHLP-DDPFFQLVSKLYEVVPPILLELGKVKNPWPNVDAHSGV 379
                                                                                                                                                                      specifically by NADH
*superfamily citrate (si)-synthase
allosteric regulation; carbon-carbon lyase; homohexamer;
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#formal_name Bacillus subtilis
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                        #length 428 #molecular-weight 47681 #checksum 7548
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 9.4%; Score 306; DB 1; Length 428; Best Local Similarity 29.3%; Pred. No. 5.24e-34; Matches 95; Conservative 95; Mismatches 98; Indels 36;
                                                                                                                                                                                                                                                                                   oxo-acid-lyase; tricarboxylic acid cycle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380 LLNHYGLTEARYYTVLFGVSRSLG 403
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Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.;
Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, E.;
Schleich, S.; Schroeter, R.; Scoffone, F.; Sekfquchi, J.;
Sekowska, A.; Schrock, R.; Scoffone, F.; Schfquchi, J.;
Sekowska, A.; Tacconi, E.; Takadishi, H.;
Takemaru, K.; Takeuchi, M.; Takadi, T.; Takahashi, H.;
Takemaru, K.; Takeuchi, M.; Tosato, V.; Uchiyama, T.;
Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.;
Wandenbol, M.; Vannier, F.; Vassarotti, A.; Vanters, P.; Wedler, F.; Wedler, H.; Wannone, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumstein, E.;
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#journal Nature (1997) 390:349-226
#title The complete genome sequence of the Gram-positive bacterium
#cross-references MUID:98044033
#accession E69658
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##cross-references GB:299116; GB:AL009126; NID:g2634723; PID:ell85682;
##experimental_source strain 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 9.3%; Score 301; DB 2; Length 372;
Best Local Similarity 28.3%; Pred. No. 4.44e-33;
Matches 96; Conservative 91; Mismatches 124; Indels 28; Gaps
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#length 372 #molecular-weight 42106 #checksum 1505
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Search completed: Fri Oct 22 16:50:35 1999 Job time: 83 secs.

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Fri Oct 22 16:50:52 1999; MasPar time 13.81 Seconds 894.613 Million cell updates/sec

Run on:

Tabular output not generated.

>US-08-702-718-4 (1-437) from USO8702718.pep 3243 1 SSNLDLRSELQELIPEQQER......LERPKSVIMEWLEKFCKRRA 437

Description: Perfect Score:

Sequence:

PAM 150 Gap 11 Scoring table:

77977 seqs, 28268293 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot37 1:swissprot Database:

Mean 50.720; Variance 85.362; scale 0.594 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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86.9%; Score 2817; DB 1; Length 471;

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01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANDOTATION UPDATE)
CITRATE SYWHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)
EUKARYOTS, VIRIDIPLANTAE, STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
CUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX. CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                  181 QVPVVAAYVYRRMYKNGQVIPLDDSLDYGGNFAHMLGFDSPQMLELMRLYVTIHSDHEGG 240
                                                                                                                                                                                                                                                                                          301 KDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYEVVPPIL 360
                                                                                                                                                                                                                                                                                                                                                                                       95 DEGIRFRGLSIPECOKLLPAAKPDGEPLPEGLLWLLLTGKVPSKEQVDGLSKELRDRATV 154
                                                                                                                                                          155 PDYVYKAIDALPVSAHPMTQFASGVMALQVQSEFQEAYEKGIHKSKSWEPTSEDSLNLIA 214
                                                                                                                                                                                                                  215 RVPVVAAYVYQRIYKDGKIIPKDDSLDYGGNFSHMLGFDDPKMLELMRLYVTIHSDHEGG 274
                                                                                                                                                                                                                                                                           275 NVSAHTGHLVASALSDPYLSFLAALNGLAGPLHGLANQEVLLWIKSVVDECGENVTTEQL 334
                                                                                                                                                                                                                                                                                                                                 335 KDYVWKTLNSGKVVPGFGHGVLRKTDPRYTCQREFALKHLPDDPLFQLVSKLYEVVPPIL 394
                                           35 SADLDLHSQLKEMIPEQQERLKKVKSDLGKAQLGNITIDVVIGGMRGMTGLLWETSLLDP 94
                                                                      1 SSNLDLRSELQELIPEQQERLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLDP 60
               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNGER E.A., HAND J.M., CASHMORE A.R., VASCONCELOS A.C.;
"Isolation of a cDNA encoding mitochondrial citrate synthase Arabidopsis thaliana.";
PLANT MOL. BIOL. 13:411-418(1989).
-:- CATALYITC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)O + OXALOACETATE.
Pred. No. 0.00e+00;
42; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METABOLISM.
SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    472 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
 Best Local Similarity 84.4%;
Matches 369; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 455 PKSVTLDWIEKNCKKAA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 PKSVTMEWLEKFCKRRA 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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154 AAVSDYVYNAIDALPSTAHPMTQFASGVMALQVQSEFQKAYENGIHKSKFWEPTYEDCLN 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           274 EGGNVSAHTGHLVGSALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGEDISK 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCLTELES-EEPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRELLLA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 EEVFALGDCRLPECQKALLPTAQSGGLNHYRRSFVASLNWKGTL-AKSKLKH-CRKTWNR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 ASIPDHVYKTIDALPITAHPMTQFCTGVMALQTRSEFQKAYEKGIHKSKFWEPTYEDCLS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 EQLKEYVWKTLNSGKVIPGYGHGVLRNTDPRYVCQREFALKHHPDDPLFQ-CCKLMKL-A 391
                                                                                                                                                                                                                                                                                                                                            36 STDLDLKSQLQELIPEHKDRLKKLKSEHGKVQLGNITVDMVIGGMRGMTGLLWETSLLDP 95
                                                                                                                                                                                                                                                                                                                                                                     8; Gaps
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DEDXIAMD.P., PARMELEE D.C., KUMAR S., WALSH K.A., TITANI K.;
"Complete amino acid sequence of porcine heart citrate synthase.";
BIOCHEMISTRY 21:2028-2036(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVANS C.I., OWENS D.D., SUMEGI B., KISPAL G., SRERE P.A.; "Isolation, nucleotide sequence, and expression of a cDNA encoding
                                                           LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE; MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACTYLA; SUIFORMES; SUINA; SUIDAE; SUS.
                                                                                                                                                                                                                                                          DB 1; Length 472;
                                                                                                                                                                                                                                                                                                  52; Mismatches 64; Indels
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01-CCT-1389 (REL. 12, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNORATION UPDATE)
CITRALE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
', 954AFA81 CRC32;
                                                                                                                                                                                                                                                                              Pred. No. 0.00e+00;
                                                                                                                                CITRATE SYNTHASE.
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                                                                                                          MITOCHONDRION
                                                                                                                                                                                                                                                          Score 2249;
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
PFAM; PF00285; citrate_synt; 1.
HSSP; P23007; SCSC.
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                                                                                                                                                                                                              52941 MW;
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Similarity 71.7%;
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309
355
407
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355 3
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472 AA;
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CISY_PIG
P00889;
                                                                                                                                                  ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
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                                                                                                                                             SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
              MEDLINE; 83010291.

REMINGTON S , WIEGAND G , HUBER R ;

"Crystallographic refinement and atomic models of two different forms of citrate synthase at 2.7 and 1.7 A resolution.";

J MOL. BIOL. 158:111-152(1982).
                                                                         MEDLINE; 91104711.
ALTER G.M., CASAZZA J.P., ZHI W., NEMETH P., SRERE P.A., EVANS C.T.;
"Mutation of essential catalytic residues in pig citrate synthase.";
BIOCHEMISTRY 29:7557-7563(1990).
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)0 +
                                                                                                                                                                                                                                                                  PIR; A29966; YKPG.
PDB; ICTS; 16-JUL-88.
PDB; 3CTS; 09-OCT-88.
PDB; 3CTS; 09-OCT-88.
PDB; 4CTS; 16-JUL-88.
PROSTIE: PS00480; CITRATE_SYNTHASE; 1.
PRAM; PF00285; CITRATE_SYNT; 1.
LYASE; TRICARROXYLIC ACID CYCLE: MITOCHONDFION; 3D-STRUCTURE; TRANSIT PEPTIDE; MEHMIATION.
ITANSIT PEPTIDE; MEHMIATION.
                                                                                                                                                                      : - SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY,
                                                                                                                                                                                                                                                                                                                                                       CITRATE SYNTHASE.
METHYLATION (TRI-).
         X-RAY CRYSTALLOGRAPHY (2.7 AND 1.7 ANGSTROMS)
                                                                                                                             PATHWAY: TRICARBOXYLIC ACID CYCLE. SUBUNIT: HOMODIMEP
                                                                                                                                                                                                                                                           EMBL; M21197; G164419; -.
                                                                                                                                                                                                                                                                                                                                                      OXALOACETATE
                                                                                                                                                              METABOLISM.
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PSHVVTMLDNFPTNLHPMSQLSAAITALNSESNFARAYAEGIHRTKYWELIYEDCMDLIA 2077
                                                                                                                                                                                                                                                                                                                                                                     208 KLPCVAAKIYRNLYREGSSIGAIDSKLDWSHNFTNMLGYTDAQFTELMRLYLTIHSDHEG 267
                                                                                                                                                                                                                                                                                                                                                                                                      240 GNVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                               LLEQGKAKNPWPNVDAHSGVLLQYYGMTEMNYYTVLFGVSRALGVLAQLIWSRALGFPLE 447
                                                                                                                                                                                                                                                                                                                  88 DEGIRFRGYSIPECQKMLPKAKGGEEPLPEGLFWLLVTGQIPTEEQVSWLSKEWAKRAAL 147
                                                                                                                                                                                                                                                                                                                                                                                                                         LRDYIWNTLNSGRVVPGYGHAVLRKTDPRYTCQREFALKHLPHDPMFKLVAQLYKIVPNV 387
                                                                                                                                                                                                                                                                                        28 ASSINLKDILADLIPKEQARIKTFRQQHGNTVVGQITVDMMYGGMRGMKGLVYETSVLDP 87
                                                                                                                                                                                                                                                                                                     1 SSNLDLRSELQELIPEQQERLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLDP 60
                                                                                                                                                                                                                                                             Score 2096; DB 1; Length 464;
Pred. No. 0.00e+00;
79; Mismatches 84; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                  181 OVPVVAAYVYRRMYKNGOVI-PLDDSLDYGGNFAHMLGFDSPOMLELMRLYVTIHSDHEG
                                                                                                                                                                                                                                                                                                                                                                                               268 GNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLVWLTQLQKEVGKDVSDEK
                                                                                                                                                                                                                                                  51529 MW; 3BC38D25 CRC32;
                                                                                                                                                                                                                                                               64.68;
                                                                                                                                                                                                                                                                    Best Local Similarity 62.1%;
Matches 269; Conservative
RPKSMSTDGLIKL 460
                                                                                                                                                                                                                                                  464 AA;
SECUENCE
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PATHWAY: TRICARBOXYLIC ACID CYCLE.
SUBUNT: HOMODINER.
SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                     MEDLINE; 91255228.

LIAO D.-1., KARPUSAS M., REMINGTON S.J.;
LIAO Structure of an open conformation of citrate synthase from chicken heart at 2.8-A resolution.";
BIOCHEMISTRY 30:6031-6036(1991).
-:-CATANTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)0 +
                                                                                                                                           TISSUE-HEART MUSCLE;
MEDLINE; 9024843.
MEDRINGS 9024843.
"Proposed mechanism for the condensation reaction of citrate
"Proposed mechanism for the condensation reaction of citrate
synthase: 1.9-A structure of the ternary complex with oxaloacetate
and carboxymethyl coenzyme A.";
BIOCHEMISTRY 29:2213-2219(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                         DR PDB: 1CSS: 15-OCT-95.

DR PDB: 1AL6: 24-DEC-97.

DR PDB: 1AM2: 24-DEC-97.

DR PROSITE: 2800000; CITRATE_SYNTHASE; 1.

DR PFAM: PFO0285; Citrate_synt; 1.

KW LYASE: TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; 3D-STRUCTURE.

T ACT_SITE 320 320

T ACT_SITE 375 375
                                                                                                                                                                                                                                                                                                                METABOLISM.
SIMILARITY: BELONGS TO THE CITFATE SYNTHASE FAMILY.
SIMILARITY: BELONGS TO THE CITFATE SYNTHASE FAMILY.
CAUTION: THIS IS AN X-RAY DETERMINED SEQUENCE WHICH WAS
ESTABLISHED USING THE SEQUENCE OF PIG CITRATE SYNTHASE AND
MODIFYING IT BASED ON THE OBSERVED ELECTRON DENSITY.
                                                                                                           EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF OPEN CONFORMATION
                                                                01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL (EC 4.1.3.7).
                                         433 AA
                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)
                                         PRT;
                                                       01-AUG-1991 (REL. 19, CREATED)
                                                                                                  GALLUS GALLUS (CHICKEN)
                                                                                                                                                                                                                                                                                                                                                                           15-APR-91.
15-APR-91.
15-APR-91
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375
375
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477
477
70
70
80
       420 RPKSVTMEWLEKF 432
                                                                                                                                                                                                                                                                                                                                                          1CSC; 15-APR-91.
2CSC; 15-APR-91.
                                                                                                                                                                                                                                                                                                                                                                                                   24-DEC-97
15-OCT-90.
                                                                                                                                                                                                                                                                                                                                                                                                                     15-JAN-93
OXALOACETATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CISY_CHICK P23007:
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5CTS;
6CTS;
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181 KLPCVAAKIYRNLYRAGSSIGAIDSKLDWSHNFTNMLGYTDAQFTELMRLYLTIHSDHEG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 LRDYIWNTLNSGRVVPGYGHAVLRKTDPRYTCQREFALKHLPGDPMFKLVAQLYKIVPNV 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 LKDYVWKILNSGKVVPGFGLGVLRKIDPRYTCQREFALKHLPDDPFFQLVSKLYEVVPPI 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 LLEQGAAANPWPNVDAHSGVLLQYYGMTEMNYYTVLFGVSRALGVLAQLIWSRALGFPLE 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 PSHVVTMLDNFPTNLHPMSQLSAAITALNSESNFARAYAEGILRTKYWEMVYESAMDLIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 GNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLGWLAQLQKAXXXAGADAS 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DEGIRFRGFSIPPECOKLLPRGGXGGEPLPEGLFWLLVTGQIPTGAQVSWLSKEWAKRAAL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SSNLDLPSELQELIPEQQEPLKKIKKEFGSFQLGNINVDMVLGGMPGMTGLLWETSLLDP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 61.5%; Score 1993; DB 1; Length 433;
Local Similarity 60.5%; Pred. No. 0.00e+00;
nes 259; Conservative 72; Mismatches 96; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      47373 MW; 6E24FE58 CPC32;
                                                                                                                                                                                                                                                                                                                                  343
364
372
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384
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312
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390
415
427
43 AA;
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Match 57.7%;
Local Similarity 59.5%;
Les 254; Conservative
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                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                     SCHIZOSACCHAROMYCES.
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365
420
482 AA;
                                                                                                                                                      453 SHSTDGLIKL 462
                                                                                                                                                                                  423 SVIMEWLEKF 432
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                        CISY_SCHPO
Q10306;
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                                                                                                                                                                                                                                                                                                         -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (BY SIMILARITY).
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDAIIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM: PF00285; citrate_synt; 1.
HSSP; P23007; 5CSC.
HYPOTHETICAL PROTEIN: LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 VAAYVYRRMYKNGQVIP-LDDSLDYGGNFAHMLGFDSPQMLELMRLYVTIHSDHEGGNVS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 RFRGYSIPECQKLLPKAKGGEEPLPEAIWWLLCTGDVPSEAQTAAITKEWNARADLPTHV 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 RFRGFSIPECOKLLPAASAGAEPLPEGLLWLLIGKVPSKEQVDALSADLRKRASIPDHV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 VRMLDNFPDNLHPMAQFIAAIAALNNESKFAGAYARGVAKASYWEYAYEDSMDLLAKLPT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 VAAIIYRNLYRDGSAVSVIDPKKDWSANFSSMLGYDDPLFAELMRLYLVIHSDHEGGNVS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                274 AHTSHLVGSALSDPYLSFSAAMAGLAGPLHGLANQEVLVFLNKIVGEIGFNYTEEQLKEW 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 YKTIDALPITAHPMIQFCTGVMALQTRSEFQKAYEKGIHKSKFWEPTYEDCLSLIAQVPV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 NLKEVLSKKIPAHNAKVKSFRTEHGSTVVQNVNIDMIYGGMRSMKGMVTETSVLDPEEGI 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 DLRSELQELIPEQQERLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLDPEEGI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0.00e+00;
76; Mismatches 99; Indels 3; Gaps
                                                                                                                                                                            EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA, RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                        01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
PROBABLE CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MITOCHONDRION (POTENTIAL).
CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                 BERKS M., SMITH A.;
SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADA3A630 CRC32;
                                                                  468 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1890;
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WORMPEP; T20G5.2; CE00513.
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51540 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 58.3%;
l Similarity 58.6%;
252; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z30423; G458482; -.
                                                                  STANDARD;
                                                                                                                                                                  CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303
349
349
404
468 AA;
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       STRAIN-BRISTOL N2;
       420 RPKSVTME 427
                                                                                                                                                                                                                                                                                              OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSIT PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                     METABOLISM.
                                                             CISY_CAEEL P34575;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (BY SIMILARITY).
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                        394 GKAKNPWPNVDSHSGVLLQYFGMTEMSFYTVLFGVSRALG-CLSQLIWARGMGLPLERPK 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 FRGYTIPECQKLLPSSPNGKQPLPESLFWLLVTGEIPTLSQVQALSADWAARSQLPKFVE 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334 VWKHLKSGQVVPGYGHAVLRKTDPRYECQREFALKHLPNDDLFKLVSILYKITPGILLEQ 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00480; CITRATE_SYNTHASE; 1.
PFAM, PF002B5; citrate_synt; 1.
HSSP, P23007; 5csc.
HYSPPTHETICAL PROTEIN; LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 LKDRLAELIPEKQAEIKKFRAEHGQDVIGEVTINQMYGGARGVRSLIWEGSVLDPNEGIR 110
244 AHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQLKDY 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAJANDREAM M.A., WALSH S.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 LRSELQELIPEQQERLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLDPEEGIR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-001-1996 (REL. 34, CREATED)
01-001-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-001-1996 (REL. 34, LAST ANNOTATION UPDATE)
PROBABLE CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77; Mismatches 95; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=972;
DEVLIN K., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALS SUBMITTED (FEB-1996) TO EMEL/GENBANK/DDBJ DATA BANKS.
-1- CATALYTIC ACTIVITY: CITRAIE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MITOCHONDRION (BY SIMILARITY). CITRATE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1870; DB 1; Length 482; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES; SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
4; 18145A7D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        482 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OXALOACETATE.
-!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44
482
319
365
83
420
84030 MW;
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PATHWAY TRICARROXYLIC ACID CYCLE
SURCELLULAR LOCATION MITOCHONDRIAL MATRIX.
CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
              291 HTGHLVGSALSSPFLSMAASLNGLAGPLHGLANOEVLNFLITMKKEIGDDLSEETIKSYL 350
                                                                                                                                                                    245 HIGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQLKDYV 304
                                                                                                                                                                                                     351 WKLLNSGRVVPGYGHAVLPKTDPRYTAQPEFALEHLPKDPMFQLVSPLYEIVPGVLTEHG 410
                                                                                                                                                                                                                                                                                         VERHASSELT P , AERT R , VOET M ., VOLCKAERT G , Twelve open reading frames revealed in the 23.6 kb segment flanking the centromere on the Saccharomyces cerevisiae chromosome XIV right
ELIDRCPPTLHPMAQFSLAVTALEHDSAFAKAYERGMNKHDYWKYEYEDCMDLIAKTVPI
                                                                                                                                                                                                                         01-FDB-1996 (REL. 28, LAST SEQUENCE UPDATE)
01-FDB-1996 (REL. 28, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CITRALE SYMTHASE, MITCHONDRIAL PRECURSOR (EC 4.1.3.7).
CITI OR LYS6 OR GLU3 OR YNROULC OR N2019.
CITI OR LYS6 OR GLU3 OR YNROULC STANST).
EUKARYOTA: FUNGI: ASCOMYCOTA: HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                       411 KTKNPYPNVDSHSGVLLQYYGLKEQSFYTVLFGVSRTLGVASQLIWDRALGLPIERPKSF
                                                                 231 AGRIYRNLYRDGVVAPIQMDKDHSYNFANVLGFANNEEFVELMRLYLTIHADHEGGNVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Isolation of the nuclear yeast genes for citrate synthase and fifteen other mitochondrial proteins by a new screening method EMBO J. 3:1773-1781(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LALO D., STETTLEP S., MARIOTTE S., GENDREAU E., THURIAUX P., "Organization of the centromeric region of chromosome XIV in Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-D273-10B;
LINDNER P., PLUECKTHUN A.;
SUBMITTED (JUL-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                          479 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUISSA M., SUDA K., SCHATZ G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YEAST 10:1355-1361(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-S288C / FY1679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YEAST 10:523-533(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-D273-10B;
MEDLINE; 85003587.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 95028151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 95208356
                                                                                                                                                                                                                                                                                                                                         471 STEALKK 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                          425 TMEWLEK 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METABOLISM
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P00890;
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C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 PDHVYKTIDALPITAHPMTQFCTGVMALQTRSEFQKAYEKGIHKSKFWEPTYEDCLSLIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  280 NVSAHTTHLVGSALSSPYLSLAAGLNGLAGPLHGRANQEVLEWLFKLREEVKGDYSKETI 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 NVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 340 EKYLWDTLNAGRVVPGYGHAVLRKTDPRYTAQREFALKHFPDYELFKLVSTIYEVAPGVL 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 KDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYEVVPPIL 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  400 TKHGKTKNPWPNVDSHSGVLLQYYGLTEASFYTVLFGVARAIGVLPQLIIDRAVGAPIER 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 EEGIRFRGRTIPEIQRELPKAEGSTEPLPEALFWLLLTGEIPTDAQVKALSADLAARSEI 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 PEHVIQLLDSLPKDLHPMAQFSIAVTALESESKFAKAYAQGVSKKEYWSYTFEDSLDLLG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 ASEQTLKEPFAEIIPAKAEEIKKFKKEHGKTVIGEVLLEQAYGGMRGIKGLVWEGSVLDP 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SSNLDLRSELQELIPEQQERLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 KLPVIASKIYRNVFKDGKITSTDPNADYGKNLAQLLGYENKDFIDLMRLYLTIHSDHEGG
                                                                                                                                                                                                                                                                                                                           LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66; Indels
SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                           CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
E -> Q (IN REF. 2).
E -> E (IN REF. 2).
W; C6896385 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1815; DB 1;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CISY_EMENI STANDARD; PRT; 474 AA 000098; 01-NOV-1997 (REL. 35, CREATED) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                             MITOCHONDRION
                                                                                                                                                                                                                                                                             PS00480; CITRATE_SYNTHASE; 1. 00285; citrate_synt; 1.
                                                                                                                                                                                                                                                                                                                                                                479
312
312 BB
413
413
53360 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 56.0%;
Local Similarity 57.1%;
                                                                                                                                                              EMBL; Z23259; G313750; -.
                                                                                                                                                                               EMBL; X00782; G3603; -.
EMBL; X77395; G496718; -.
EMBL; Z71616; E239778; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                             PIR; A01110; YKBY.
PIR; S35390; S35390.
                                                                                                                                                                                                                                                          SGD; L0000341; CIT1
PROSITE; PS00480; C
PFAM; PF00285; Citr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        479 AA;
                                                                                                                                                                                                                                                                                                             ; 5csc
                                                                                                                                                                                                                                                                                                                                              MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 460 PKSFSTE 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 PKSVTME 427
                                                                                                                                                                                                                                                                                                                                                                                          312
358
413
58
78
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                                                                                                                                                                                                                                                                                                             HSSP; P23007
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CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                         TRANSIT
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462 STE 464 : | 425 TME 427

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                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX. CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               365 KVKNPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRALGLPLERPKSV 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 LKETFADKLPGELEKVKKLRKEHGNKVIGELTLDQAYGGARGVKCLVWEGSVLDSEEGIR 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 FRGLTIPECQKLLPKAPGGEEPLPEGLFWLLLTGEVPSEQQVRDLSAEWAARSDLPKFIE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 FRGFSIPECQKLLPAASAGAEPLPEGLLWLLLTGKVPSKEQVDALSADLRKRASIPDHVY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 ELIDRVPSTLHPMAQFSLAVTALEHESAFAKATAKGINKKDYWNYTFEDSMDLIAKLPTI 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 KTIDALPITAHPMTQFCTGVMALQTRSEFQKAYEKGIHKSKFWEPTYEDCLSLIAQVPVV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222 AAKIYRNVFKDGKVAPIQKDKDYSYNLANQLGFADNKDFVELMRLYLTIHSDHEGGNVSA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    282 HTTHLVGSALSSPMLSLAAGLNGLAGPLHGLANQEVLNWLTEMKKVVGNDLSDQSIKDYL 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   342 WSTLNAGRVVPGYGHAVLRKTDPRYTSQREFALRKLPDDPMFKLVSQVYKIAPGVLTEHG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305 WKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYEVVPPILLELG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              402 KTKNPYPNVDAHSGVLLQYYGLTERNYYTVLFGVSRALGVLPQLIIDRAFGAPIERPKSF 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE
                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                       "Cloning and characterization of the citA gene encoding the mitochondrial citrate synthase of Aspergillus nidulans."; MOL. CELLS 7:290-295(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1778; DB 1; Length 474; Pred. No. 0.00e+00;
                                                      EMERICELLA NIDULANS (ASPERGILLUS NIDULANS).
EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PLECTOMYCETES;
EUROTIALES; TRICHOCOMACEAE; EMERICELLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MITOCHONDRION (POTENTIAL).
                    4.1.3.7).
                                                                                                                                                                                       PARK B.W., HAN K.H., LEE C.Y., LEE C.H., MAENG P.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY.
D97E1E91 CRC32;
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE) CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITRATE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PS00480; CITRATE_SYNTHASE; 1.
PFAM: PF00285; citrate_synt; 1.
HSSP; P23007; 5CSC.
                                                                                                                                                                                                                                                                                                     -! - PATHWAY: TRICARBOXYLIC ACID CYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΒY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Β¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                474 AA; 52223 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U89675; G2138332; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                     97306446.
                                                                                                                                                                                                                                                                                                                                                                METABOLISM.
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                                                                                                                                                      STRAIN=FGSC
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 HTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQLKDYV 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 KTIDALPITAHPMTQFCTGVMALQTRSEFQKAYEKGIHKSKFWEPTYEDCLSLIAQVPVV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 AAKIYRNVFKDGKVAPIQKDKDYSYNLANQLGYGDNNDFVELMRLYLTIHSDHEGGNVSA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            282 HTTHLVGSALSSPMLSLAAGLNGLAGPLHGLANQEVLNWLTKMKAAIGNDLSDEAIKNYL 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 LKETFAEKLPAELEKVKKLRKEHGSKVIGEVTLDQAYGGARGVKCLVWEGSVLDSEEGIR 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 FRGRTIPECQELLPKAPGGQEPLPEGLFWLLLTGEIPTEQQVRDLSAEWAARSDLPKFIE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 LRSELQELIPEQQERLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLDPEEGIR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0.00e+00;
74; Mismatches 100; Indels 1; Gaps
                                                                                                                                                                                                                                                                   EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PLECTOMYCETES;
EUROTIALES; TRICHOCOMACEAE; MITOSPORIC TRICHOCOMACEAE; ASPERGILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 ELIDRCPSTLHPMSQFSLAVTALEHESAFAKAYAKGINKKDYWNYTFEDSMDLIAKLPTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSIT PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 OSHIDA Y., MIYAKE K., KANAYAMA S., KIRIMURA K., USAMI S.;
SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MITOCHONDRION (BY SIMILARITY). CITRATE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 475;
                                                       01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST EXQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNORATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -! - SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.

"", 48D237BC CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS00480; CITRATE_SYNTHASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00285; citrate_synt; 1.
HSSP; P23007; 5CSC.
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Local Similarity 58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D63376; G927641; -.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  475
310
356
411
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                                                                                                                                                                                                                                         ASPERGILLUS NIGER.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-WU-2223L;
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CISY_ASPNG
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                             P51044;
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                                                                                                                                                                                                                                                                                                                                                                                                       CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               342 WSTLNAGOVVPGYGHAVLRKTDPPYVSQREFALRKLPDDPMFKLVSQVYKIAPGVLTEHG 401
                                                            92 FRGRTIPDIQKELPKAPGGEEPLPEALFWLLLTGEVPTEAQTRALSEEFAARSALPKHVE 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 ELIDRSPSHLHPMAQFSIAVTALESESQFAKAYAKGVHKSEYWKYTYEDSIELLAKLPTI 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 LKQRLEEILPAKAEEVKQLKKDYGKTVIGEVLLEQAYGGMRGIKGLVWEGSVLDPIEGIR 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 LRSELQELIPEQQERLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLDPEEGIR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                               402 KTKNPYPNVDAHSGVLLQYYGLTEANYYTVLFGVSRALGVLPQLIIDRALGAPIERPKSY
                                                                                                                                                                                                                                                               EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES; CANDIDACEAE; CANDIDA
                                                                                                                                                                                                                                                                                                                            UEDA M., SANUKI S., KAWACHI H., SHIMIZU K., ATOMI H., TANAKA A.;
SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE.
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;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 56.4%; Score 1767; DB 1; Length 467; Similarity 56.4%; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84; Mismatches 99; Indels
                                                                                                                                                                                          01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.11.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEE342A9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITRATE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                      467 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB001565; G1871439; -. PROSITE; PS00480; CITRATE_SYNTHASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: TRICARBOXYLIC ACID CYCLE.
                                                                                                                                                                    PRT;
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HSSP; P23007; 5CSC.
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                                                                                                                                                                                                                                                         CANDIDA TROPICALIS (YEAST)
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                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           467 AA;
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    OXALOACETATE
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347
402
                                                                                                                                                                                                                                                                                                                                                                                                                    METABOLISM.
                                                                                               462 STE 464
                                                                                                                      425 TME 427
                                                                                                                                                                    CISY_CANTR
P79024;
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ACT_SITE
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-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
-!- DEVELOPMENTAL STACE: ABUNDANT AFTER 6-12 HRS OF GROWTH. IT IS
NOT SIGNIFICANTLY EXPRESSED AFTER 24 HRS, WHICH IS SEVERAL HRS
AFTER ENTERING THE STATIONARY PHASE OF GROWTH.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                272 AHTTHLVGSALSSPFLSLAAGLNGLAGPLHGRANQEVLEWLFKLREELNGDYSKEAIEKY 331
                                                                                                                                                                                                                                                                                                                         304 VWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYEVVPPILLEL 363
                                                                                                                                                                                                                                                                                                                                                                                          392 GMTKNPWPNVGSHSGVLLQYYGLTEESFYTVLFGVSRAFGVLPQLILDRGLGMPIERPKS 451
                                                                                                                                                                                                                                                                                                                                                                                                                                212 AAKIYRNVFHDGKLPAQIDSKLDYGANLASLLGFGENKEFLELMRLYLTIHSDHEGGNVS 271
                                                                                                                                                                                                                                                            332 LWDTLNAGRVGPGYGHAVLRKTDPRYTAQREFALKHMPDYELFKLVSNIYEVAPGVFDQH 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEREA I., CONTRERAS E.T., OUNG T., BOWMAN E.J., BOWMAN B.J.;
"Characterization of the cit-1 gene from Neurospora crassa encoding
the mitochondrial form of citrate synthase.";
MOL. GEN. GENET. 242:105-110(1994).

-i- CATALVIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)O +
OXALOACETATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKAPYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PYRENOMYCETES;
SORDARIALES; SORDARIACEAE; NEUROSPORA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MITOCHONDRION (POTENTIAL)
CITRATE SYNTHASE.
BY SIMILARITY.
: E6281B97 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       469 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00480; CITRATE_SYNTHASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00285; citrate_synt; 1.
HSSP; P23007; 5CSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52002 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M84187; G168775; -. PIR; S41563; S41563.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33
469
352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 94104594.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        452 FSTE 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      424 VTME 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CISY_NEUCR
P34085:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
SEQUENCE
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Score 1761; DB 1, Length 469,

54.38,

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                                                                                                                                                                                                            158 ELIDRCPSDLHPMAQLSLAVTALEHTSSFARAYAKGINKKEYWGYTFEDSMDLIAKLPTI 217
                                                                                                                                                                                                                               HTTHLVGSALSSPFLSVAAGLNGLAGPLHGLANQEVLNWLTEMKKVIGDDLSDEAITKYL 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 FRGKTIPECQELLPKAPGGKEPLPEGLFWLLLTGEVPSEQQVRDLSAEWAARSDVPKFIE 157
                                                                                                                                                                                                                                                                                218 AARIYONVFKGGKVAAVQKDKDYSFNFANQLGFGDNKDFVELLRLYLTIHTDHEGGNVSA 277
                                                                                                                                                                                                                                                                                                                                                                                          245 HTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQLKDYV 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Mitochondrial and nonmitochondrial citrate synthases in Saccharomyces cerevisiae are encoded by distinct homologous genes."; MOL. CELL. BIOL. 6:4509-4515(1986).
                                                        38 LKERFAELLPENIEKIKALRKEHGSKVVDKVTLDQVYGGARGIKCLVWEGSVLDAEEGIR 97
                                                                                          6 LRSELQELIPEQQERLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLDPEEGIR 65
                       3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 FRGFSIPECOKLLPAASAGAEPLPEGLLWLLLIGKVPSKEQVDALSADLRKRASIPDHVY
                                                                                                                                                                                                                                                                                                                     186 AAYVYRRMYKNGQVIPLDDSLDYGGNFAHMLGF-DSPQMLELMRLYVTIHSDHEGGNVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                 338 WDTLNAGRVVPGYAHAVLRKTDPRYSAQRKFAQEHLPEDPMFQLVSQVYKIAPKVLTEHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            398 KTKNPYPNVDAHSGVLLQHYGLTEANYYTVLFGVSRAIGVLPQLIIDRAVGAPIERPKSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE; 92254505.
BITEAU N., FREMAUX C., HEBRARD S., MENARA A., AIGLE M., CROUZET "The complete sequence of a 10.8kb fragment to the right of the chromosome III centromere of Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIAO X., SMALL W.C., SRERE P.A., BUTOW R.A.;
"Intramitochondrial functions regulate nonmitochondrial citrate synthase (CIT2) expression in Saccharomyces cerevisiae.";
MOL. CELL. BIOL. 1:38-46(1991).
-:- CATALYTIC ACTIVITY: CITRAIE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 87089811.
ROSENKRANTZ M., ALAM T., KIM K.-S., CLARK B.J., SRERE P.A.,
                     81; Mismatches 103; Indels
Best Local Similarity 56.7%; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
CITCAITE SYNTHANSE, PEROXISOMAL (EC 4.1.3.7).
CITCAIT OR YCRO05C OR YCR5C OR YCR043.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  460 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- SUBCELLULAR LOCATION: PEROXISOMAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SACCHAROMYCETACEAE; SACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-24 FROM N.A.
                     245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       458 STDKWIE-ICKK 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          425 TME-WLEKFCKR 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CISZ_YEAST
P08679:
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                                                                                                                                                                                                                                                                                                                                                         278
                   Matches
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-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  366 VKNPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRALGLPLERPKSVT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 FRGRTIADIQKDLPKAKGSSQPLPEALFWLLLTGEVPTQAQVENLSADLMSRSELPSHVV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 QLLDNLPKDLHPMAQFSIAVTALESESKFAKAYAQGISKQDYWSYTFEDSLDLLGKLPVI 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 AAKIYRNVFKDGKMGEVDPNADYAKNLVNLIGSKDEDFVDLMRLYLTIHSDHEGGNVSAH 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               266 TSHLVGSALSSPYLSLASGLNGLAGPLHGRANQEVLEWLFALKEEVNDDYSKDTIEKYLW 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              326 DTLNSGRVIPGYGHAVLRKTDPRYMAQRKFAMDHFPDYELFKLVSSIYEVAPGVLTEHGK 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 KTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYEVVPPILLELGK 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              386 TKNPWPNVDAHSGVLLQYYGLKESSFYTVLFGVSRAFGILAQLITDRAIGASIERPKSYS 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 LKERFSEIYPIHAQDVRQFVKEHGKTKISDVLLEQVYGGMRGIPGSVWEGSVLDPEDGIR 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                MICROBODY TARGETING SIGNAL (POTENTIAL) 9E93E2FD CRC32;
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                                                                                                                                                                                                                                                                                                                                                                           LYASE, TRICARBOXYLIC ACID CYCLE; PEROXISOME; MULTIGENE FAMILY ACT_SITE 293 293 BY SIMILARITY.

ACT_SITE 339 BY SIMILARITY.

ACT_SITE 394 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1701; DB 1; Length 460
Pred. No. 0.00e+00;
90; Mismatches 105; Indels
                                  -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REL. 21, CREATED)
(REL. 21, LAST SEQUENCE UPDATE)
(REL. 28, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                             PROSITE; PS00342; MICROBODIES_CTER; PROSITE; PS00480; CITRATE_SYNTHASE;
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                                                                                                                                                                                                                                                                                                                                              PFAM; PF00285; citrate_synt; 1.
HSSP; P23007; 5CSC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 52.5%;
Similarity 53.8%;
                                                                                                                                                                                               EMBL; Z11113; G3299; -. EMBL; M14686; G171227; -. EMBL; M54982; G171229; -. EMBL; X59720; E264468; -.
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                                                                                                                                                                                                                                                                                                                                                                                                 293
339
460
                                                                                                                                                                                                                                                                                               SGD; L0000342; CIT2.
                                                                                                                                                                                                                                                           PIR; A25393; YKBYC.
YEPD; 5440; -.
                  METABOLISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Sin 227;
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01-MAR-1992 (
01-FEB-1994 (
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ACT_SITE
SITE
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441 FGLPIERPGSADLKWFHDKY 460

S G

295 ISTEQLKDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYE 354

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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                              CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201
                                   TETRAHYMENA THERMOPHILA.
EUKARYOTA: ALVEOLATA: CILIOPHORA: OLIGOHYMENOPHOREA: HYMENOSTOMATIDA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 SMDLIAKIPRVAAIIYRHKYRDSKLIDSDSKLDWAGNYAHMMGFEQHVVKECIRGYLSIH 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 CDHEGGNVSAHTTHLVGSALSDPYLSYSAGVNGLAGPLHGLANQEVLKWLLQFIEEKGTK 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 QGIIFRGYTIPQLKEFLPKADPKAADQANQEPLPEGIFWLLMTGQLPTHAQVDALKHEWQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 SDHEGGNVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGEN 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 VSDKDIEDYVDHVISSGRVVPGYGHAVLRDTDPRFHHQVDFSKFHLKDDQMIKLLHQCAD 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 SQTNLKKVIAEIIPQKQAELKEVKEKYGDKVVGQYTVKQVIGGMRGMKGLMSDLSRCDPY 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 SNLDLRSELQELIPEQQERLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLDPE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91; Mismatches 124; Indels 10; Gaps
                                                                                                                                                                                                                                    BIOCHEM. BIOPHYS. RES. COMMUN. 174:1028-1034(1991).
-!- FUNCTION: STRAID POPTENI UNCOUNDE IN OPAL MOPPHOGENESIS AND
IN PRONUCLEAR BEHAVIOR DURING CONJUGATION. RESPIRATORY ENZYME.
-!- CATALYTIC ACTIVITY: CITRAIE + COA - ACETYL-COA + H(2)0 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 NRGTVNQDCVNFILNLPKDLHSMTMLSMALLYLQKDSKFAKLYDEGKISKKDYWEPFYED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 KRASIPDHVYKTIDALPITAHPMTQFCTGVMALQTRSEFQKAYEKG-IHKSKFWEPTYED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 CLSLIAQVPVVAAYVYRRMYKNGQVIPLDDSLDYGGNFAHMLGFDSPQMLELMRLYVTIH
                                                                                                                                             NUMATA O., TAKEMASA T., TAKAGI I., HIRONO M., HIRANO H., CKIBA J.
WATANABE Y.;
                                                                                                                                                                                               Tetrahymena 14-nm filament-forming protein has citrate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE;
                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION - MITOCHONDRIAL MATRIX AND CYTOPLASMIC
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7) (14 NM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1451; DB 1; Length 462; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY BELONGS TO THE CITRATE SYNTHASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY.
786A39BC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITRATE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MITOCHONDRION.
                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 22-40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D90117; E33571; -.
PIR; JN0130; JN0130.
PROSITE: PS00480; CITRATE_SYNTHASE; 1.
PFAM; PF00285; citrate_synt; 1.
HSSP; P23007; SCSC.
                                                                                                                                                                                                                                                                                                                                      PATHWAY: TRICARBOXYLIC ACID CYCLE. SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52575 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 44.7%;
Similarity 48.9%;
                                                                            ETRAHYMENINA; TETRAHYMENA.
                FILAMENT-FORMING PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             462 AA;
                                                                                                                                       MEDLINE; 91128358
                                                                                                                                                                                                                                                                                                                                                                                                  CYTOSKELETON.
                                                                                                                                                                                                                                                                                                                   OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOSKELETON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
SEQUENCE
                                                                                                                                                                                                                     activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRICARBOXXLIC ACID CYCLE; MULTIGENE FAMILY.

IE 315 BY SIMILARITY.

IE 361 BY SIMILARITY.

IE 419 419 BY SIMILARITY.

484 486 MICROBODY TARGETING SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102; Mismatches 123; Indels 26; Gaps
                                                                                                                   CISX_YEAST STANDARD; PRT; 486 AA.

P43635;
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
01-NOV-1995 (REL. 35, LAST ANNOTATION UPDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEARSON D., BOWMAN S., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
SUBMITTED (APR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WANG Y., AHMED A., BUSSEY H., FORTIN N., FRIESEN J.D., HALL J. STORMS R.K., VO D.H., WINNEIT E.;
STORMITTED (XXX-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-i - CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METABOLISM.
-!- SIMILAPITY· BELONGS TO THE CITRATE SYNTHASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CW04;
JIA Y.K., BECAM A.-M., SLONIMSKI P.P., HERBERT C.J.;
SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1261; DB 1;
Pred. No. 1.32e-268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         806F987D CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGD; L0002855; CIT3.
PROSITE; PS00342; MICROBODIES_CTER; 1.
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                            SACCHAROMYCETACEAE; SACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00285; citrate_synt; 1.
HSSP; P23007; 5CSC.
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414 LGLPLERPKSVTMEWL-EKF 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 38.9%;
1 Similarity 45.2%;
207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X88846; G895889; -. EMBL; Z48951; G763000; -. EMBL; Z71255; E236811; -. EMBL; U31900; G939735; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         486 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Best Local
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24 SSALTLKEALENVIPKKRDAVKKLKACYGSTF-VGPITISSVLGGMKGNQSMFWQGTSLE 82

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- SUBUNIT: HOMOHEXAMER.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                           224 LE---LMRLYVIIHSDHEGGNVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEV 280
                                                                                                                                                                                                                                                                                                                                                                                                                                           340 - LP-D-DPFFQLVSKLYEVVPPILLELGKVKNPWPNVDAHSGVLLNHYGLTEARYYTVLF 396
                                                                                                                                                                                       119 S-IPDHVYKTIDALPITAHPMTQFCTGVMALQTRSEFQKAYEKG-IHKSKFWEPIYEDCL 176
                                                                                                                                                                                                                                            203 NLIASLPLLTGRIYSNITNEGHPLGQYSEEVDWCTNICSLLGMTNGTNSSNTCNLTSQQS 262
                                                                                                                                                                                                                                                                                                                                                                                                                  323 VRFLIEMNSNIS-SIAREQEIKDYLWKILNSNRVIPGYGHAVLRKPDPRFTAMLEFAQKR 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         382 PIEFENDKNVLLMOKLAEIAPKVLLEHGKSKNPFPNVDSASGILFYHYGIRELLFFTVIF 441
                                                                  83 PEHGIKFQGLTIEECQNRLPNTGIDGDNFLPESMLWLLMTGGVPTFQQAASFRKELAIRG 142
                                                                                                         60 PEEGIRFRGFSIPECQKLLPAASAGAEP-LPEGLLWLLTGKVPSKEQVDALSADLRKRA 118
                                                                                                                                                     143 RKLPHYTEKVLSSLPKDMHPMTQLAIGLASMNKGSLFATNYQKGLIGKMEFWKDTLEDSL 202
                                                                                                                                                                                                                                                                                   177 SLIAQVPVVAAYVYRRMYKNGQVI-PLDDSLDYGGNFAHMLGF----DSP-----QM- 223
                                                                                                                                                                                                                                                                                                                               LDFINLMRLYTGIHVDHEGGNVSAHTTHLVGSALSDPYLSYSSGIMGLAGPLHGLAAQEV 322
                      1 SSNLDLRSELQELIPEQQERLKKIKKEFGS-FQLGNINVDMVLGGMRGMTGLLWETSLLD 59
SCHENDEL F.J., AUGUST P.R., ANDERSON C.R., HANSON R.S., FLICKINGER M.C.,
"Cloning and nucleotide sequence of the gene coding for citrate synthase from a thermotolerant Bacillus sp.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthase from a thermotolerant Bacillus sp.";
APPL. ENVIRON. MICROBIOL. 58:335-345(1992).
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -! - SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              442 GCSRAMGPLTQLVWDRILGLPIERPKSLNLEGLEALTK 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     397 GVSRSLGICSQLIWDRALGLPLERPKSVTMEWLEKFCK 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1992 (REL. 23, CREATED)
01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-ETB-1994 (REL. 28, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00480; CITRATE_SYNTHASE; 1.
PFAM; PF00285; citrate_synt; 1.
HSSP; Q53554; 1AJ8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A43936; A43936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BACILLUS COAGULANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-ATCC 55182; MEDLINE; 92171501.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CISY_BACCO
P27660;
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Score 323; DB 1; Length 373;
Pred. No. 9.74e-44;
82; Mismatches 119; Indels 25; Gaps 18;
                                                                                                                                                                                                                            53 LLLEGTIPNEAEKQHLEETLKQEYDVPDEIIQVLSLLPKTAHPMDALRTGVSVL-A-S-F 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 MLGFDSPQMLELMRL--YVTIHSDHEGGNVSAHTGHLVGSPLSDPYLSFAAALNGLAGPL 272
                                                                                                                                                                                                                                                                                                                                                             164 MITGKKPTELEEKIFDRSLVLYSEHELPN-STFTARVIASTLSDLYGALTGAVASLKGHL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 HGGANEAVM----EMLQD-AQTV--EGFKHLLHDKLSKKEKIMGFGHRVYMKKMDPRAAM 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273 HGLANQEVLLMIKSVVDECGENISTEQLKDYVWKTLNSGKVVPGFGLGV-LRKIDPRYIC 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       332 OREFALKHLPDDDFFFQLVSKLYEVVPPILLELGKVKNPWPNVDAHSGVLLNHYGLTEARY 391
                                                                                                                                                                                                                                                                               95 LLLTGKVPSKEQVDALSADLRKRASIPDHVYKTIDALPITAHPMTQFCTGVMALQTRSEF 154
                                                                                                                                                                                                                                                                                                                                  110 DTELLNREHSTNL-KRAYQ--L-L-GKIPNIVANSYHILHSEEPVQPLQD-LSYSANFLY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276 MKE-ALKELSAVNGDDLLLQMCEAGEQIMRE--E-KGLFPNLDYYAAPVYWKLGIPIPLY 331
LYASE, TRICARBOXYLIC ACID CYCLE; ALLOSTERIC ENZYME.
ACT_SITE 252 262 BY SIMILARITY.
ACT_SITE 314 BY SIMILARITY.
SEQUENCE 373 AA; 41970 MW; BC8B68C6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: Fri Oct 22 16:51:58 1999 Job time : 66 secs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             392 YTVLFGVSRSLGICSQLI 409
                                                                                                                           Match 10.0%;
Local Similarity 28.9%;
es 92; Conservative
                                                                                                                              Query Match
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Run on:

Fri Oct 22 16:52:16 1999; MasPar time 27.64 Seconds 863.073 Million cell updates/sec

Tabular output not generated.

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(1-437) from US08702718.pep
3.243
1 SSNLDLRSELQELIPEQQER......LERPKSVTMEWLEKFCKRRA 437 Title:

Description: Perfect Score:

Sequence:

PAM 150 Gap 11 Scoring table:

179066 seqs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremb19 Database:

1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human 5:sp\_nvertebrate 6:sp\_nnammal 7:sp\_mhc 8:sp\_organolle 9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified 13:sp\_vertebrate 14:sp\_virus

Mean 48.796; Variance 86.952; scale 0.561 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES		
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Result		Query					
No.	Score	Match	Match Length	DB	ID	Description	Pred. No.
П	3243	100.0	437	10	096544	CITRATE (SI)-SYNTHASE	0.00e+00
7	2867	88.4	472	10	080433		0.00e+00
m	2834	87.4	474	10	064869		0.00e+00
4	2800	86.3	469	10	024135	_	0.00e+00
5	2637	81.3	471	10	043175	ETHANOLAMINE AMMONIA-L	0.00e+00
9	2166	66.8	339	10	024259	CITRATE (SI)-SYNTHASE	0.00e+00
7	2072	63.9	466	4	075390	CITRATE SYNTHASE (EC 4	0.00e+00
60	270	8.3	372	Ч	028929	CITRATE SYNTHASE (CITZ	8.07e-31
6	256	7.9	379	-	032705	CITRATE SYNTHASE (EC 4	5.18e-28
10	239	7.4	427	7	068883	CITRATE SYNTHASE (EC 4	1.19e-24
11	240	7.4	431	7	033066	CITRATE SYNTHASE (EC 4	7.59e-25
12	228	7 0	379	۲,	034002	CITRATE SYNTHASE.	1.67e-22
13	226	7.0	411	C4	053115	CITRATE SYNTHASE (FRAG	4.08e-22
14	223	6.9	356		054382	CITRATE SYNTHASE (EC 4	1.55e-21
15	223	6.9	411		059777	CITRATE SYNTHASE (EC 4	1.55e-21
16	222	9.8	411	7	059775	CITRATE SYNTHASE (EC 4	2.41e-21
17	221	9.9	411	~	060047	CITRATE SYNTHASE (EC 4	3.76e-21
18	219	ğ.	411	7	059779	CITRATE SYNTHASE (EC 4	9.10e-21
19	219	6.8	411	7	P77936	CITRATE SYNTHASE (EC 4	9.10e-21
20	218	6.7	411	C a	059469	CITRATE SYNTHASE (EC 4	1.42e-20

-	1.76e-18	3.64e-17	2.65e-13	4.10e-10	1.36e-09	1.35e-09	1.36e-09	2.99e-09	4.62e-08	2.15e-07	3.15e-07	1.12e-01	2.12e-01	5.47e-01	4.00e-01	1.02e+00	1.38e+00	1.02e+00	7.47e-01	1.87e+00	1.38e+00	7.47e-01	1.87e+00	7.47e-01
E SYNTHASE (	CITRATE SYNTHASE (EC 4	HYPOTHETICAL 31.0 KD P	ACYL-COA OXIDASE 1 (EC	PCRV.	CITRATE SYNTHASE (FRAG	HYPOTHETICAL 40.8 KD P	CODED FOR BY C. ELEGAN	CODED FOR BY C. ELEGAN	DNA POLYMERASE III, SU	ACYL-COA OXIDASE 5 (EC	INSOLUBLE PROTEIN.	REPLICASE.	NRD2 CONVERTASE (EC 3.	YLR466WP.										
91	9	P94325	070008	059236	23	059238	059234	030966	059237	P77822	008395	066147	074934	030527	045540	055851	P91198	28	083970	074938	002402	083424	035836	013559
7	C1	~	~	~	7	7	7	~	N	7	~	7	~	7	7	7	S	Ŋ	7	m	2	14	11	m
429	410	434	390	322	315	318	319	349	321	319	393	295	689	294	299	375	378	555	572	669	738	791	1229	1382
	•	6.2	٠	5.0	4.9	6.4	6.4	4.8	4.6	4.5	4.4	3.3	۳. ۳	3.5			3.1	3.1						3.1
212	207	200	179	161	158	158	158	156	149	145	144	108	106	103	104	101	100	101	102	66	100	102	66	102
21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	<b>7</b>	41	42	43	44	45

## ALIGNMENTS

181 QVPVVAAYVYRRMYKNGQVIFLDDSLDYGGNFAHMLGFDSFQMLELMRLYVTIHSDHEGG 240

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156 PEHVYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKTKYWEPTYEDSITLIA 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 PDHVYKTIDALPITAHPMTQFCTGVMALQTRSEFQKAYEKGIHKSKFWEPTYEDCLSLIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 QLPVVAAYIYRRMYKNGQSISTDDSLDYGANFAHMLGYDSPSMQELMRLYVTIHTDHEGG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 NVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQL 300
                                                                                               241 NVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQL 300
                                                                                                                                      KDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYEVVPPIL 360
                                                                                                                                                                              301 KDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFGLVSKLYEVVPPIL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 EEGIPFRGLSIPECQKLLPGAKPGGEPLPEGLLWLLLTGKVPTKEQVDALSAELRSRAAV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 EEGIRFPGFSIPECQKLLPAASAGAEPLPEGLLWLLLTGKVPSKEQVDALSADLPKRASI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           276 NVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVSECGENVTKEQL 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 ASDLDLRSQLKELIPEQQERIKKLKAEHGKVQLGNITVDMVLGGMRGMTGLLWETSLLDP 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SSNLDLRSELOELIPEQOERLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLDP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUKAPYOTA; VIPIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
ASTERIDAE; ARALIALES; APIACEAE; DAUCUS.
                                                                                                                                                                                                                                      181 QVPVVAAYVYRRMYKNGQVIPLDDSLDYGGNFAHMLGFDSPQMLELMRLYVTIHSDHEGG
                                                                                                                                                                                                                   361 LELGKVKNPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRALGLPLER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-i- CITPATE SYNTHASE IS FOUND IN NEAPLY ALL CELLS CAPABLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.4%; Score 2867; DB 10; Length 472; 85.4%; Pred. No. 0.00e+00; ative 42; Mismatches 22; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CV. MS YONSUN;
TAKITA E., KOYAMA H., SHIRANO Y., SHIBATA D., HARA T.;
CDNA encoding carrot mitochondrial citrate synthase.";
SUBKITIED (AUG-1998) TO EMBL/GENBANK/DBU DATA BANKS.
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D46C38CC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                    472 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -:- SIMILARITY: TO OTHER CITRATE SYNTHASES.
BMBL, ABOIT159; D1033521. -
PROSITE: PSOO480; CITRATE_SYNTHASE; 1.
LYASE; TRICARBOXYLIC ACLD CYCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITRATE SYNTHASE (EC 4.1.3.7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-00-1998 (TREMBLREL. 08, 01-NOV-1998 (TREMBLREL. 08, 01-NOV-1998 (TREMBLREL. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              larity 85.4%;
Conservative
                                                                                                                                                                                                                                                                                                421 PKSVTMEWLEKFCKRRA 437
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(TREMBLREL.
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Matches 373; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 KDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYEVVPPIL 360
                     396 TELGKVKNPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRAIGICSQLVWDRALGLPLER 455
                                                                                                                       361 LELGKVKNPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRALGLPLER 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 PDYVYNAIDALPSTAHPMTQFASGVMALQVQSEFQKAYENGIHKSKFWEPTYEDCLNLIA 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276 NVSAHTGHLVGSALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGEDISKEQL 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                396 TELGKVKNPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRALGLALER 455
336 KDYIWKTLNSGKVVPGYGHGVLRNTDPRYICQREFALKHLPDDPLFQLVSNLFEVVPPIL 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 EEGIRFRGLSIPECQKVLPTAQSGAEPLPEGLLWLLLTGKVPSKEQVEALSKDLANRAAV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 STDLDLKSQLQELIPEQQDRLKKLKSEHGKVQLGNITVDMVIGGMRGMTGLLWETSLLDP 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA, VIRIDIPLANTAE; SIREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SSNLDLRSELQELIPEQQERLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 RVPVVAAYVYRRMYKNGDSIPSDKSLDYGANFSHMLGFDDEKVKELMRLYITIHSDHEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 NVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CV. COLUMBIA;
ROUNGLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
SYKES S.M., KARL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
SOMERVILLE C.R., VENTER J.C.;
SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2834; DB 10; Length 4'
Pred. No. 0.00e+00;
39; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: TO OTHER CITRATE SYNTHASES.
EMBL; AC004521; G3128180; -.
INASE; PS00480; CITRATE_SYNTHASE; 1.
INASE; TRACRBOXYLIC ACID CYCLE.
SEQUENCE 474 AA; 52782 MW; 64FF2AC6 CRC32;
                                                                                                                                                                                                                                                                                          474 AA
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                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQ)
01-AUG-1998 (TREMBLREL. 07, LAST ANN
                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 85.3%;
Matches 371; Conservative
                                                                                                                                                                456 PKSVTMEWLENHCKKSS 472
                                                                                                                                                                                                       421 PKSVTMEWLEKFCKRRA 437
                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OXALOACETATE
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064869
064869;
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361 LELGKVKNPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRALGLPLER 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155 PDHVYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLIA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 KDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYEVVPPIL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 DEGIRFRGLSIYECQKVLPAAKPGGEPLPEGLLWLLLTGKVPSKEQVDSLSQELRSRATV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 SSGLDLRSELQELIPEQQDRLKKLKSEHGKVQLGNITVDMVLGGMRGMTGLLWETSLLDP 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Gaps
                                                                                                                                                                              NICOTIANA TABACUM (COMMON TOBACCO).
WENGRYCHAA, VIRIDIDLANTAE, STREPTOPHYTA, EMBRYOPHYTA, EVERYCHYTES, SPERMATOPHYTA, MAGNOLIOPHYTA, EUDICOTYLEDONS, ASTERIDAE, SOLANANAE, SOLANALES, SOLANACEAE, NICOTIANA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 QVPLVAAYVYRRMYKNGNTIPKDDSLDYGANFAHMLGFSSSDMHELMKLYVTIHSDHEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 NVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 NVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KDYAWKTLKSGKVVPGFGHGVLRKTDPRYTCQREFALKHLPEDPLFQLVAKLYEVFLQFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QNLAKL-NPWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALGLPLER
                                                                                                                                                                                                                                                    STRAIN-CV. SNN;
LA COGNATA U., LANDSCHUETZE V., WILLMITZER L., MUELLER-ROEBER B.;
PLANT CELL PHYSIOL. 0:0-0(0).
-'- CATALYTIC ACTIVITY: CITPATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                OF.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 469;
                                                                                                                                                                                                                                                                                                                               CELLS CAPABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34; Mismatches 27; Indels
                                                                                                                  01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2800; DB 10;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                       PFAM: PF00285; citrate_synt; 1.
LYASE; TRICARBOXXLIC ACID CYCLE.
SEQUENCE 469 AA; 52492 MW; 6BE3C325 CRC32;
                                                                                                                                                                                                                                                                                                                            -!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL OXIDATIVE METABOLISM.
                                                                                               469 AA
                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: TO OTHER CITRATE SYNTHASES.
EMBL; X84226; E137432; -.
                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00480; CITRATE_SYNTHASE; 1.
                                                                                                                                                                                                                                                                                                                   PATHWAY: TRICARBOXYLIC ACID CYCLE
                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 86.3%;
Best Local Similarity 85.7%;
Matches 373; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   456 PKSVTMDWLEAHCKK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PKSVTMEWLENHCKK 468
                                             421 PKSVTMEWLEKFCKR 435
                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                nrr 4
024135
024135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      335
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                                                                                 RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENISK 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334 EQLKDYVWKTLNSGKVVPGFGHGVLRKTVPRYTCQREFAMKHLPEDPLFQLVSKLYEVFL 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 SSGLDLRSELVQELIPEQQDRLKKIKSDMKG-SIGNITVDMVLGGMRGMTGLLWKPHYLD 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAINTENENTY, 30.0343.1.

"MILOCHORDIAL GITTATE STORTH STOR
                                                                                                                                                                                                                                                                                                                             EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
ASTERIDAE; SOLANANAE; SOLANALES; SOLANACEAE; SOLANUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         394 LFLQNLAKLK-PWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 ISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKYWEPTYEDSMNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 IAQVPLVAAYVYRRMYKNGDTIPKDESLDYGANFAHMLGFSSSEMHELLMRLYVTIHSDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 2637; DB 10; Length 4
Pred. No. 0.00e+00;
41; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     024259;
01-37N-1998 (TREMBLREL. 05, CREATED)
01-37N-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE (S1)-SYNTHABE (EC 4.1.3.7) (CONDENSING ENZYME)
(CITRATE CONDENSING ENZYME) (CITROGENASE)
                                                                                                        ETHANOLAMINE AMMONIA-LYSSE (EC 4.3.1.7).

SOLANUM TUBEROSUM (POTATO).

EURAROTA: VIRIDIPLANA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 471 AA; 52612 MW; BC96A65C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       339 AA.
                                                      471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 81.3%;
Matches 356; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         453 LERPKSVIMEWLENQCKK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               418 LERPKSVTMEWLEKFCKR 435
043175 PRELIMINARY;
043175, 03175, 01-NOV-1996 (TREMBLREL. C
01-NOV-1996 (TREMBLREL. 0
01-JAN-1999 (TREMBLREL. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-CV. DESIREE;
MEDLINE; 96073431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  o24259
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          POPULUS DELTOIDES X POPULUS BALSAMIFERA SUBSP, TRICHOCARPA.
EUKARYOTA: VIPIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
                                                                                                                                                                                                                                                                                                                                                                  280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GIHKSKYWEPTYEDSLSLIARVPIVASYIYRRIYKDGKVIPMNDSLVIGGNFSHMLGFDS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 GIHKSKFWEPTYEDCLSLIAQVPVVAAYVYRRMYKNGQVIPLDDSLDYGGNFAHMLGFDS 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEMOELMRLYVTNHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 LLWIKSVVEEGGENITTEQUKDYVWKTLNSGKVVPGFGHGVLPKTVPPYTCQPEFALKHL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         281 LLWIKSVYDECGENISTEQLKDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHL 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 PDDPLFQLVSKLYEVVPPVLTQLGKVKNPWPNVDAHSGVLLNYYGLTEARYYTVLFGVSR 300
                                                                                                                                                                                                                                                                                                                                                 1 MPTKEQVGALSKELRDRALVHDYVFKAIDALPVTAHPMTQFATGVMALQVQSEFQKAYEK 60
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning and sequence analysis of human citrate synthase cDNA."; SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)0 +
                                                                                                                   LA COGNATA U., LANDSCHUETZE V , WILLMITZEP L., MUELLEP-POEREP P PLANT CELL PHYSIOL. 0\cdot0\cdot0(0)
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)0 +
                                                                                                                                                                                                                                                                                                               .;
0
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-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF
                                                                                                                                                                                                                                                                          66.8%; Score 2166; DB 10; Length 339; 85.4%; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                               29; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C0532604 CRC32;
                                                                                                                                                                                                                                         SEQUENCE 339 AA; 37834 MW; B2DA24A9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 SIGICSQLIWDRALGLPLERPKSVTMELLENHCKK 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401 SLGICSQLIWDRALGLPLERPKSVTMEWLEKFCKR 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    466 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - ! - SIMILARITY - TO OTHER CITRATE SYNTHASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF047042; G3288815; -. PROSITE; PS00480; CITRATE_SYNTHASE; 1. LYASE, TRICARBOXYLIC ACID CYCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                    EMBL, X84227, E276838; -. PFAM; PF00285; citrate_synt; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51706 MW;
                                                               VIOLALES; SALICACEAE; POPULUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATARRHINI; HOMINIDAE; HOMO
                                                                                                                                                                                                                                                                                              85.4%;
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         466 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OXALOACETATE
                                                                                                                                                                       OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GOLDENTHAL M.J.;
                                                                                                                                                                                                                                                                                                             286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I I SSUE-HEART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T 7
075390
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                                                                                                                                                                                                                         LYASE.
                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                 QQ
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DB 4; Length 466;

63.9%; Score 2072;

Query Match

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88 DEGIRFRGFSIPECQKLLPKAKGGEEPLPEGLFWLLVTGCIPTEEQVSWLSKEWAKRAAL 147
                                                                                                                                                                                                  61 EEGIRFRGFSIPECQKLLPAASAGAEPLPEGLLWLLLTGKVPSKFQVDALSADLFKRASI 120
                                                                                                                                                                                                                                                                                           121 PDHVYKTIDALPITAHPMTOFCTGVMALOTRSEFOKAYEKGIHKSKFWEPTYEDCLSLIA 180
                                                                                                                                                                                                                                                                                                                                                                               181 QVPVVAAYVYRRMYKNGQVI-PLDDSLDYGGNFAHMLGFDSPQMLELMRLYVTIHSDHEG 239
                                                                                                                                                                                                                                                                                                                                                                                                                            268 GNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLVWLTQLQKEVGKDVSDEK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328 LRDYIWNTLNSGRVVPGYGHAVLRKIDPRYTCQREFALKHLPNDPMFKLVAQLYKIVPNV 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         388 LLEQGKAKNPWPNVDAHSGVLLQYYGMTEMNYTTVLFGVSRALGVLAQLIWSRALGFPLE 447
                                                               28 ASSINLKDILADLIPKEQARIKIFRQQHGKTVVGQIIVDMMYGGMPGMKGLVYFTSVLDP 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
RICHAPDSON D.L., KERLAYAGE A.R., GRAHAM D.E., KYPPIDES N.C.,
RICHAPDSON D.L., VERLAYAGE A.R., GRAHAM D.E., KYPPIDES N.C.,
KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
RIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
PETERSON S., PEICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOII LOVETREBEK R., GOCAPURE J.D., WEIDMAN J.F., MCDONALD L., UITERBACK T.,
COTTON M.D., SPRIGGS T., BATIACH P., KAINE B.P., SYKES S.M.,
SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
MANSON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
                  Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 GNVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEO
                                                                                                           1 SSNLDLRSELQELIPEQQERLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLDP
                                                                                                                                                                                                                                              148 FSHVVTMLDNFPTNLHFMSQLSAAVTALNSESNFAQAYARGISFTKYWELIYEDSVDIJA
                                                                                                                                                                                                                                                                                                                                       208 KLPCVAAKIYRNLYWEGSGIGAIDSNLDWSHNFTNMLGYTDHQFTELMRLYLTIHSDHEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARCHAEOGLOBUS FULGIDUS.
ARCHAEA; EURYARCHAEOTA; ARCHAEOGLOBALES; ARCHAEOGLOBACEAB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.3%; Score 270; DB 1; Length 372; Best Local Similarity 27.2%; Pred. No. 8.07e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of the hyperthermophilic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sulphate-reducing archaeon Archaeoglobus fulgidus.";
NATURE 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
Pred. No. 0.00e+00;
75; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42270 MW; DB9662BC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-VC-16 / DSM 4304 / ATCC 49558;
MEDLINE; 98049343.
KLENK H.-P., CLAYTON R.A., TOMB J -F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00285; citrate_synt; 1.
Best Local Similarity 62.1%;
Matches 272; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                448 RPKSMSTEGLMKFVDSKS 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          420 RPKSVTMEWLEKFCKRRA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE001011; G2649234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITRATE SYNTHASE (CITZ)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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028929;
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387 TEARYYTVLFGVSRSLGICSQLIWDRALGLPLERPKS 423

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Ouery Match 7.9%; Score 256; DB 1; Length 379;
Best Local Similarity 28.2%; Pred. No. 5.18e-28;
Matches 95; Conservative 78; Mismatches 142; Indels 22; Gaps 19;
                                                                                                                                                                                                                                                                                       90 EGLLWLLLTGKVPSKEQVDALSADLRKRASIPDHVYKTIDALPITAH-PMTQFCTGVMAL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 PRAKILGAKS-EALGEAAG-DM--KWYEMSVAIEEYIGEEKGLAPNVDFYSASTYYQMGI 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 EGLIMILITGKVPSKEQVDALSADLRKRASIPDHVYKTIDALPITAHPMIQFCTGVMALQ 149
                                                                                                                                    154 AANFLYMLHGEEPTKTAERALDMDLILHAEHEL-NASTFAARIAASTLADIYACVVAATG 212
                                                                                                                                                                                                                             209 GGNFAHML-GFDSPQMLE-LMRLYVIIHSDHEGGNVSAHTGHLVGSPLSDPYLSFAAALN 266
                                                                                                                                                                                                                                                                   213 ILMGPLHGGAAQEVM---R-MLREVASPRRAE---EYVKRKIEAGERIMGFGHRVYRGVM 265
                                                                                                                                                                                                                                                                                                                                              266 DPRAELLR-YLAKRLAAEG----STKWFEISEAIAKAAYKYKKLLPNVDFYSASVYANLG 320
                                                                                                                                                                                                                                                                                                                                                                      326 DPRYTCQREFALKHLPDDPFFQLVSKLYEVVPPILLELGKVKNPWPNVDAHSGVLLNHYG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 EEVLYLLWHGALPTGEELDAFSDELAAHRDLDDGVLDVARELAEQDESPMAALRTLVSAM 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 SAYDESA-DFE-DV-TDR--EVNLEKAKRITAKMPSVLA-AYARFRRGDDYVEPDESLNH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 AANFLYMLNGEEPNEVLAETFDMALVLHADH-GLNASTFSAMVTSSTLSDLYSAVTSAIG 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209 GGNFAHMLGFDSP-QML-ELMRLYVIIHSDHEGGNVSAHTGHLVGSPLSDPYLSFAAALN 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 GLAGPLHGLANQEVLLWIKSVVDECGENISTEQLKDYVWKTLNSGKVVPGFGLGVLRKTD 326
                                                                                                            44 EEVAYLLLYGELPKKYELQDFKIELAERRELPPQI---I-GL-LT-H-LPPYTHPMVVLR 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARCHAEA; EURYARCHAEOTA; HALOBACTERIALES; HALOBACTERIACEAE; HALOFERAX
92; Conservative 87; Mismatches 130; Indels 29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-WFD II;
MADDOCKS D.G., CONNARIS H., HOUCH D.W., DANSON M.J.;
SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ002075; E1154178; -.
PFAM; PF00285; citrate_synt; 1.
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01-NOV-1998 (TREWBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (EC 4.1.3.7) (FRAGMENT).
HALOBACTERIUM VOLCANII (HALOFERAX VOLCANII).
                                                                                                                                                                                                                                                                                                                                                                                                                        321 IPDDLFVNI-FAMGRISGWTAHII-EQYENNRLIRPRA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                             386 LTEARYYTVLFGVSRSLGICSQLIWDRALGLPLERPKS 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           329 PID-LYTPIFAVSRAGGWIAHVL-EQYEDNRLIRPRA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   379 AA; 41848 MW; 480EAC2F CRC32;
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01-JAN-1998 (TREMBLREL.
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89 ILLYGEKPTQEEYDEFRITVTRHTMIHEQIIRLFHAFRRDSHPMAVMC-GIIGALA-AFY 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 HDSLD--VNNPRHRE-I-AA-FRLLSKMPTMAAMCYK--YSIGQPFVYPRND-LSYAGNF 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 KNYDPRATVMRETCHEVLKELGTKDDLLEVAMELEHIALNDPYFIEK-K-LYPNVDFYSG 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            323 RKTDPRYICQRE--FA-LKHL-PDDPFFQLVSKLYEVVPPILLELGKVKNPWPNVDAHSG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            n Match
7.4%; Score 239; DB 2; Length 427;
Local Similarity 27.1%; Pred. No. 1.19e-24;
les 88; Conservative 96; Mismatches 103; Indels 38; Gaps
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BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=LI2;
HORSWILL A.R., DUDDING A.R., ESCALANTE-SEMERENA J.C.;
SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: CITRAIE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE METABOLISM.
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01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (EC 4.1.3.7).
GLTA.
                                                                                                      (TREMBLREL. 07, CREATED)
(TREMBLREL. 07, LAST SEQUENCE UPDATE)
(TREMBLREL. 07, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: TO OTHER CITRATE SYNTHASES.
EMBL: AF056043; G3025888; -.
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
LYASE; TRACARBOXYLC ACID CYCLE.
SEQUENCE 427 AA; 48106 MW; F5AB9869 CRC32;
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                                                                                                                                                                                                            CITRATE SYNTHASE (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BADCOCK K., CHURCHER C.M.;
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                                        PRELIMINARY;
                                                                                              01-AUG-1998 (TREMBLREL.
01-AUG-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                 SALMONELLA TYPHIMURIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                           01-AUG-1998
                                                                                                                                                                                                                                                                                                                                                       SALMONELLA.
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033066
033066;
RESULT 10
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Q53115;
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                                                                                                                                                                                                                                                                                                                       Score 240; DB 2; Length 431;
Pred. No. 7.59e-25;
95; Mismatches 106; Indels 29; Gaps 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GERIKE U., DANSON M.J., RUSSELL N.J., HOUGH D.W.;
"Sequencing and expression of the gene encoding a cold-active citrate synthase from an Antarctic bacterium, strain DS2-3R.";
EUR. J. BIOCHEM. 248:49-57(1997).
EMBL: U89544; G2431774; -.
PFAM: PF00285; citrate_synt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 M---L-G--FDS-PQML-ELMRLYVTHSDHEGGNVSAHTGHLVGSPLSDPYLSFAAALN 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261 ALWGPLHGGANQAVLEMLEGIR-ESGDDVGG-FVQK-VKNCQAGVKLM-GFGHRVYKNYD 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 LLIYGELPATDQLAEFTHRIQRHTMLHEDLKRFYDGFPRNAHPMPVLSSVVNAL-S-AYY 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                 149 QDALD-PMDNGQV-ELS--T-IRLLAKLPTIAAYAYKKSVGQPFLYP-DNAFSLVENFLR 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                203 MTFGLPAEPYEPDPEVVRALDMLFI-LHADHEQ-NCSTSTVRLVGSSRANLFTSISGGIN 260
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                                                                                                     EIGLMEIER K., HONORE N., WOODS S.A., CAUDRON B., COLE S.T.; "Use of an ordered cosmid library to deduce the genomic organization
                                                                                                                                                                                                    :!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF
                                                                                                                                of Mycobacterium leprae.";
40L. MICROBIOL. 7:197-206(1993).
-!- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)0
                                    PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                     PROSITE; PS00480; CITRATE_SYNTHASE; 1.
PFAM; PF00285; citrate_Synt; 1.
LYASE; TRICARBOXYLIC ACID CYCLE.
SEQUENCE 431 AA; 48111 MW; ICFA87BB CRC32;
                                                                                                                                                                                                             OXIDATIVE METABOLISM.
-!- SIMILARITY: TO OTHER CITRATE SYNTHASES.
EMBL; 299494; E350411; -.
                                                                                                                                                                                    .! - PATHWAY: TRICARBOXYLIC ACID CYCLE
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Best Local Similarity 27.7%;
Matches 88; Conservative
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01-JAN-1998 (TREMBLREL
01-NOV-1998 (TREMBLREL
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                          SEQUENCE FROM N.A.
                                                                              SEQUENCE FROM N.A.
                                                                                           MEDLINE; 93188700
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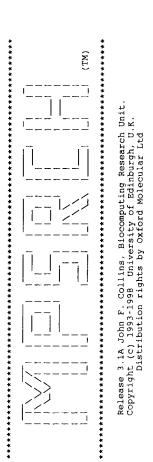
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18;
                                                                                                                               Gaps 11;
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                                                                                                                                                                                                                                       227 MRLYVTIHSDHEGGNVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKS 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 IGIRKDESLDEAATRSKAWWVDALAQKKKVMGFGHRVYKNGDSRVPTMKS-ALDAMIKHY 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 DRPEMIG-LYNGLEAAMEEAKQIK---PNLDYPAGPTYNLMGF-DTEMFTPLFIAARITG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 PFFQLVSKLYEVVPPILLELGKVKNPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLG 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333 REF-ALKHLPDDDFFFQLVSKLYEVVPPILLELGKVKNPWPNVDAHSGVLLNHYGLTEARY 391
                                                                                                                                                                                              118 EANLEKAMSLLATFPSVVAYDQRRR-RGEELIEPREDLDYSANFLWMTFGEEAAPEVVEA 176
                                                                                                                                                                                                                                                                                                                              177 FNVSMILYAEH-SFNASTFTARVITSTLADLHSAVTGAIGALKGPLHGGANEAVMHTFEE 235
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                                                                                                                               69; Mismatches 106; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RICKETTSIALES;
RICKETTSIACEAE; RICKETTSIEAE; RICKETTSIA.
                                                          y Match 7.0%; Score 228; DB 2; Length 379; Local Similarity 26.7%; Pred. No. 1.67e-22; nes 69; Conservative 69; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 7.0%; Score 226; DB 2; Length 411; Local Similarity 28.6%; Pred. No. 4.08e-22; es 72; Conservative 70; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-AB BACTERIUM.
STRAIN-AB BACTERIUM.
RAOULT D., RYDKINA E., ROUX V., EREMEEVA M., BALAYEVA N.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EKBL: U59712; G1390003; -.
PFAM; PF00285; citrate_synt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
379 AA; 41832 MW; 47DB0E16 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                411 AA; 46189 MW; 9CCB3291 CRC32;
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01-NOV-1996 (TREMBLREL. 01, LAST SEQ
01-NOV-1998 (TREMBLREL. 08, LAST ANN
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6.9%; Score 223; DB 2; Length 356;
28.7%; Pred. No. 1.55e-21;
Ative 69; Mismatches 86; Indels 24; Gaps 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 FKEADYELTAIRMIAKIPTIAAMSYK--YSIGQPFVYPDNSLDFTENFLHMM-FATPCEK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 FWEPTYE-DCLSLIAQVPVVAAYVYRRMYKNGQVIPL-DDSLDYGGNFAHMLGFDSP-QM 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 YKVNPVVKNALNKIFILHADHEQ-NASTSTVRIAGSSGANPFACVSTGIASLWGPAHGGA 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277 NQEVLLWIKSV--VDECGENISTEQLKDYVWKTLNSG-KVVPGFGLGVLRKTDPRYTCQR 333
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                                                                                                                                                                                                                                                             DAVIS M.J., YING Z., BRUNNER B.R., PANTOJA A., FERWERDA F.H.;
"Rickettsial relative associated with papaya bunchy top disease.";
CURR. MICROBIOL. 36:80-84(1998).
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
OXALOACETATE.
                                                                                                                                                                                                                                                                                                                                               -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE METABOLLSM.
-!- SIMILARITY: TO OTHER CITRATE SYNTHASES.
EMBL, U76908; G2894797; -..
PROSITE; PSO0480; CITRATE_SYNTHASE; 1.
LYASE; TRICARBOXYLIC ACID CYCLE.
                                                                                                                                     RICKETTSIA SP.
BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RICKETTSIALES;
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RICKETTSIACEAE; RICKETTSIEAE; RICKETTSIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=HA-91;
RAOULT D., RYDKINA E., POUX V., EREMEEVA M., BALAYEVA N.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                 01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (EC 4.1.3.7) (FRAGMENT).
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (EC 4.1.3.7) (FRAGMENT).
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                    356 AA
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                    PRT;
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Matches 72; Conservative
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                  PRELIMINARY;
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                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-PUERTO RICO; MEDLINE; 98087556.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 207 KYTVNPIIKNALNKIFILHADHEQ-NASTSTVRIAGSSGANPFACISTGIASLWGPAHGG 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276 ANQEVILWIKSV-VDEC-GENISTEQLKDYVWKTLNSG-KVVPGFGLGVLRKTDPRYTCQ 332
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                                                                                                                                                                                                                                                                                                            Query Match 6.9%; Score 223; DB 2; Length 411;
Best Local Similarity 29.0%; Pred. No. 1.55e-21;
Matches 73; Conservative 67; Mismatches 88; Indels 24; Gaps
                     OXIDATIVE METABOLISM.
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF
                                                                                                                                                                                                                                            411 411 411 411 411 411 AA; 46162 MW; 9921533A CRC32;
                                                                               -!- PATHWAY: TRICKRBOXYLIC ACID CYCLE.
-!- SIMILARITY: TO OTHER CITRATE SYNTHASES.
EMBL; U59731, G1390011; -.
PROSITE: PSO0480; CITRATE_SYNTHASE; 1.
PFAM; PF00285; citrate_synt; 1.
LYASE; TRICARBOXYLIC ACID CYCLE.
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392 YTVLFGVSRSLG 403
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n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch\_nn

Sat Oct 23 20:18:09 1999; MasPar time 3158.85 Seconds 1533.004 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-702-718-5 (1-1747) from US08702718.seq 1747 Description: Perfect Score:

N.A. Sequence:

TABLE default Gap 6 Scoring table:

Nmatch STD

646147 seqs, 1385953633 bases x 2 Searched:

Dbase 0; Query 0

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

Database:

1:em\_bal 2:em\_ba2 3:em\_fun 4:em\_htg 5:em\_hum1 6:em\_hum2
7:em\_in 8:em\_om 9:em\_or 10:em\_ov 11:em\_pat 12:em\_ph
13:em\_pl 14:em\_ro 15:em\_sts 16:em\_vi
genbank111

17:95 bal 18:9b ba2 19:9b htg1 20:9b htg2 21:9b in1 22:9b in2 23:9b om 24:9b ov 25:9b pat 26:9b ph 27:9b pll 28:9b pll 29:9b prl 30:9b prz 31:9b prz 32:9b ro 33:9b st 34:9b st 35:9b sy 36:9b un 37:9b vi

Mean 12.066; Variance 12.847; scale 0.939 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ					
Result No.	Score	Query Match	Query Match Length DB	DB	ΩI	Description	Pred. No.
-	1747	100.0	1747	25	A46547	Sequence 3 from Patent	0.00e+00
7	1747	100.0	1747	27	NTCITSYNH	N. tabacum mRNA for cit	0.00e+00
m	1238	70.9		25	A46545	Sequence 1 from Patent	0.00e+00
4	1238	70.9		27	STCITS	S.tuberosum mRNA for m	0.00e+00
S	848	48.5		27	AB017159	Daucus carota mRNA for	0.00e+00
9	818	46.8		27	CMU19481	Citrus maxima citrate	0.00e+00
7	726	41.6		25	A46546	Sequence 2 from Patent	2.29e-258
ω	726	41.6		27	BUCITSYNH	B. vulgaris mRNA for ci	2.29e-268
σ	655	37.5		27	ATMTCITRN	Arabidopsis thaliana m	7.23e-240
10	296	34.1		27	PHCITSYNH	Populus hybrid mRNA fo	3.18e-216
11	274	15.7		31	AF047042	Homo sapiens citrate s	2.34e-88
12	273	15.6	1455	23	PIGCITSYN	Porcine citrate syntha	5.77e-88
13	210	12.0		27	SCMTCISNA	S.cerevisiae mitochond	1.946-63

/codou\_start=1
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/db\_xref="PID:2300712"
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/tb\_xref="GI:2300712"
/translation="MVFYRGVSLLSKLRSRAVQQTNLSNSVRWLQVQTSSGLDLRSEL

/EC\_number-"4.1.3.7"

Yeast gene for citrate S. cerevisiae chromosom S. cerevisiae N2019, N2 Candida tropicalis DNA S. pombe chromosome I c Yeast (S. cerevisiae) C S. cerevisiae chromosom Yeast (S. cerevisiae) C Aspergillus niger mRNA N. crassa mitochondrial M. Muyveromyces lactis D M. Crassa mitochondrial		PAT 07-MAR- 17. PAT 07-MAR- 18. PAT 07-MAR- 18
SCCS01 SCYNC0 SCN201 AB0015 SPAC6C SC1 YSCC1RI YSCCIRI ASNCIT NEUCIT	CETACOL G13212 G13212 CETACOO ATACOO ATACOO SCC113 SCC113 SCCHRA 166494 166494 166494 ASCHISA ANUSAMX ANUSAMX ACOO41 ACOO41	ALIGNMENTS  1747 bp DNA  GI:2300711  GDacco.  a tabacum  a; Viridiplantae; Strephyte;  bytes; Spermatophyta;  e; Solananee; Solanane
248899917 889017 889017 889017 889017 89017 8018	4 8096 21 4 8096 21 4 80 34 4 80 34 118324 28 12398 28 2709 27 1709 27 17218 25 7218	AL 1747 bp 171 GI:2300711 7.1 GI:2300711 7.1 GI:2300711 11 Llophytes; Sperma 11 Spermanae; Sperma 11 Lophytes; Sperma 12 Ser Solamanae; Sperma 12 Ser Solamanae; Sperma 12 Ser Solamanae; Lan 12 Ser Solamanae; Lan 13 Ser Solamanae; Lan 14 WO 9524487-A 3 15 WO 9524487-A 3 15 WO 9524487-A 3 16 WO 9524487-A 3 17 WO 9524487-A 3 18 WO 9524487-A 3 19 Publication DE 4 10 Publication AU 2 10 Cordanion Qual 10 Location Qual 11 1747
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LSIYECĞKULPAAKPGGEPLPEGLLMILLIGKVPSKEQVDSLSQELRSRATVPDHVYK
TIDALPVTAHPMIQRATGVMALOVQSEFOKAYEKGIHKSKIMEPIYEDSMSIJAQVPL
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QELIPEQQDRLKKLKSEHGKVQLGNITVDMVLGGMRGMTGLLWETSLLDPDEGIRFRG
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                                                                                                                     1021 ATCAAATCTGTTGTAGAGGAGTGTGGGGGAGAACATTTCCAAAGAGCAGTTGAAAGACTAC 1080
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                                GCTCACACACACCACTGGTTGCTAGTGCTTTGTCAGACCCTTACCTCTCCTTCGCTGCT
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                                                 481 AAAGAGCAAGTGGATTCATTGTCTCAGGAATTGCGAAGTCGTGCTACTGTCCCCGATCAT 540
       421 GGGGGAGAGCCCTTGCCTGAAGGTCTTCTCTGGCTTCTTTTAACAGGAAAGGTGCCATCA 480
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KDYAWKTLKSGKVVPGFGHGVLRKTDPRYTCQREFALKHLPEDPLFQLVAKLYEVFLQ
FLONLAKLNPWPNVDAHSGVLLNYYGLTEARYXTVLFGVSRALGICSQLIWDRALGLP
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TIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKLWEPTYEDSWSLIAQVPL
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euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
Asteridae; Solananae; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 1747)
La Cognata, U., Landschuetze, V., Willmitzer, L. and Mueller-Roeber, B. Plant Cell Physiol. In press
2 (bases 1 to 1747)
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Genbiologische Forschung, Berlin GmbH, Ihnestrasse 63, 14195
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                                                                                                                                                                                                                                                                                            /organism="Nicotiana tabacum"
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Best Local Similarity 100.0%;
Matches 1747; Conservative
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                                                                                                                                    La Cognata, U.
Direct Submission
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Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
Asteridae; Solananae; Solanales; Solanaceae; Solanum, Potatoe;
                                     1561 AGCCAAGGTAGGTCGCATTAGGATGTTCATCGATTGGCTTAGTACGGTTTTGAAAGATTT 1620
                                                                                                                                        1621 TGGTTGTGTATTTTCAGTTTTCGGTTTTAAAAATGTTATACCAATACCTTATCGATATAAA 1680
                                                                                                                                                                             Mueller-Roeber, B., Landschuetze, V. and La, C.U.
PROCESSES FOR INHIBITING AND FOR INDUCING FLOWER FORMATION IN
PLANTS
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73. .1488
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Pred. No. 0.00e+00;
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HOECHST SCHERING AGREVO GMBH (DE)
Other publication DE 4438821 960425
Other publication DE 443566 960328
Other publication AU 2067995 950925
Other publication DE 4408629 950914.
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/protein_id="CAA02908.1"
/db_xref="PID:e306252"
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Submitted (20-SEP-1993) V. Landschuetze, Inst. fuer Genbiologische Forschung, Berlin GmbH, Ihnestr. 63, 14195 Berlin, FRG
2 (bases 1 to 1891)
Landschutze, V., Muller-Rober, B. and Willmitzer, L.
Mitochondrial citrate synthase from potato: predominant expression in mature leaves and young flower buds
Planta 196 (4), 756-764 (1995)
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S.tuberosum mRNA for mitochondrial citrate-synthase.
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/note="ethanolamine ammonia-lyase"
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/db_xref="PID:9483510"
/db_xref="G1:483510"
/db_xref="SPTREMBL:043175"
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/clone_lib="leaf library"
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VQELIPEQODRLKKIKSDMKGSIGNITVDMVLGGMRGMTGLLWKPHYLDPDEGIRFRG
LSIPECQYLDAARPGGEPLPEGLLMILLTGKYRYSKEQVIS 18GIASEGIISLIIMY
TIIDALPYTAHPMTGFATGWAGLQVGSEFQRAYEKGIHKSKWEPTYEDSMNIIAQVP
LVAAYVYRRWYKNGDTIPKDESLDYGANFAHMLGFSSSEMHELLMRLYVTIHSDHEGG
                                                                                                    NVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLMIKSVVEEGGENISKE
GLODYVWKILLINSGKVYPGFGHGVLRKTVPRYTCQREFAMKHLPEDPLEQLVSKLYEVF
LLLFLONLAKLRVPWPUDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALG
LPLERPKSVTMEWLENQCKKA"
/translation="MVFYRSVSLLSKLRSRAVQQSNVSNSVRWLQVQTSSGLDLRSEI
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                                                                                                                                                                                                                                                      Score 1238; DB 27; Length 1891;
Pred. No. 0.00e+00;
0; Mismatches 93; Indels 18;
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Best Local Similarity 92.8%;
Matches 1439; Conservative
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; Asteridae; Aralhales; Aplaceae; Daucus.

1 (bases 1 to 1859)
Takita,E., Koyama,H., Shirano,Y., Shibata,D. and Hara,T.
Supriect Submission
Submisted (26-AUG-1998) to the DDBJ/EMBL/GenBank databases. Eiji
Takita, Gifu University, Laboratory of Plant Cell Technology, Faculty of Agriculture; Yanagido 1-1, Gifu, Gifu 501-1193, Japan (E-mail:takita@cc.gifu-u.ac.jp, Tel:+81-58-293-2911,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Daucus carota (cultivar:MS Yonsun) suspension cultured cells cDNA
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                                                                                                                                                                                                     987 TCATGGTTTAGCCAATCAGGAAGTTTTGCTATGGATCAAATCTGTTGTAGAGGAGTGTGG 2046
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TCATGGTTTAGCCAATCAGGAAGTTTTGCTATGGATAAAATCTGTTAGAAGAATGTGG
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                                                                                                              927 IGCTITGICAGACCCTIACCICTCCTICGCIGCTGCTTIGAAIGGTTIAGCIGGACCACT
                                                                                                                                                                                                                                                                                                                                        1116 GGTTGTCCCTGGTTTTGGACATGGAGTTCTGCGAAAGACTGTACCAAGATGCCA
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Takita, E., Koyama, H., Shirano, Y., Shibata, D. and Hara, T.
CDNA encoding carrot mitochondrial citrate synthase
Published Only in DataBase (1998) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AB017159 1859 bp mRNA PLN 01-S
Daucus carota mRNA for citrate synthase, complete cds.
AB017159
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Daucus carota
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LKELIPEQORELRKIKAEHGKVQLGNITVDWYLGGWRGWTGLLWETSLLDPEEGIRFR
GLSIPECGKLLPGARFGGEPLBEGLLWLLLGKVPTKEOVDALSAELRSRAAVPEHVY
KTIDALDVTAHRWTGPATGYWALQVQSEFQRAYEKGIHKTKYWEPTYEDSITLAQLP
VVAAYIYRRWYKNGGSISTDDSLDYGANFEKGIHKTKYWEPTYEDSITLIAQLP
VVAAYIYRRWYKNGGSISTDDSLDYGANFAHMLGYDSFWQELMRLYVTIHTDHEGGN
LKDYIWKTLANSGKVPGTGHGVLRNTDPRYTCQREFALKHLPDDPLFGULVSNLFEVYP
PILTELGKVKNPWPNVDAHSGVLLRNTDPRYTCQREFALKHLPDDDPLFGULVSNLFEVYP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 GAGCCAIGGIGITICIAICGCGGGGITICICIGCIGICAAAGCIGCGTICICGAGCGGTCC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 AGCAGTCGAACCTCAGTAATACAGTGCGTTGGTTTCAAGTGCAGACCTCCGCTTCTGATC 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 848; DB 27; Length 1859;
Pred. No. 0.00e+00;
0; Mismatches 271; Indels 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 TCAAGTCAGAGCATGGAAAGGTTCAATTGGGAAACATCACAGTTGATATGGTTCTTGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    332 TTAAAGCAGAACATGGAAAGGTTCAGCTGGGAAACATAACTGTTGATATGGTACTTGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGAGCAAGTGGATTCATTGTCTCAGGAATTGCGAAGTCGTGCTACTGTCCCCGGATCATG
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                                                           /cultivar-MS Yonsun'
/db_xref-"taxon:4039"
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1. 156
/gene-"DoCS"
                                                                                                                                                                                                                                                                                               /product-"citrate synthase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    563 t
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                                                                                                                                                                                                                                                                                                                                                             /db_xref="PID:9349367"
/db_xref="GI:3493367"
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1576. .1859
1838. .1843
                                                                                                                                                                                                                                                  /EC_number="4.1.3.7"
/codon_start=1
Location/Qualifiers
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                                                                                                                                                                                                       157. .1575
/gene="DcCS"
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Best Local Similarity 80.7%;
Matches 1155; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1232 ACACAGATCCAAGATACATGTCACAGAGAGTTTGCTTTAAAGCATTTACCTGATGATC 1291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1352 GCAAGGTAAAGAACCCCTGGCCAAATGTTGATGCCCATAGTGGGGGTACTGCTGAATCATT 1411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1412 ATGGCCTAACAGAAGCCAGATATTATACTGTTCTCTTTGGAGTATCGAGGGCCATTGGTA 1471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1319 ATGGTTTAACTGAAGCAAGATATTATACGGTCCTCTTTGGTGTATCAAGAGCTCTTGGCA 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1472 TITGITCTCAGCTGGTATGGGACAGAGCTCTTGGATTACCACTTGAGAGGCCAAAAAGTG 1531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1112 TCAAGTCTGTGGTTTCCGAATGCGGAGAAATGTAACTAAGGAACAATTGAAAGATTATA 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1022 TCAAATCTGTTGTAGAGGAGTGTGGGGAGAACATTTCCAAAGAGCAGTTGAAAGACTACG 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1172 TCTGGAAAACATTAAACAGCGGGAAGGTTGTTCCTGGATATGGACATGGTGTTCTGCGTA 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1142 AGACTGATCCAAGATACACATGCCAGAGAGTTCGCTTTGAAGCATTTGCCTGAAGATC 1201
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                                                                    752 AAACAAAGTATIGGGAGCCAACAIAIGAGGACTCTATIACTITAATIGCTCAATIACCAG 811
                                                                                       872 ATTCTCTAGATTATGGTGCAAACTTTGCCCACATGCTTGGTTACGATAGTCCCAGCATGC 931
GIGICATGGCCCTCCAGGTICAAAGTGAATTTCAGAAGGCATACGAGAAAGGGATTCACA 751
                                                                                                                                             812 TIGTAGCAGCTTATATCTATCGCAGGATGTACAAGAATGGACAAAGTATATCCACGGATG 871
                                                                                                                                                                                                                                                                                        932 AAGAGCITATGAGGCTITACGITACTATCCATACTGACCATGAAGGTGGAAACGTTAGTG 991
                                                                                                                                                                                                                                                                                                                             842 ATGAGCTTATGAAGCTCTATGTCACGATACACAGTGATCATGAAGGTGGTAACGTCAGTG 901
                                                                                                                                                                                                                                       pummelo.
Citrus maxima
Citrus mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
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/db_xref-"G1:674676"
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AIDALPVSAHPMTQFASGVMALQVQSEFQEAVEKGIHKSKSWEPTSEDSLNLTARVPY
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SAHTGHLVAAGLSDPYLSFLAALNGLAGPLHGLANOBYLLMIKSVVDECGENVTTEQL
KDYWKTLDROKKVVBGFGHGVLRKTDPRYTCQREFALKHLPDDPLFGLVSKLYEVVPP
ILTKLGKVRNPWPNAHSGVLLNHFGLAEARYYTVLFGVSRSLGIGSQLIMDRALGL
PLERPKSVTLDWIEKNCKKAA"
                                                     Canel,C., Bailey-Serres,J. and Roose,M.
Physiological and molecular genetic studies of acid accumulation in
                                                                                                                                             Thesis (1994) Botany & Plant Sciences, University of California at
                                                                                                                                                                                                                                                                                           Submitted (04-JAN-1995) Camilo Canel, University of California at Riverside, Botany & Plant Sciences, Riverside, CA 92521-0124, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="Siamese sweet (pummelo 2240)"
/note="There is a single copy of the cit gene in the citrus genome. A single transcript with an estimated length of 1,850 nucleotides can be detected in juice cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111. .1469
/gene="it"
/function="synthesis of citrate from oxaloacetate and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function="synthesis of citrate from oxaloacetate and acetylCoA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 AACAGICTAATCTCAGTAATTCAGTGAGATGGCTTCAAATGCAAAGCTCTGCTGATCTTG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 GAACCATGGCGTCCCTCAGGAGCGCCACTGCGCTCTCGCCCTCCGGTTCTCGCGTGGGC 111
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Magnoliopsida; Rutanae; Sapindales; Rutaceae; Citrus
1 (bases 1 to 1733)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="citrate synthase precursor"
/protein_id="AAA82743.1"
/db_xref="PID:9624676"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="juice tissue"
/dev_stage="immature"
1.56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       512 t
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                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Citrus maxima"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:37334"
/sex="hermaphrodite"
/cell_type="juice cell"
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/gene="cit"
57. .1472
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SKEQVDALSADLRKRASIPDHVYKTIDALPITAHPMTGFCTGVWALGTRSEFGKAYEK
GIHKSKFWEPTYEDGLSLIAQVPVVAAYVYRRAYKNGOVIPLDDSLDYGGNFAHMLGF
DSPQMLELMRLYVTIHSDHGGNVSAHTGHLVGSPLSDPYLSFAALNGLAGFLHGLA
NOEVLLWIKSVVDEGCENISTEGLKOYVWKTLNSGKVVPGFGLGVLRKTDRRYTCORE
FALKHLPDDPFFQLVSKLYEVVPPILLELGKVKNPWPNVDAHSGVLLNHYGLTEARYY
TVLFGYSRSLGICSQLIWDRALGLPERPKSVTMEWLEKFCKRRA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beta vulgaris
Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
1 (bases 1 to 1551)
1312 GTITGGCTGAGGCAAGATATTATACTGTTCTTTTTGGAGTATCAAGGAGTCTTGGGATCT 1371
                                                                                                                      1322 GTTTAACTGAAGCAAGATATTATACGGTCCTCTTTGGTGTTCAAGAGCTCTTGGCATTT 1381
                                                                                                                                                                     1372 GCTCTCAGTTGATATGGGACCGAGCTCTTGGGCTGCCACTTGAGAGGCCAAAAAGTGTAA 1431
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Pred. No. 2.29e-268;
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HOECHST SCHENIG AGREVO GMBH (DE)
Other publication DE 4438821 966425
Other publication DE 4435366 960328
Other publication AU 2067995 956925
Other publication DE 4408629 956914.
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/strain="2UCHTLINIE 5S 0026"
/db_xref="taxon:3555"
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/protein_id="CAA02909.1"
/db_xref="PID:e306423"
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                          121 GTATTGGGCGGAATGAGAGGAATGACTGGTTTACTTTGGGAGACTTCCTTACTCGACCCA 180
                                                                                                                                              292 GITCTTGGTGGAATGAGAGGAATGACAGGATTACTGTGGGAAACCTCATTACTTGACCCC 351
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/translation-*SSNLDLRSELQELIPEQOERLKKIKKEFGSFOLGNINVDMVLGG
MRGWTGLLWETSLLDPEEGIRFRGFSPPEGOKLTPAASAGAEPLFPGGLJLWLLLTGKVP
SKEQVALGABLRKRASIPDHVYKTIDALPITAHPMTGFCTGVWALGTRSFFQKASFK
GIHKSKFWEPPTYEDGLSLIAQVPVYAAYYFRNYKNGQVIPLDDSLDYGGNFAMLGF
DSPQWLELMRLYVTHSDHEGGNVSHTTGHLVGSPLSDPYLSFAALNGLAGPLHGLA
NQEVLUMIKSKVDEGGENISTBQLKDYVWKTLNSKKVVPGFGLGVLRKTDPRYTCQRE
TALKHLDDDPFFQLVSKLYFVPPILLELGSVVKNPWPNVDAHSGVLLRYTGQRE
TVLFGVSRSLGICSQLIMDRALGLPLERPKSVTMEWLEKFCKRRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotá; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; Caryophyllales; Chenopodiaceae; Beta.
1 (bases 1 to 1551)
La Cognata,U., Landschuetze,V., Willmitzer,L. and Mueller-Roeber,B.
                        1201 AGTCTTGGAATATGCTCACAGCTTATATGGGACCGAGCTCTTGGCTTGCCGCTAGAGAGG 1260
1369 GCTCTTGGCATTTGCTCTCAGCTAATTTGGGACCGGAGCTCTTGGATTGCCACTAGAGAGG 1428
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Genbiologische Forschung, Berlin GmbH, Ihnestrasse 63, 14195
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/protein_id="CAA59010.1"
/db_xref="PID:e137433"
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/db_xref="taxon:3555"
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/db_xref="GI:1556380"
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                                                                                                       181 GAAGAGGTATCCGGTTCAGGGGTTTTTCTATACCTGAATGCCAGAAACTTTTACCCGCT 240
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PUVAAYVYRRMYKNGDSIPSDKSLDYGANFSHMLGFDDERLKELMRLTSPSTVMHEGG
WYSHFGHLYGSALSDPYLSFAAALUGLAGPLHGLANGKSWFEGGEDISKE
QLKEYWMKILNSGKYLPGYGHGYLRNTDRYVCQREFALKHFDDPLFQCCKLMKLAS
CLIELESEEPWPNVDAHSGYLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRELLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation-"MVFFRSVSAFTRLRSRVGGGGSSLSNSVKWIGMGSSTDLDLKSG
LOELIPEHKDRLKKLKSEHGKVQLGNITVDMVIGGMRGMTGLLWETSLLDPEEVFALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DCRLPECQKALLPTAQSGGLNHYRRSFVASLNWKGTLAKSKLKHCRKTWNRAAVSDYV
YNAIDALPSTAHPMTQFASGVMALQVQSEFQKAYENGIHKSKFWEPTYEDCLNLIARV
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1680)
1 (bases 1 to 1680)
1 (nger,E.A., Hand,J.M., Cashmore,A.R. and Vasconcelos,A.C.
Isolation of a cDNA encoding mitochondrial citrate synthase from Arabidopsis thaliana
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 300; Indels 17; Gaps 16;
                        1369 GCTCTTGGCATTTGCTCTCAGCTAATTTGGGACCGAGCTCTTGGATTGCCACTAGAGAGG 1428
                                                                                                                                                                                                                                                Arabidopsis thaliana mRNA for mitochondrial citrate synthetase, X17528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 GGGCCAACAATCTTCACTCAGCAATTCTGTCAGATGGATTCAGATGCAGAGCTCTACCGA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 GGTCCAACAGACAAATCTTAGCAACTCTGTGCGGTGGCTTCAAGTCCAAACCTCTTCTGG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 CCTGGACCTGAAGTCGCAGCTGCAAGAGTTAATTCCGGAACACACAAGACCGTCTGAAGAA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 TCTTGATCTGCGTTCTGAGCTGCAAGAATTGATTCCAGAACAACAGGATCGCCTAAAGAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 ACTGAAGTCAGAACATGGGAAGGTCCAACTGGGAAACATCACTGTTGATATGGTTATTGG 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 TGGAATGAGAGAATGACAGGATTACTGTGGGAAACCTCATTACTTGACCCCGATGAAGG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350 TATICGCTTTAGGGGAITGTGGACTTCCTGAGTGCCAGAAAGCCCTATTACCTACTGCCC 409
                                                                                                                                                                                                                                  26-NOV-1997
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Length 1680;
                                                                                                         1261 CCAAAGAGTGTCACTATGGAATGGCTTGAAAAGTTTTGTAA 1301
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/db_xref="taxon:3702"
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/product="citrate synthetase"
/protein_id="can3570.1"
/db_xref="PID:e1188578"
/db_xref="PID:e1188578"
/db_xref="SWISS-PROT:P20115"
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X17528.1 GI:11243
citrate synthase.
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1301 ACCACTATGGTCTAACCGAAGCAAGGTACTACACCGTGCTCTTTGGTGTTTCAAGGAGTC 1360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1067 AAGAATATGTTTGGAAAACATTAAACAGTGGCAAGGTTATTCCGGGATATGGTCACGGTG 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCTGCGCAATACTGATCCAAGATATGTATGCCAAAGAGAATTTGCCTTGAAGCATCATC 1186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1313 ACTATTATGGTTTAACTGAAGCAAGATATTATACGGTCCTCTTTGGTGTATCAAGAGCTC 1372
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                                                                                                                                                                                 475 CCAICA-AAAGAGCAAGIGGAIICAIIGICICCAGGAAIIGCGAAGICGIGCIACIGICCC 533
                                                                                                                                                                                                                                                                        534 CGATCATGTATACAAAACTATTGATGCCTTACCAGTCACAGCTCATCCAATGACTCAGTT 593
                                                                                                                                                                                                                                                                                                                      588 IGCTAGCGGTGTTATGGCCCTCCAGGTGCAAAGTGAGTTTCAAAAGGCATATGAGAATGG 647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              654 GATTCACAAATCAAAGTTATGGGAACCGACATATGAGGATTCCATGAGTTTGATTGCTCA 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 IGTICCTGTIGIAGCIGCAIAIGIIIAICGAAGGAIGIAIAAGAAIGGIGAIICCAIICC 767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             774 TAAGGATGACTCACTGGATTATGGTGCAAATTTTGCTCACATGCTTGGTTTCAGTAGCTC 833
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                                           410 AGTCTGGAGGCTTGAACCATTACCGGAGGTCTTTTGTGGCCTTCTTAACTGGAAAGGTA 469
                                                                                                                                       470 CCTTAGCAAAGAGCAAGTTGAAGCACTGTCGAAAGACTTG-GAAC-CGTGCTGCTGTGTC 527
360 AATTCGCTTTCGGGGCTTGTCTA-TGAATGCCA-AAAGG--TATTACCTGCAGCAA 415
                                                                                         416 AGCCTGGGGGAGAGC-CCTTGCCTGAAGGTCTTCTCTGGCTTCTTTTAACAGGAAAGGTG 474
                                                                                                                                                                                                                                                                                                                                                 528 AGATTATGTGTACAATGCCATCGATGCTCTGCCTTCCACAGGTCATCCAATGACTCAATT
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/translation="MPTKEQYGALSKELRDRALVHDYVFKAIDALPVTAHPWTQFATG
VMALQYQSEFOKAYEKGIHKSKYWEPTYEDSLSLIARVPITASYINRIYKDGKVIPM
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FAAALNGLAGPLHGLANQEVLLWIKGYVEDGGENITTEQLKDYWWTLNSGKVVPGFG
HGVLRKTVPRYTGCREFALKHLPDDPLPQLYSKLYEVYPPVLTQLGKVKNPWPNVDAH
SGYLLNYYGLTEARXYTVLFGVSRSIGICSQLIWDRALGLPERPKSVTMELLENHCK
                                                                                                                                                                                                                                                                                             1 (bases 1 to 1378)
La Cognata, U., Landschuetze, V., Willmitzer, L. and Mueller-Roeber, B. Plant Cell Physiol. In press
2 (bases 1 to 1378)
La Cognata, U.
                                                                                                                                            citi gene; citrate synthase.

Populus balsamifera subsp. trichocarpa X Populus deltoides.

Populus balsamifera subsp. trichocarpa X Populus deltoides.

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae; Violales; Salicaceae; Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 ITCATGATTATGICITIAAGGCCATTGAIGCCTTACCIGTCACIGCICAICCAAIGACIC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     530 TCCCCGATCATGTATACAAACTATTGATGCCTTACCAGTCACAGCTCATCCAATGACTC 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 AGTITGCAACTGGTGTTATGGCCCTACAGGTTCAGAGTGAATTTCAAAAAGCCTATGAAA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      590 AGITIGCIACIGGAGICAIGGCICITICAGGIICAAAGIGAAITICAAAAGGCATAIGAGA 649
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                     28-OCT-1996
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Submitted (23-JAN-1995) U. La Cognata, Institute fuer
Genbiologische Forschung, Berlin GmbH, Ihnestrasse 63, 14195
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/codon_start=1
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/product="citrate (si)-synthase"
/protein_id="CAA59009.1"
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PHCITSYNH 1378 bp MRNA Populus hybrid mRNA for citrate synthase.
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                                                                                                                                                                                                                                                                                                          1130 GAGTICTGGGCAAGACTGATCCAAGAIACACAIGCCAGAGAGTTGGCTTTGAAGCATT 1189
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                                                         314 TICCTATGAATGACTCTTTGGTTATAGGTGGAAATTTTTCACACATGTTGGGATTTGATA 373
                                                                                                                                   374 GICCIGAAAIGCAAGAGCIIAIGAGGCIIIAIGIIACIAACCAIAGIGACCAIGAAGGIG 433
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cloning and sequence analysis of human citrate synthase cDNA
                                                                                                                                                         1249 TTACAGAACTTGGCAAAGTTAAA--CCCTTGGCCAAATGTTGATGCCCACAGTGGTGTGT
                   710 CTCAAGTTCCACTTGTTGCTGCTTATGTTTATCGCAGGATGTACAAGAACGGCAACACTA
                                                                                             770 TACCTAAGGATGACTCACTGGATTATGGTGCAAATTTTGCTCACATGCTTGGTTTCAGTA
                                                                                                                                                                                                           434 GGAATGTCAGTGCTCATACTGGTCACTGGTTGCTAGTGCACTTTCAGATCCTTATCTTT
                                                                                                                                                                                                                                                890 GTAACGTCAGTGCTCACACAGGTCACTTGGTTGCTAGTGCTTTGTCAGACCCTTACCTCT
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974 GGCCAAAGAGTGTTACAATGGAATTGCTTGAGAATCACTGCAAGAAAGC 1022
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Homo sapiens citrate synthase mRNA, complete cds.
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Goldenthal, M.J.
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2 (bases 1 to 1401)
Goldenthal, M.J.
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QARIKTFRQQHGKTVVGQITVDMMYGGMRGMKGLVYETSVLDPDEGIRFRGFSIPECQ
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NLYWEGSGIGAIDSNLDWSHNFTNMLGYTDHQFTELMRLYLTIHSDHEGGNVSAHTSH
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TLNSGRVVPGYGHAVLRKTDPRYTCQREFALKHLPNDPMFKLVAQLYK I VPNVLLEQG
KAKNPWPNVDAHSGVLLQYYGMTEMNYYTVLFGVSRALGVLAQLIWSRALGFPLERPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        719 TCACCAACATGTTAGGCTATACTGATCAGTTCAGTTGAGCTCATGGGCCTGTACCTCA 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 ATGAAACATCAGTTCTTGATCCTGATGAGGGCATCCGTTTCCGAGGCTTTAGTATCCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 274; DB 31; Length 1401;
Pred. No. 2.34e-88;
0; Mismatches 458; Indels 6
                                                                                                                                                                             /note="isolated from a 22-year old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340 t
                                                                                                                                                                                                                                                                                 /product="citrate synthase"
/protein_id="AAC25560.1"
/db_xref="PID:93288815"
                                    /organism-"Homo sapiens"
/db_xref-"taxon:9606"
                                                                                                                                 /tissue_type="heart"
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                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="GI:328881
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                                                                                                   /sex="male"
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Local Similarity 62.3%;
hes 768; Conservative
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779 CCATCCACAGTGACCATGAGGGTGGCAATGTAAGTGCCCATACCAGCCACTTGGTGGGCA 838

FEATURES

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Chromosome 12.
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ORIGIN
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KMLFKAKGGEEPLPEGLFWLLVTGQIPTEEOVSWLSKEWAKRAALFSHVTMLDNFFT
NLHPMGQLSAAITALMSESNPARAYAEGIHRTKYWELIYEDCMDLIAKLEVVARAIYR
NLYREGSSIGAIDSKLHTMMAYTDAQFTEIMKLYTTIHSDHEGGNVSAHTSH
LVGSALSDPYLSFAAAMNGLAGPLHGLANQFVLWLTQLQKEVGKDVSDEKLRDYIKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MALLTAAARLFGAKNASCLVLAARHASASSTNLKDILADLIPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rtebrata; Eutheria; Artiodactýla; Sulformes; Silna; Suldae; Sus. (bases 1 to 1455)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolation, nucleotide sequence, and expression of a cDNA encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1259 ACACGGICCTGTTTGGGGTGTCACGAGCATTGGGIGTACTGGCACAGCTCATCTGGAGCC 1318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1343 ATACGGTCCTCTTTGGTGTATCAAGAGCTCTTGGCATTTGCTCTCAGCTAATTTGGGACC 1402
                                                                                                                                                           986 ITCATGGTTTAGCCAATCAGGAAGTTTTGCTATGGATCAAATCTGTTGTAGAGGAGTGTG 1045
                                                                                                                                                                                               959 GCAAAGATGTGTCAGATGAGAAGTTACGAGACTACATCTGGAACACACTCAACTCAGGAC 1018
                                                                                                                                                                                                                               1046 GGGAGAACATTTCCAAAGAGCAGTTGAAAGACTACGCTTGGAAAACATTGAAAAGTGGCA 1105
                                                                                                                                                                                                                                                                   1019 GGGTTGTTCCAGGCTATGGCCATGCAGTACTAAGGAAGACTGATCCGCGATATACCTGTC 1078
                                                                                                                                                                                                                                                                                                      1106 AGGTTGTCCCTGGTTTCGGACATGGAGTTCTGCGCAAGACTGATCCAAGATACACATGCC 1165
                                                                                                                                                                                                                                                                                                                                            1139 TGTACAAGATTGTGCCCCAATGTCCTCTTAGAGCAGGGTAAAGCCAAGAATCCTTGGCCCA 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1226 TCTACGA-AGTGTTCCTCCAATTCTTACAGAACTTGGCAAAGTTAA--ACCCTTGGCCAA 1282
                                                                                       926 GIGCITIGICAGACCCITACCICTCCTICGCIGCIGITIGAAIGGITIAGCIGGACCAC 985
                                                                                                                         839 GIGCCCTITCCGACCCTIACCIGICCTITIGCAGCAGCCAIGAACGGGCIGGCAGGGCCIC 898
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                                                                                                                                                                                                                                                                                                                                                              1199 ATGTAGATGCTCACAGTGGGGTGCTGCTCCAGTATTATGGCATGACGGAGATGAATTACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="citrate synthase precursor (EC 4.1.3.7)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Porcine citrate synthase mRNA, complete cds. M21197
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citrate synthase.
Porcine kidney, cDNA to mRNA, clone PCS4.
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/protein_id="AAA31017.1"
/db_xref="PID:9164419"
/db_xref="GI:164419"
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Biochemistry 27, 4680-4686 (1988)
89000665
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KAKNPWPNVDAHSGVLLQYYGMTEMNYYTVLFGVSRALGVLAQLIWSRALGFPLERPK
SMSTDGLIKLVDSK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    389 AATGCCAAAAGGTATTACCTGCAGCAAAGCCTGGGGGAGAGCCCTTGCCTGAAGGTCTTC 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           449 TCTGGCTTCTTTTAACAGGAAAGGTGCCATCAAAAGAGCAAGTGGATTCATTGTCTCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1455;
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                                                                                                                           8. .88
/note="citrate synthase signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                Score 273; DB 23;
Pred. No. 5.77e-88;
                                                                                                                                                                                                                                                                                              333 t
                                                                                                                                                                                                                                                  /note="citrate synthase"
363 c 386 g 33
                                                                                                                                                                                                                                                                                                                                                                                                                / Match 15.6%;
Local Similarity 63.3%;
nes 743; Conservative
                                                                                                                                                                                                          .1399
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/clone="Plasmid pFCS1 (Suissa et al., EMBO J. 3, 1773-1781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
1084 CAAAGAGAGTTTGCTCTGAAACACCTGCCTCATGACCCCATGTTTAAGCTGGTTGCTCAG 1143
                                                                                                                                1225 CTCTACGAAGTGTTCCTCCAATTCTTACAG-AACTTGGCAAAGTTAA--ACCCTTGGCCA 1281
                                                                                                                                                                            1204 AATGTGGATGCTCACAGTGGGGTGCTGCTCCAGTACTATGGCATGACGGAGATGAACTAC 1263
                                                                                                                                                                                                                   1282 AATGTTGATGCCCACAGTGGTGTTGTTGAACTATTATGGTTTAACTGAAGCAAGATAT 1341
                                                                                                                                                                                                                                                               1264 TACACAGTCCTGTTCGGGGTATCACGGGCACTGGGTGTATTAGCACAGCTCATCT5GAGC 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maxtinsried, D-82152, Feter Linuuer, Frotein Engineering, Maxtinsried, D-82152, Fed. Rep., Germany 4 (bases 1 to 1481)
Suissa,M., Suda,K. and Schatz,G.
Isolation of the nuclear yeast genes for citrate synthase and lifteen other mitochondrial proteins by a new screening method 85003587
                                         1165 CAGAGAGAGTICGCTTTGAAGCATTTGCCTGAAGATCCACTGTTTCAACTGGTTGCAAAA 1224
                                                                                                                                                                                                                                                                                        SCMTCISNA 1481 bp DNA PLN 17-FEB-1997
S.cerevisiae mitochondrial citrate synthase gene, complete CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="SGD:L0000341"
/db_xref="SGD:L0000341"
/evidence-experimental
/product="the processing site has been determined by
direct_N.terminal protein sequencing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 1481)
Lindner,P and Plueckthun,A
The effect of point mutations in the hinge of yeast citrate
                                                                                       1144 CTGTACAAGATTGTGCCCAATGTCCTCCTGGAACAGGGCAAGGCTAAGAATCCTTGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thesis (1993) Protein Engineering, Max-Planck-Institut fue:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (05-JUL-1993) Peter Lindner, Protein Engineering,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Saccharomyces cerevisiae"
/strain="D273-10B"
/db_xref="taxon:4932"
                                                                                                                                                                                                                                                                                                                                                    1324 CGAGCCTTAGGCTTCCCTCTAGAGGGCCCAAG 1356
                                                                                                                                                                                                                                                                                                                                                                                           1402 CGAGCTCTTGGATTGCCACTAGAGAGGCCAAAG 1434
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mitochondrial citrate synthase.
baker's yeast.
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GKLPVIASKIYRNVFKDGKITSTDPNADYGKNLAQLLGYENKDFIDLMRLYLTIHSDH
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SKCTIEKYLMDTLNAGRYVPGYGHAVLRKTDPRYTAQREFALKHFDYSELFKLVSTY
EVARGVLTREGKTRWAPNYDSHSGYLLQYYGLTEASFYTVLFGVARAIGVLPQLIID
RAVGAPIERPKSFSTEKYKELVKKIESKN"
                                                                                                                                                                                                  LKERFAEIIPAKAEEIKKFKKEHGKTVIGEVLLEQAYGGMRGIKGLKUWEGSVLDPEEG
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                                                                                                                                                                            /translation-"MSAILSTISKSFLSRGSTRQCQNMQKALFALLNARHYSSASEQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 AGGTATTAGATTTAGGGGTCGTACTATTCCAGAAATTCAAAGGGAACTACCAAAGGCTGA 362
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                /db_xref="SGD:L0000341"
/db_xref="SGD:L0000d1a1" citrate synthase"
/protein_id="CAA8078:.1"
/db_xref="PID:9313750"
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Pred. No. 1.94e-63;
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/db_xref-"SWISS-PROT:P00890"
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Best Local Similarity 60.3%;
Matches 688; Conservative
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citrate synthase; synthase.
Daker's yeast.
Saccharomyces cerevisiae
Eukaryota; Fungi: Ascomycota; Hemiascomycetes; Saccharomycetales;
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1 (Dases 1 to 2427)
Suissa,M., Suda,K. and Schatz,G.
Isolation of the nuclear yeast genes for citrate synthase and fifteen other mitochondrial proteins by a new screening method EMBO J. 3 (8), 1773-1781 (1984)
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                                                                                                                                                                                                                                843 ITCTGCCCATACTACACATTTAGTGGGTTCTGCCTTATCTTCGCCATACTTATCTTTGGC
                                                                                                                                                                         957 IGCIGCITIGAAIGGITIAGCIGGACCACTICAIGGITIAGCCAAICAGGAAGITIIGCI
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 783 ITITAITGACTTAATGAGACTATATTTAACTATTCATTCTGATCATGAAGGTGGTAACGT
                                                                                                                                                                                                          963 ATGGCTATTTAAATTGAGAAGAAGTGAAAGGTGACTATTCAAAAGAAACAATTGAAA-
                                                                                                                                                                                                                                                                               1022 AGTACTIGIGGGAIACTIIGAACGCAGGGAGAGTIGTICCIGGTIAIGGCCAIGCGGTII
                                                                                                  897 CAGIGCICACACAGGICACTIGGIIGCIAGIGCIIIIGICAGACCCIIACCICICCCIICGC
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/db_xref="taxon:4932"
376. .1818
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/protein_id="CAA25359.1"
/db_xref="PID:93603"
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Yeast gene for citrate synthase.
X00782
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//Translation="MGAILSTTSKSFLSRGSTRQCQNMQKALFALLNARHYSSASEQT
//Translation="MGAILSTTSKSFLSRGSTRQCQNMQKALFALLNARHYSSASEQT
GIRFRGRIPPERAGETELPEALEWILLTGEIPUDAQVKALSADLAARSEI
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GALLDVLASKTIRNVFRDGRIAVTALESESKFAKAYAQGVSKKEWSYTFEDSLDL
HEGGRUYSARTIRNVFRDGRITSTDAMDVGKNLAOLLGYBENGFIDLMAKLYLTHSD
HEGGRUYSAHTTHLVGSALSSPYLSLAAGLNGLAGPLHGRANDEVLENLFRLBEDVGD
YSKETIEKYLMDTLNAGRVVDGTGHAVLRKTDPRYTAQREFALKHFPDYELFKLVSTI
YEVAPGVLTKHGKTRWPNNDSHSGYLLQYTGLTEASFYTVLFGVARAIGVLPQLII
DRAVQAPIERPKSELVKELVKKIESKN"

439 C. 757 t.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         777 GGATGACTCACTGGATTATGGTGCAAATTTTGCTCACATGCTTGGTTTCAGTAGCTCTGA
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                                                                                                                                                                                                                                                                                                                                                                             Score 210; DB 27; Length 2427; Pred. No. 1.94e-63;
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/db_xref="GI:3603"
/db_xref="SWISS-PROT:P00890"
                                                                                                                                                                                                                                                                                                                                                                          Query Match 12.0%;
Best Local Similarity 60.3%;
Matches 688; Conservative
                                                                                                                                                                                                                                                                                              757
                                                                                                                                                                                                                                                                                           BASE COUNT
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Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (29-APR-1996) Data collected by MIPS on behalf of the European yeast chromosome XIV sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152 Martinsried, FRG: E-mail: Mewes@mips.embnet.org
                                                                                                                                                                         1580 AGCATGGTAAAACTAAGAACCCATGGCCAAATGTTGATTCACATTCCGGTGTTTATTGC 1639
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1460 TGAGAAAACTGATCCTCGTTATACGGCTCAACGTGAATTCGCATTGAAACATTTCCCAG 1519
                                          1136 TGCGCAAGACTGATCCAAGATACACATGCCAGAGAGAGTTCGCTTTGAAGCATTTGCCTG 1195
                                                                                       ATTACGAGITATITAAGITGGTCTCCACCAITIAIGAAGITGCCCCCAGGGGITTITAACIA 1579
                                                                                                                              1196 AAGATCCACTGTTTCAACTGGTTGCAAAACTCTACGAAGT-GTTCCTCCAATTCTTACAG 1254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCYNR001C 4391 bp DNA PLN 11-A
S.cerevisiae chromosome XIV reading frame ORF YNR001c.
Z71616 <u>Y</u>13139
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Aert,R., Verhasselt,P., Voet,M. and Volckaert,G.
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/db_xref="taxon:4932"
/chromosome="XIV"
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/db_xref="SWISS-PROT:P00890"
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/note="CEN element CDE I"
150. .234
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/protein_id="CAA96277.1"
/db_xref="PID:e239778"
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/gene="CIT1"
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/note="solo-tau"
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1783 TAATITTACCCAGCAGATCTAACGAATCTICAAATGTATAGCTCCAATATICTITGTTGGA 1842
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Search completed: Sat Oct 23 21:11:13 1999 Job time: 3184 secs.

Survival motor neuron Human survival motor Human secreted protei Human secreted protei Pl4(T) allergen clone Birch pollen P.4 alle Plasmid pMG3C9 used t Human superoxide-dism Human mucosal lymphoc

Q22352 Q89191 104682 Q23462 T03885 Q44265 Q12154 Q25185

1582 22 11582 22 251848 56 25184 56 472 56 700 14 10046 12 2229 4 2229 4 3333 16 7859 7

T28259 T18831 V84588 V54124 V84530

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MasPar time 392.61 Seconds 953.450 Million cell updates/sec
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                                                                                               Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd
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(1-1747) from US08702718.seq
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Listing first 45 summaries
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Rat allograft inflamm

Q99380 T69172

44 9 10 14 10 36 36

V84473

785 880 1118

Oligonucleotide

Trypanosoma cruzi ant Human secreted protei Rat SmLIM/CRP2 cDNA.

Nucleotide sequence o Human growth regulato Oligonucleotide probe

V09269

V37488

pSW6 for expression o Shuttle vector pSW6. pSW6 expression vecto Human secreted protei Human secreted protei Plant CAD enzyme DNA Plant CAD enzyme DNA

V34290 V34253 V23913

V23914 V73000

1454 42 1474 42 1521 58 1694 50 1875 49

V33190

V33033

Deg-1 gene.

020263

Human foetal brain se Secreted protein BD38 Dictyostelium plasmid Human plasminogen wit Plasminogen gene from

Q11710 Q11998

5153 21 5153 21 5852 2 6010 2

T30347

006648

ALIGNMENTS

Petunia EPSP synthase Human secreted protei Human YAP CDNA.

Q37189 V59663

Dirofilaria immitis t

DNA encoding plant citrate synthase - used to regulate flower formation, to improve storage of tubers, etc. and to reduce sprouting claim 7: Page 60-63: 87pp; Bnglish.

To identify a cDNA from tobacco which codes for citrate synthase, a cDNA bank of leaf tissue from tobacco was prepd. Plaques of this cDNA bank were screened using a radioactive DNA probe which comprises Solanum tuberosum citrate synthase cDNA probe which comprises Solanum tuberosum citrate synthase cDNA (704199), one of the clones was sequenced. The nt. sequence is sequence 1747 Bp; 490 A; 335 C; 400 G; 522 T; (AGRE ) HOECHST-SCHERING AGREVO GMBH. La Cognata U, Landschutze V, Muller-rober B, Landschuetze 25-JAN-1996 (first entry)
Tobacco citrate synthase cDNA.
Citrate synthase; flower formation; ss.
Nicotiana tabacum r 1 T04201 standard; cDNA to mRNA; 1747 Location/Qualifiers 70..1476 /\*tag= a 14.SEP-1995. 07-MAR-1995. 09-MAR-1994; DE-408629. 22-SEP-1994; DE-438586. 19-OCT-1994; DE-438821. La Cognata U, Lands Mueller-roeber B; WPI; 95-328278/42. P-PSDB; R82840. W09524487-A 

DB 16; 100.0%; Score 1747; Query Match

0.00e+00 0.00e+00 0.00e+00 7.45e-08 7.45c-03 1.44e-06

Potato citrate syntha Potato citrate syntha Sugar beet citrate sy Base substituted E.co Spinach debranching c Base substituted E.co Survival motor neuron

T04199 T03410 T04200 N81164 T31478 N81164 T28255

1891 1891 1551 204 3437 204 1558

Human survival motor

0.00e+00

Tobacco citrate synth

T04201

1747

16 16 17

1747 1238 1238 726 46

Description

Q

DB

Query Match Length

Score

Result

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Mean 9.616; Variance 7.859; scale 1.224

Statistics:

60:part60

49:part49 5 54:part54 5 59:part59 6

Length 1747;

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P-PSDB; R82838
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                                                    1 gctcttgggatctatttcctctctctatttctccctaggtaaaagttaatttgttgattt 60
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Best Local Similarity 100.0%; Pred. No. 0.00e+00;
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               Matches 1747; Conservative
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DNA encoding plant citrate synthase - used to requiate flower formation,
1021 ATCAAATCTGTTGTAGAGGAGTGTGGGGGAGAACATTTCCAAAGAGCAGTTGAAAGACTAC 1080
                                          gcttggaaaacattgaaaagtggcaaggttgtccctggtttcggacatggagttctgcgc 1140
                                                                                1081 GCTTGGAAAACATTGAAAAGTGGCAAGGTTGTCCCTGGTTTCGGACATGGAGTTCTGCGC 1140
                                                                                                                           1141 aagactgatccaagatacacatgccagagagagttcgctttgaagcatttgcctgaagat 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JAN'1996 (first entry)
Potato citrate synthase cDNA.
Citrate synthase; flower formation; tuber storage; ss.
Solanum tuberosum.
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La Cognata U, Landschutze V, Muller-rober B,
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07-MAR-1995.
09-MAR-1994. DE-408629.
22-SEP-1994. DE-433861.
19-OCT-1994, DE-438821.
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WPI; 95-328278/42.
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Page 3

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0; Mismatches 93; Indels 18; Gaps 14;
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to improve storage of tubers, etc. and to reduce sprouting claim 5; Page 53-56; B7pp; English.

To identify a cDNA from potato which codes for citrate synthase, a cDNA fragment of citrate synthase from Arabidopsis thaliana was firstly amplified using A.thaliana cDNA and oligos T04202 and T04203 which are complementary to the 5' or 3' end of the coding region of introduce BamHI clavage sites at both ends of the amplified cDNA for citrate synthase. The oligos additionally introduce BamHI clavage sites at both ends of the amplified cDNA fragment. a cDNA library was prepd. from potato leaves and screened with A. thaliana citrate synthase cDNA. Positive clones were purified and sequenced. Then t sequence is given in T04199.
                                                                                                                                                                                                                                                                                                                                                                                                                                               ggtaaaagttaattttttttgattttcgcgagcaatggtgttctaccgtagcgtttcgttg 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 GGIAAAAGITAATITGII-GAITITIGCGAGCCAIGGIGIICIAICGCGGCGIIICICIG 96
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                                                                                                                                                                                                                                                                                                                                         3; DB 16; Length 1891;
0.00e+00;
                                                                                                                                                                                                                                                                                                                                         Score 1238;
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Local Similarity 92.8%;
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876 aatacacagtgatcatgaaggtggtaatgtcagtgctcacacccggtcacttggttgctag 935
                                       867 GATACACAGGGGATCAIGAAGGIGGTAACGTCAGTGCTCACACAGGGTCACTTGGTIGCTAG 926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potato citrate synthase gene.
Citrate synthase; inhibitor; increased storage capacity; potato;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Landschutze V, Muller-Roeber B, Landschuetze V;
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09.MAR-1994; 408629.

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P-PSDB; R86383.
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also new CS sense and anti-sense DNA sequences
Claim 6; Page 15-19; 35pp; German.
The potato citrate synthase (CS) gene or CDNA sequence encoding CS
(T03410) may be used to produce antisense CS sequences. CS DNA
sequences are useful for altering CS activity in plants. Antisense
CS sequences can be used to inhibit CS expression in plants and has
the effect of inhibiting flower formation and by doing so improves
the plant's storage capacity. This is partic. useful in crop plants
of any kind but esp. useful in potatoes. In addition to altering CS
activity the DNA sequences can also be used to identify similar
sequences in the genomes of other plants and in the production of
transgenic plants with altered CS activity.
Sequence 1891 BP: 512 A; 370 C; 425 G; 584 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acctcattaccttgaccctgatgagggaattcgcttccggggggttgtctatacctgaatg
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Best Local Similarity 92.8%;
Matches 1439; Conservative
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DNA encoding plant citrate synthase - used to requlate flower formation, to improve storage of tubers, etc. and to reduce sprouting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        987 TCATGGTTTAGCCAATCAGGAAGTTTTGCTATGGATCAAATCTGTTGTAGAGGAGTGTGG
                                                                                                                                                                                                                                                                                     1047 GGAGAACATTICCAAAGAGCAGTIGAAAGACIACGCTIGGAAAACATIGAAAAGTGGCAA
                                                                                                                                                                                                                                                                                                                              1116 ggttgtccctggttttggacatggagttctgcgaaagactgtaccaagatatacatgcca
                                                                                                                                                                                                                                                                                                                                                                    1107 GGIIGICCCIGGIIICGGACAIGGAGIICIGCGCAAGACIGAICCAAGAIACACAIGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1236 ctacgaagttttcctcctgttcttacagaacttggcaaagttaaaaccttggccaaatgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1476 caagaaagcatgaattgtttgaaatete-gegageataaaa-cacaatgtataateteta
876 aatacacagtgatcatgaaggtggtaatgtcagtgctcacacccggtcacttggttgctag
                                      867 GATACACCAGTGATCATGAAGGTGGTAACGTCAGTGCTCACACAGGTCACTTGGTTGCTAG
                                                                                                                                                                                                                                                                                                                                                                                                             1176 gagagagttegetatgaageatttgeetgaagateeactgttteaaetggttteaaaet
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1167 GAGAGAGTICGCITIGAAGCAITIGCCIGAAGAICCACIGITICAACIGGITGCAAAACI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1227 CTACGAAGTGTTCCTCCAATTCTTACAGAACTTGGCAAAGTTAAAACCTTGGCCAAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1347 GGTCCTCTTTGGTGTATCAAGAGCTCTTGGCATTTGCTCTCAGCTAATTTGGGACCGAGC
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                                                                                 tgctttgtctgatccttacctctcctttgctgctgctttgaatggtttagccggaccact
                                                                                                                      927 IGCTITGICAGACCCTIACCICTCCTICGCIGCTGCTITGAATGGTITAGCTGGACCACT
                                                                                                                                                               996 tcatggtttagccaatcaggaagttttgctatggataaaaatctgttgtagaagaatgtgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1534 tgaataattgcttgacaaagcactcctttcttgggggacaagataggtcg 1583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1527 IGAATAATIGCTIGAGAAAGCAGTITITITITIGGAGC-CAAGGTAGGICG 1575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Landschutze V, Muller-rober
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sugar beet citrate synthase cDNA.
Citrate synthase; flower formation; ss.
Ceta vulgaris strain Zuchtlinie 58 0026
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
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19-OCT-1994; DE-438821.
(AGRE ) HOECHST-SCHERING AGREVO GMBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JAN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        952 TTCGCTGCTGCTTTGAATGGTTTAGCTGGACCACTTCATGGTTTAGCCAATCAGGAAGTT 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   781 tttgcagcagcattaaatggtttggctgggccactccatggattagccaaccaggaagtc 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        841 ctgctgtggattaaatcagttgttgatgaatgtggagagaacatctcgacagagcagttg 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 541 caagttcctgttgttgcagcttatgtttatcggaggatgtataagaatggacaagtaata 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            721 aatgttagtgcacacactggccatttggtgggtagtccactttcagatccttatttgtca 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 gaagagggtatccggttcaggggtttttctatacctgaatgccagaaacttttacccgct 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 gcaagtgctggtgcagagccattgcctgaaggtcttctttggcttcttttaaccggaaag 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gttcctagcaaagagcaagtagatgctctatcagcagatttacgaaaacgtgcttctatc 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 ttttgcactggtgttatggccttacagactcgaagcgaatttcagaaggcatatgagaaa 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cogotygatgactcocttgattatggtggaaatttogcacacatgttgggatttgatago 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             661 cctcagatgcttgagctgatgcgcctttatgtcacaattcacagtgatcatgagggtgga 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       892 AACGICAGIGCICACACAGGICACTIGGIIGCIAGIGCIIIGICAGACCCIIACCICICC 951
                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ctgaagaagataaagaaagaatttggaagtttccagctggggaatatcaatgttgacatg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 gtattgggcggaatgagaggaatgactggtttactttgggagacttcćttactcgaccca 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 712 CAAGTICCACTIGIIGCIGCIIAIGIIIAICGCAGGAIGIACAAGAACGGCAACACATAA 771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           832 TCTGACATGCATGAGCTTATGAAGCTCTATGTCACGATACACAGTGATCATGAAGGTGGT 891
                                                                                                                                                                                                                                                                                                                                                                                      172 TCTTCTGGTCTTGATCTGCGTTCTGAGCTGCAAGAATTGATTCCAGAACAACAACAGGATCGC 231
                                                                                                                                                                                                                                                                                                                                      tectetaacettgaeettegtteagagttacaagaaetgatteetgaacaaggaaega 60
       To identify a cDNA from sugar beet which codes for citrate synthase, a cDNA bank of leaf tissue from sugar beet was prepd. Plaques of this cDNA bank were screened using radioactive DNA probes which comprise a mixture of Solanum tuberosum citrate synthase cDNA (104199) and Nicotian tabacum citrate synthase cDNA (see T04201). One of the clones was sequenced. The nt. sequence is given in 104200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            472 GIGCCATCAAAAGAGCAAGIGGAITCAIIGICICCAGGAAIIGCGAAGICGIGCIACIGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      532 CCCGATCATGTATACAAAACTATTGATGCCTTACCAGTCACAGCTCATCCAATGACTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232 CTAAAGGAAGCTCAAGTCAGAGCATGGAAAGGTTCAATTGGGAAACATGATATG
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                                                                                                                                                                                                                                  Score 726; DB 16; Length 1551;
Pred. No. 0.00e+00;
0; Mismatches 277; Indels 3
                                                                                                                                                                                       458 T;
                                                                                                                                                                                         370 G;
                                                                                                                                                                                                                                     Query Match 41.6%; Score 726; Best Local Similarity 78.5%; Pred. No. 0 Matches 1021; Conservative 0; Mismat
                                                                                                                                                                                         268 C;
Claim 6; Page 57-60; 87pp; English.
                                                                                                                                                                                       455 A;
                                                                                                                                                                                         1551 BP;
                                                                                                                                                                                            Sequence
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                                                                                                                                                                                    1021 cctgatgacccattttttcaattggtgtcaaagttgtatgaagtggtgctcctattcta 1080
                                                                                                                                                                                                                                                                                                          1309 TTGAACTATTATGGTTTAACTGAAGCAAGATATTATACGGTCCTCTTTGGTGTATCAAGA 1368
                                            1072 AAAGACTACGCTTGGAAAACATTGAAAAGTGGCAAGGTTGTCCCTGGTTTCGGACATGGA 1131
                                                                                                                                     Introducing random point mutations into nucleic acods - by prepn of single stranded template, annealing a primer, elongation, misincorporation, completion of molecules and screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mistincipolation of misterials and streening.
Random point mutations were introduced into the alpha fragment of
E.coli beta-galactosidase. The wild type sequence was obtained as a
E.coli beta-galactosidase. The wild type sequence was obtained as a
E.coli beta-galactosidase. The wild type sequence was obtained as a
E.coli beta-galactosidase. The wild type sequence was obtained as a
E.coli beta-galactosidase. The wild type sequence was obtained as a
E.coli beta-galactosidase. The wild type securical caping the molecules which terminate at all
possible nucleotide positions within a specified region. The
variable 3' ends generated in this way are used as primers for reverse transcriptase. Mucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system.
The sequence covers all 176 difft base substitutions, most of which See also PB0575.
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901 aaagattatgtttggaagacactaaacagtggcaaggttgtacctggatttggtctagga
                                                                                             gtattgcggaagacagatccaagatacacatgccaaagagaatttgcgttgaagcacttg
                                                                                                                                                                                                                                   1192 CCTGAAGATCCACTGTTTCAACTGGTTGCAAAACTCTACGAAGTGTT-CCTCCAATTCTT
                                                                                                                                                                                                                                                                                  1081 ttagagettggaaaggtaaagaatecatggeetaatgttgatgeteatagtggagttttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-NoV-1990 (first entry) assess alpha-fragment. Base substituted E.coli beta-galactosidase alpha-fragment; brooli beta galactosidase alpha-fragment; base substitutions; ss. Escherichia coll.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 C; 17 G; 11 T; 108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
WPI; 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.6%; Score 46; DB 1; Length 204; 8.7%; Pred. No. 7.45e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1261 ccaaagagtgtcactatggaatggcttgaaaagttttgtaa 1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1429 CCAAAGAGTGTCACAATGGAGTGGCTTGAGAACCATTGCAA 1469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function=multiple cloning site 187..204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N81164 standard; DNA; 204 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 A;
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03-APR-1987; US-034819.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 BP;
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Matches 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
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94 yrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynvhnhnncnc 153

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Matches
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PARTHER THE FERNING SERVICE OF THE FERNING SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding a de-branching enzyme - for modifying the branching degree of amylopectin starch synthesised in plants

25 Claim 1, Page 64-67, 90pp; English.

26 Claim 1, Page 64-67, 90pp; English.

27 A partial CDNA clone (T31478) codes for a spinach debranching enzyme (DE) (R98371) useful for modifying the branching degree of amylopectin synthesised in plants. It was obtd. by PCR amplification of CDNA (From a spinach leaf CDNA library using probes (T31480-81) based on CF from a spinach leaf CDNA library using probes (T31480-81) based on CF peptides (R98385-86). The clone can be incorporated into a vector and used for prodn. of recombinant DE, or used in the breeding of transgenic plants, transgenic potatoes showed increased be activity properties. Ribozyme or antisense sequences can be used to reduce the DE activity of transgenic plants. The modified starches have clood and industrial applies.

26 Cod and industrial applies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               751 TACAAGAACGCAACACTATACCTAAGGATGACTCACTGGATTATGGTGCAAATTTTGCT 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                        Spinach debranching enzyme cDNA.
Debranching enzyme: R enzyme: spinach: potato; amylopectin; starch;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.6%; Score 46; DB 21; Length 3437
11.9%; Pred. No. 7.45e-08;
trive 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function=multiple cloning site 187..204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virgin I;
                                                                154 ccbnnhvchnvhbnnhrnwayvrhdarrddvh 185
                                                                                           | : ::: :: ::: :::: | 811 CACATGCTTGGTTTCAGTAGCTCTGACATGCA 842
                                                                                                                                                                                 T 6
T31478 standard; cDNA to mRNA; 3437 BP
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22-DEC-1994; DE-447387.
(GENB-) INST GENBIOLOGISCHE FORSCHUNG.
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201..3095
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nes 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-NOV-1990 (first entry)
                                                                                                                                                                                                                                                18-SEP-1996 (first entry)
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30-MAR-1988; 105163.
03-APR-1987; US-034819.
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                                                                                                                                                                                                                                                                                                                        transgenic plant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Emmermann M, Kossr
WPI; 96-309595/31.
                                                                                                                                                                                                                                                                                                                                           Spinacea oleracea.
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                                                                                                                                                                                                                          T31478;
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1090 TITICCAAGCGIAGICITICAAC-IGCICITIGGAAAIGITCICCCCACACICCICIACA 1032
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                                                              Introducing random point mutations into nucleic acods -
by prepn of single stranded template, annealing a primer, elongation,
misincorporation, completion of molecules and screening.
Disclosure, p. English.
                                                                                                                                                                         E.coli beta galactosidase. The wild type sequence was obtained as single stranded template and an oligonucleotide was hybridised to it to generate a popp of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are misincorporated by the amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which See also P89575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
                                                                                                                                                               of
as
to
                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 T; 108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 hyvybbbvynvhnhnncncccbnnhvchnvhbnnhrnwayvrhdarrddvhccv 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1031 ACAGATTTGATCCATAGCAAAACTTCCTGATTGGCTAAACCATGAAGTGGTCCA 978
                                                                                                                                                               Random point mutations were introduced into the alpha fragment
            Lebtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
WPI: 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Survival motor neuron gene, clone T-BCD541.
Survival motor neuron; SMN: spinal muscular atrophy, SMA;
T-BCD541; C-BCD541; amytrophic lateral sclerosis; ALS;
primary lateral sclerosis; PLS; ss.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43; DB 1; I
Pred. No. 1.44e-06;
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/note= "beginning of exon 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note- "beginning of exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note- "beginning of exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 C;
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/note= "beginning
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T28255 standard; cDNA; 1558 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reaton 2.5%;
Local Similarity 13.2%;
hes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 A;
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(SUSO) SUOMEN SOKERI OY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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/label= Exon-8

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EP-711833-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated survival motor neuron gene - used to develop prods. for the diagnosis and treatment of motor neuron diseases claim 1: Fig 3A; 29pp; English.
The SMM gene is a chromosome 5-SMA (Spinal Muscular Atrophy) determining gene. Sequences of clone T-BCD541 and clone C-BCD541 are provided in T28255 and T28259, respectively.
SMN sequences can be used for detecting neuron disorders having symptoms of muscular weakness with or without sensory changes such as amytrophic lateral sclerosis (ALS), SMA, primary lateral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 10; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-001-1996 (first entry)

Human survival motor neuron gene cDNA clone T-BCD541.

Survival motor neuron gene; SMN gene; spinal muscular atrophy; chromosome 5-SMA determining gene; amytrophic lateral sclerosis; primary lateral sclerosis; arthrogryposis multiplex congenita; diagnosis; gene therapy; T-BCD541; ss.
                                                                                                                                                                                                                                                                                                                                                                                                           402 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1558;
                                                                                                                                                                                                                                                                                                                                                                                                           336 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43; DB 22; 1 Pred. No. 1.44e-06;
                                                                                                                                           (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
Melki J, Munnich A;
                                                  /note= "beginning of exon 8"
                                                                                                                                                                                                                                                                                                                                                                                                           283 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 34..918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Exon-7
922..1483
/*tag= i
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/label= Exon-4
661..756
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T18828 standard; cDNA; 1560 BP.
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/label= Exon-5
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/label= Exon-6
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/label= Exon-2
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/label= Exon-3
                                                                                                                                                                                                                                                                                                                                                                                                       537 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.5%;
Best Local Similarity 84.1%;
Matches 53; Conservative
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                   /*tag= i
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                                  /numper=
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                                                                                     24-APR-1996.
19-OCT-1994; 402353.
19-OCT-1994; EP-402353.
                                                                                                                                                                                                                                                                                                                                                                                      sclerosis (PLS), etc.
Sequence 1558 BP;
                                                                                                                                                                              WPI; 96-202055/21.
                                                                                                                                                                                                  P-PSDB; R96991
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                                                                     EP-708178-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T18828;
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Welki J. Munnichs.
Welki J. Solosof.

New isolated survival motor neuron gene - used to develop prods. for the diagnosis and treatment of motor neuron diseases.
Claim 4: Fig 2A; 29pp: English.

The SMN gene is a chromosome 5-SMA (Spinal Muscular Atrophy)
determining gene. Sequences of clone T-BCD541 and clone C-BCD541
are provided in T28255 and T28259, respectively.
SMN sequences can be used for detecting neuron disorders having symptoms of muscular weakness with or without sensory changes such as amytrophic lateral sclerosis (ALS), SMA, primary lateral Sclerosis (PLS), etc.
Scquence 1582 BP; 562 A; 285 C; 335 G; 400 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                  murine equiv. - useful to develop primers and probes for in vitro detection of motor neuron diseases e.g. spinal muscular atrophy claim 1; Fig 3; 47pp; English.
A cDNA sequence (T18828) was detd. for the human survival motor neuron (SMN) gene T-BCD541 (see also T18868). This telomeric gene is responsible for motor neuron diseases of the spinal muscular atrophy (SMA) type. The SMN gene is lacking or truncated in 98% of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atrophy (SWA) type. The SMN gene is lacking or truncated in 98% of SWA patients. The gene was discovered using a complex system of restriction mapping, distinguishing the Erel from the Eren by Southern blot, and determination of the differences between the Erel in SMA patients by genetic and physical mapping. It can be used in gene therapy protocols to correct disorders present in SMA, anthropylosis multiplex congenita patients, to produce large quantities of recombinant SMN protein (see also R94963), and to design probes and primers (118833-65) useful for detecting or
                                                                                                                                                                                                                                                       Human survival motor neuron gene T-BCD541, variant C-BCD541 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    402 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 2.5%; Score 43; DB 22; Length 1560; Local Similarity 84.1%; Pred. No. 1.44e-06; nes 53; Conservative 0; Mismatches 10; Indels 0
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Survival motor neuron; SMN; spinal muscular atrophy, SMA;
T-BCD541; C-BCD541; amytrophic lateral sclerosis; ALS;
primary lateral sclerosis; PLS; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        337 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-APR-1996.
19-0CT-1994; 402353.
10-0CT-1994; EP-402353.
(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
15-WAY-1996.
19-0CT-1995; 402335.
19-CCT-1994; EP-402335.
(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        282 C;
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34..918
/*tag= a
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T28259 standard; cDNA; 1582 BP.
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13-OCT-1996 (first entry)
                                                                                                                                                    Munnich A;
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Sequence 1560 BP;
                                                                                                                                                                               WPI; 96-232098/24.
P-PSDB; R94963.
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A CDNA sequence (T18831) was detd. for the human survival motor neuron (SMN) variant gene C-BCD541. This centromeric gene differs from the SMN telomeric gene cDNA clone T-BCD541 (T18828) by a nucleocides. The C-BCD541 gene is unable to correct in vivo a deficiency of the T-BCD541 gene responsible for motor neuron diseases of the spinal muscular atrophy type. A variation
                                                                                                                                                                                                            Human survival motor neuron variant gene cDNA clone C-BCD541.
Survival motor neuron gene: SNN gene: spinal muscular atrophy:
chromosome 5-SNA determining gene; amytrophic lateral sclerosis;
primary lateral sclerosis; arthrogryposis multiplex congenita;
diagnosis; gene therapy; C-BCD541; ss.
  Score 43; DB 22; Length 1582; Pred. No. 1.44e-06;
                           0; Mismatches 10; Indels
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/note= "base 873 (t) is c is T-BCD541"
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19-0CT-1995, 402335.
19-0CT-1994; EP-402353.
(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
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/label= Exon-2
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/label= Exon-6
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/label= Exon-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Exon-7
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2.5%;
Best Local Similarity 84.1%;
Matches 53; Conservative
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WPI; 96-232098/24
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Human secreted protein; quel 178 clone HETAR54.

Human secreted protein; quel 178 clone HETAR54.

Human; secreted protein; fusion protein; quel therapy; protein therapy;

Human; secreted protein; fusion protein; quel therapy; protein therapy;

dayolatist; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;

developmental abnormality; foetal deficiency; blood; allergy; renal; developmental abnormality; foetal deficiency; blood; allergy; renal; ds:

inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;

cognitive disorder; schlarophrenia; prostate; obesity; osteoclast; thymus;

osteoporosis; arthritis; testis; lung; thyroidtis; thyroid; digestion;
endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                   Ouery Match 2.5%; Score 43; DB 22; Length 1582;
Best Local Similarity 84.1%; Pred. No. 1.44e-06;
Matches 53; Conservative 0; Mismatches 10; Indels 0; Gaps
of sequence within intron 7 of the C-BCD541 genomic sequence results in an alternatively spliced transcript that lacks exon 7 and a truncated SMN protein (R94965) lacking the exon 7-encoded C-terminal region. 562 A; 283 C; 335 G; 402 T;
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US-048884.
US-048893.
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US-048897.
US-048900.
US-048916.
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US-048970.
US-048974.
US-049373.
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18-DEC-1997; US-070923
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05-SEP-1997; U
05-SEP-1997; U
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06-JUN-1997;
06-JUN-1997;
06-JUN-1997;
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05-SEP-1997;
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     888888
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Gaps

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Human secreted protein gene 120 clone HHPTD20.
Human secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue, cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflaumation; ischaemis oshock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Membrane protein(s) BA0306 and BA2303 - useful for, e.g. treatment and prevention of arteriosclerosis and restenosis Claim 16; Page 90-95; 141pp; Japanese.
This sequence encodes the human BA0306 membrane protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                             17-DEC-1998 (first entry)
Human membrane protein BA0306 coding sequence.
Membrane protein; BA0306; BA2303; arteriosclerosis; coronary restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention also relates to the human BA2303 membrane protein. The two membrane proteins are specifically expressed in mammals during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arteriosclerosis and coronary restenosis. The membrane proteins, fragments of them, and antibodies against them are useful in the treatment and prevention of arteriosclerosis and restenosis. Transgenic mice expressing the extracellular region of the membrane proteins are useful as models for studying these disorders.

Sequence 2519 BP; 766 A; 439 C; 809 T;
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                                                 Ouery Match 2.5%; Score 43; DB 56; Length 1848; Best Local Similarity 97.8%; Pred. No. 1.44e-06; Matches 44; Conservative 0; Mismatches 1; Indels
452 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_except= (pos: 1015..1017, aa: Xaa)
/transl_except= (pos: 1492..1494, aa: Xaa)
/transl_except= (pos: 1582..1542, aa: Xaa)
/transl_except= (pos: 1582..1544, aa: Xaa)
/transl_except= (pos: 1609..161, aa: Xaa)
/transl_except= (pos: 1693..1695, aa: Xaa)
/note= "Xaa= unspecified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_except= (pos: 289..291, aa: Xaa)
                                                                                                                                                                                    345 C;
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1..1785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NISB ) JAPAN TOBACCO INC.
Nakamura Y, Tanaka T, Tsukada S;
WPI; 98-481206/41.
                                                                                                                                                                                                                                                                                                                              RESULT 13

LO V54124 standard; DNA; 2519 BP. AC V54124;
DT 17-DEC-1998 (first entry)
DE Human membrane protein BA0306; BA2303, KW Membrane protein; BA0306; BA2303, KW Homorapy; human; Gs.
S Homo sapiens. Location/Qualifie FT Key Liransl_except= (ransl_except= FT CDS Location/Gualifie FT CDS Location Gualifie FT CDS Location Gualifie FT CDS Location Gualifie FT CDS COMPAN TOBACO INC.
DR Membrane protein(s) BA0306 and By PT AND ROCATION Of arteriosclerosis and coronary recommend prevention of arteriosclerosis and coronary recommend of them and prevention of arteriosclerosis and coronary recommend of the conservation of the conservation of arteriosclerosis and coronary recommend managed to sequence extracellula CDS Sequence S519 BP; 766 A; 766 A;
575 A;
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Sequence 1848 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders disorders. Immune diseases, inflammation or blood disorders disorders claim 4; Page 440-441; 772pp; English.

The invention relates to nucleic acid sequences (V84411 to V84633) encoding human secreted proteins (W88534 to W88756). The secreted protein gene sequences are deposited with the ATCC under deposit numbers ATCC 209011, 209080, 209081, 209082, 209087, 209008, 209009, 209010, 209011, 209081, 209081, 209083, 209084, 209085, 209511. Host sequences are used for the recombinant production of the secreted proteins. The polynucleotide and amino acid sequences are useful for are
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New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological
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Brower LA, Carter KC. Dillon PJ, Ebner R, Endress GA, Fan P. Feng P, Ferrie AM, Fischer CL, Florence C, Florence K, Greene JM, Hu J, Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z; WPI; 99-053665/05.
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US-057646.
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US-057776.
US-048876.
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US-048898.
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05-SEP-1997; US-057666.
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PR 05-SEP-1997; US-057760.

PR 05-SEP-1997; US-057761.

PR 05-SEP-1997; US-057761.

PR 05-SEP-1997; US-057774.

PA (UNAA.) HUMAN GENOME SCI INC.

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PI FORTENCE K. Greene JM. HU J. Kyaw H. Laflent DW.

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Epitopes; pollen; food allergy; Fageles; IgE antibodies;
hyposensitisation; ss.
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/note= "epitope for IgE binding"
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Best Local Similarity 89.1%; Pred. No. 2.64e-05;
Matches 41; Conservative 2; Mismatches 3.
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Q22352 standard; DNA; 700 BP.
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11-APR-1991; US-6838.
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PA (BIOM-) BIOMAY BIOTECH PROD.

PI Valenta R. Duchene M. Pettenburger K, Breitenbach M. Kraft D;
Rumpold H Scheiner O;
BR WPI: 92-096895/12.

DR P-PSDB: R22261.

PT Allergens - for treatment and diagnosis of pollen or food
PT allergy, and for purificn. of Pl4 allergens
Claim 2; Fig 4; 68pp; English.

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Search completed: Sat Oct 23 22:08:20 1999 Job time : 401 secs.

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US-08-702-718-5.rni

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                                                                                                                  Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd
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n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch\_nn Sat Oct 23 22:08:38 1999; MasPar time 126.78 Seconds 1191.820 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-702-718-5 (1-1747) from US08702718.seq 1747 Description: Perfect Score: N.A. Sequence:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 Nmatch STD: 165359 seqs, 43243793 bases x 2 Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

n-issued
1:5A\_COMB 2:5B\_COMB 3:5C\_COMB 4:PCT9\_COMB 5:backfiles1

Statistics:

Mean 9.068; Variance 5.849; scale 1.550

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Query Match Length DB	DB	DI	Description	Pred. No.
7	48	2.7	7218	7	US-08-232-	Sequence 14, Applicati	7.31e-13
0	47	2.7	7218	(4)	US-08-232-	Sequence 14, Applicati	1 2.63e-12
e	40	2.3	700	٦	US-07-846-	1, A	0 1.72e-08
4	40	2.3	700	-	US-08-469-	Sequence 1, Applicatio	1.72e-08
S	40	2.3	1046	Н	US-08-361-	Sequence 4, Applicatio	0 1.72e-08
9	40	2.3	1046	m	US-08-484-	Sequence 4, Applicatio	3 1.72e-08
7	40	2.3	1080	<b>→</b>	US-08-225-	-	0 1.72e-08
80	41	2.3	3933	4	PCT-US95-0	-1	5.00e-09
6	41	2.3	3933	Н	US-08-199-	٦,	5.00e-09
10	40	2.3	7859	Н	US-07-854-	Sequence 4, Applicatio	J.72e-08
11	40	2.3	7859	٣	US-08-450-	Sequence 15, Applicati	1.72e-08
12	38	2.2	84	m	US-08-738-	Sequence 3, Applicatio	0 1.98e-07
13	38	2.2	84	m	US-08-664-	Sequence 3, Applicatio	3 1.98e-07
14	38	2.2	85	٦	US-08-120-	97,	1.98e-07
15	38	2.2	85	m	US-08-478-	Sequence 97, Applicati	1.98e-07
c 16	38	2.5	350	П	US-08-171-	Sequence 14, Applicati	i 1.98e-07
17	39	2.5	836	m	-869-80-SD	Sequence 7, Applicatio	5.85e-08
18	39	2.2	880	3	US-08-616-	,	5.85e-08
19	39	2.2	1454	٣	US-08-713-	Sequence 7, Applicatio	5.85e-08
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## ALIGNMENTS

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STREET: 1800 Diagonal Road, Suite 500
STREET: 1800 Diagonal Road, Suite 500
STATE: VA
COUNTRY: USA
ZID: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
                                              Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Patent No. 567036
Patent No. 567036
Patent No. 567036
PAPLICANT: DORNER, F.
APPLICANT: SCHETFLINGER, F.
APPLICANT: FATANER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
TELEFRAM: (703)883-4109
TELEEX: 899140
T. 1
US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP.
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AGG-1991 ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
PRICA PAPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
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Similarity 3.6%; Pred. No. 7.31e-13;
7, Conservative 113; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: BOHEFLINGER, F. APPLICANT: FALKENER, F. G. TITLE OF INVENTION: RECOMBINANT FOWLDOX VIRUS NUMBER OF SEQUENCES: 52
COPRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
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US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
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ATTORNEY/AGENT INFORMATION:
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LENGTH: 7218 base pairs
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHAPACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
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Gaps 0;
                                                                                                                                                                      494 TCCACTTGCTCTTTTGATGGCACCTTTCCTGTTAAAAGAAGCCAGAGAAGACCTTCAGGC 435
                                                                                                                                                                                                                                                           374 CCCCGAAAGCGAATTCCTTCATCGGGGTCAAGTAATGAGGTTTCCCACAGTAATGCTGTC 315
                                                                                                                                                                                                                                                                                                                                                                            314 ATTCCTCTCATTCCACCAAGAACCATATCAACTGTGATGTTTCCCAATTGAACCTTTCCA 255
                                                                                                                                                                                                                                                                                                                                                                                                                        254 IGCICIGACITCITITAGGCGAICCIGITGITCIGGAAICAAITCITGCAGCIC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Valenta, Rudolf
APPLICANT: Valenta, Michael
APPLICANT: Duchene, Michael
APPLICANT: Pettenburger, Karin
APPLICANT: Kraft, Dietrich
APPLICANT: Rumpold, Helmut
APPLICANT: Scheiner, Otto
TITLE OF INVENTION: Birch Pollen Allergen P14 for Diagnosis
TITLE OF INVENTION: and Therapy of Allergic Diseases
                                                                                                                                           0,
                                                                     CLONE: pTZgpt-F1s
SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
                                                                                                                Length 7218;
                                                                                                             Ouery Match 2.7%; Score 47; DB 2; Length 7218;
Best Local Similarity 4.3%; Pred. No. 2.63e-12;
Matches 13; Conservative 160; Mismatches 126, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Pelease #1.0, Version #1 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-846-992-1 STANDARD; DNA; UNC; 700 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/353,844
FILING DATE: 18-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/07/846,992
FILING DATE: 19920606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/07846992
Sequence 1, Application US/07846992
Patent No. 5583046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Jones III, Harry C
REGISTRATION NUMBER: 20,280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
LENGIH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
COUMTY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
               TYPE: nucleic acid
STRANDEDNESS: single
                                     IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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Gaps
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APPLICANT: Van Emmelo, John
APPLICANT: De Oliveria, Dulce E.
APPLICANT: De Souza, Maria-Helena
APPLICANT: Van Montagu, Marc
TILLE OF INVENTION: PLANTS WITH MODIFIED FLOWERS, SEEDS OR
TILLE OF INVENTION: EMBRYOS
                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                      LIBRARY: POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN SEQUENCE 700 BP; 212 A; 127 C; 181 G; 180 T; 0 OTHER.
                                                                                                                                                                                                                                                                                       Length 700;
                                                                                                                                                                                                                                                                                                                         1; Indels
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UCUSAMBLE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,467B
FILING DATE: 22-DEC-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,492
FILING DATE: 04-APR-1991
PRIOR APPLICATION NUMBER: WO PCT/EP90/01275
FILING DATE: 01-ANG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 89 402 224.3
FILING DATE: 01-ANG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 89 402 224.3
FILING DATE: 04-ANG-1999
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: P.O. Box 1404
CIIY: Alexandria
                                                                                                                                                                                                                                                                                       Score 40; DB 1; Le
Pred. No. 1.72e-08;
0; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 5
US-08-361-467B-4 STANDARD; DNA; UNC; 1046 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Schulman, Robert M.
REGISTRATION NUMBER: 31,196
REFERNCE/DOCKET NUMBER: 010830-027
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08361467B Sequence 4, Application US/08361467B Patent No. 5633441 GENERAL INFORMATION:
APPLICANT: De Greef, Willy
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                       ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Betula verrucosa
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Virginia
COUNTRY: United States
ZIP: 22313-140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                LENGTH: 700 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                        Query Match 2.3%;
Best Local Similarity 97.6%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DO
                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                 HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                Gaps
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APPLICANT: Pettenburger, Karin
APPLICANT: Pettenburger, Karin
APPLICANT: Raft, Dietrich
APPLICANT: Rumpold, Helmut
APPLICANT: Schoiner, Otto
TITLE OF INVENTION: Birch Pollen Allergen P14 for Diagnosis
TITLE OF INVENTION: and Therapy of Allergic Diseases
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                ;
0
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Pred. No. 1.72e-08;
                                                                                                                                                                                                                                                                                                                                                             1; Indels
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CARPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FC Compatible
COMPUTER: TBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/469,555
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/846,992
FILING DATE: 06-JUN-1992
APPLICATION NUMBER: US/07/846,992
FILING DATE: 18-WAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                            ORGANISM: Betula verrucosa
IMMEDIATE SOURCE:
SEQUENCE 700 BP; 212 A; 127 C; 181 G; 180 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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US-08-469-555-1 STANDARD; DNA; UNC; 700 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6530-011
       REFERENCE/DOCKET NUMBER: 6530-011
                                  TELEPHONE: (212) 790-9001
TELERA: (212) 869-8864/9741
TELEA: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH 700 base pairs
TYPE: NUCLEIC AND STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08469555
Sequence 1, Application US/08469555
Patent No. 5648242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Jones III, Harry C
REGISTRATION NUMBER: 20,280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 65
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Valenta, Rudolf
                                                                                                                                                                                                                                                                                                                              Query Match 2.3%;
Best Local Similarity 97.6%;
Matches 41; Conservative
                                                                                                                                                                                              CDNA
                                                                                                                                                                         linear
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                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: CDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York
                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                           HYPOTHETICAL: NAMI - SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: 1
STATE:
                                                                                                                                                                                                                                                                                                                                Query Match
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0; Gabs
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TITLE OF INVENTION: PLANTS WITH MODIFIED FLOWERS, SEEDS OR
TITLE OF INVENTION: EMBRYOS
                                                                                                                                             Score 40; DB 1; Length lu4o;
Pred. No. 1.72e-08;
....matches 7; Indels
                                                                                                                               SEQUENCE 1046 BP; 360 A; 254 C; 166 G; 266 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 04-APR-1991
PRIOR APPLICATION DATA:
PPLICATION NUMBER: WO PCT/EP90/01275
FILING DATE: 01-AUG-1990
PRIOR APPLICATION DATA:
PRIOR APPLICATION WUMBER: EP 89 402 224.3
FILING DATE: 04-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                         7T 6
US-08-484-332C-4 STANDARD; DNA; UNC; 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Schulman, Robert M.
REGISTATION NUMBER: 31,196
PEFERNCE/POCKET NUMBEP: 010830-093
TELECOMMUNICATION INFORMATION:
TELEFNONE: (703) 836-6620
TELEFAX: (703) 836-52021
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/484,332C
FILING DATE: 7-JUNE-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/681,492 FILING DATE: 04-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/361,467 FILING DATE: 22-DEC-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                      Van Emmelo, John
De Oliveria, Dulce E.
De Souza, Maria-Helena
                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08484332C Sequence 4, Application US/08484332C Patent No. 5767374
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1046 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: De Greef, Willy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                        Query Match 2.3%;
Best Local Similarity 87.0%;
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Alexandria
                                                                                                    IMMEDIATE SOURCE:
CLONE: 3C9
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
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2.3%; Score 40; DB 1; Length 1080;
Best Local Similarity 90.0%; Pred. No. 1.72e-08;
Matches 45; Conservative 0; Mismatches 5; Indels
                                                                                                                        Length 1046;
                                                                                                                                               7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: cDNA
SEQUENCE 1080 BP; 229 A; 281 C; 359 G; 211 T; 0 OTHER.
                                                                                                SEQUENCE 1046 BP; 360 A; 254 C; 166 G; 266 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                 APPLICANT: YU, ET AL.
TITLE OF INVENTION: Superoxide Dismutase-4
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART 6 OLSTEIN
                                                                                                                     / Match 2.3%; Score 40; DB 3; L
Local Similarity 87.0%; Pred. No. 1.72e-08;
nes 47; Conservative 0; Mismatches 7
                                                                                                                                                                                                                                               US-08-225-757B-1 STANDARD; DNA; UNC; 1080 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET VUMBER: 325800-106
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-11700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,757B
FILING DATE: 11 APR-94
                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08225757B Sequence 1, Application US/08225757B Patent No. 5506133 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                           6 BECKER FARM ROAD
                                            TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
IMMEDIATE SOURCE:
CLONE: 3C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: FERRARO, GREGORY D. REGISTRATION NUMBER: 36,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1080 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
SEQUENCE CHARACTERISTICS:
LENGTH: 1046 base pairs
                      nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC:
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 6 BECKER FAR
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LINEAR
                       TYPE: nucleic STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                       Query Match
                                                                                                                                                                                                                                                             XXXXXX
                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 126..179
SEQUENCE 3933 BP; 938 A; 1062 C; 1074 G; 859 T; 0 OTHER.
                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02044
FILING DATE: herewith
                                                                                         TITLE OF INVENTION: Novel integrin alpha subunit NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield and Sacks, P.C. STREET: 600 Atlantic Avenue
T 8
PCT-US95-02044-1 STANDARD; DNA; UNC; 3933 BP.
                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/199,776
FILING DATE: 18 February 1994
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: 86,637
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
INFORMATION FOR SEQ. DI NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3333 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-199-776-1 STANDARD; DNA; UNC; 3933 BP. xxxxxxx
                                            Sequence 1, Application PC/TUS9502044 Sequence 1, Application PC/TUS9502044 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
CELL TYPE: mucosal lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mat_peptide
180..3659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: sig_peptide
LOCATION: 126..179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
126..3662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                              ADDRECT BOUNT TAY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
ORGANISM: HOM
                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO
                                                                                                                                                                            COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
                                                                                 APPLICANT:
                       XXXXXX
 RESULT
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APPLICANT: Brenner, Michael B.
APPLICANT: Parker, Christina M.
ITLLE OF INVENTION: No. 5594120el integrin alpha subunit
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.3%; Score 41; DB 1; Length 3933
Best Local Similarity 90.2%; Pred. No. 5.00e-09;
Matches 46; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: sig_peptide
LOCATION: 126..179
SEQUENCE 3933 BP; 938 A; 1062 C; 1074 G; 859 T; 0 OTHER.
                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,776
                                                                                                                ADDRESSEE: Wolf, Greenfield and Sacks, P.C. STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .T 10
US-07-854-596B-4 STANDARD; DNA; UNC; 7859 BP.
                                                                                                                                                                                                                                                                                                                              B0801/7020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/07854596B Sequence 4, Application US/07854596B Patent No. 5434073 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/COCKET NUMBER: B0801
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEPHONE: 617-720-3501
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3933 base pairs
        Sequence 1, Application US/08199776
Sequence 1, Application US/08199776
Patent No. 5594120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
CELL TYPE: mucosal lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: CDNA tO MRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dawson, Keith M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
180..3659
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126..3662
                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                       Boston
                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                              COUNTRY: US
ZIP: 02210
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                       CITY: B
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0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 2.3%; Score 40; DB 1; Length 7859; Local Similarity 81.3%; Pred. No. 1.72e-08; es 52; Conservative 0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Stem Cell Inhibiting Proteins NUMBER OF SEQUENCES: 178
NUMBER OF SEQUENCES: 178
ADDRESSEE: HALE and DORR
STREET: 60 State Street
                                                                                                       COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic acids
CORRESPONDENCE ADDRESS:
                                                           ADDRESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JT 11
US-08-450-905B-15 STANDARD; DNA; UNC; 7859 BP.
                                                                                                                                                                                                       APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-JUN-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15, Application US/08450905B Sequence 15, Application US/08450905B Patent No. 5856301 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               92,337
                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: MCDOINE], John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,33
TELEPHONE: 312-715-1000
TELEFAN: 312-715-1204
TELEX: 910-21-5317
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 7859 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 1..7859
                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: circular MOLECULE TYPE: CDNA
                                                                       STREET: Ten Sc
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 60 StacITY: Boston STATE: MAZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5638 AAAA 5641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1744 AAAA 1747
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                                                                                              STATE:
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0; Gaps
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APPLICANT: MCCO9, John
APPLICANT: MCCO9, John
APPLICANT: LaVallie, Edward
APPLICANT: Rate, Lisa
APPLICANT: Rete, Lisa
APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 7859 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA
SEQUENCE 7859 BP; 2317 A; 1656 C; 1600 G; 2286 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 7859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,905B
FILING DATE: 26-MAR.1995
PRIOR APPLICATION NUMBER: 07/982,759
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9127319.3
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: GB 9221587.0
FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAMM: BAKER, HOLLE L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 102.378.120DV-2
TELECOMMUNICATION INFORMATION:
TELEGRATION FOR SEO ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 7859 DASS PAILS
TWIND: NOTE: ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 3; Losted. No. 1.72e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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US-08-738-367-3 STANDARD; DNA; UNC; 84 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Genetics Institute, Inc. 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08738367
Sequence 3, Application US/08738367
Patent No. 582768
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 8/ cm.
CITY: Cambridge
STATE: Massachusetts
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Best Local Similarity 81.3%;
Matches 52; Conservative
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LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Evans, Cheryl
APPLICANT: Evans, Cheryl
APPLICANT: Bowman, Michael
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 37
CORRESCONDENCE ADDRESS:
                                                                                                                                                                                                        ô
                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                      Length 84;
                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,367
FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                          Score 38; DB 3; Lour Pred. No. 1.98e-07; 0; Mismatches 3
                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE 84 BP; 76 A; 0 C; 0 G; 7 T; 1 OTHER.
                                                                                                                                                                                                                                                                        .T 13
US-08-664-596B-3 STANDARD; DNA; UNC; 84 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/664,596B
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08664596B Sequence 3, Application US/08664596B Patent No. 5807703 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 848-824
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                           ATTORREY AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPAN: (617) 498-824
TELEPAN: (617) 876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TENTE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                              Jacobs, Kenneth
McCoy, John
LaVallie, Edward
                                                                                                                                                                                     Query Match 2.2%;
Best Local Similarity 93.0%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02140
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                           XXXXXX
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APPLICANT: KING, PETER H.
APPLICANT: LEVINE, TODD
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE
TITLE OF INVENTION: RECOGNITION, BINDING AND EXPRESSION OF RIBONUCLEIC ACIDS
TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION
UNMBER OF INVENTION: 101
CORRESPONDENCE: 101
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
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STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.2%; Score 38; DB 1; Length 85; Best Local Similarity 88.0%; Pred. No. 1.98e-07; Matches 44; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/120,827
FILING DATE: 15-SEP-193
CLLASSIFICATION: US-S25495man F.
REGISTRATION: No. 5525495man F.
NAME: Oblon, No. 5525495man F.
REGISTRATION NUMBER: 24 618
REFERENCE/DOCKET NUMBER: 714-158-0 CIP
TELEFAX: (703)413-220
                                                                                                                                                                                    3; Indels
                                                                                                                   Score 38; DB 3; Length 84;
Pred. No. 1.98e-07;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown MOLECULE TYPE: CDNA SEQUENCE 85 BP; 50 A; 5 C; 10 G; 20 T; 0 OTHER.
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE 84 BP; 76 A; 0 C; 0 G; 7 T; 1 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                          JT 14
US-08-120-827-97 STANDARD; DNA; UNC; 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 97, Application US/08120827
Sequence 97, Application US/08120827
Patent No. 5525495
GENERAL INFORMATION:
APPLICANT: KEENE, JACK D.
APPLICANT: KING, PETER H.
                                                                                                                         Query Match 2.2%;
Best Local Similarity 93.0%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U.S.A.
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Sequence 97, Application US/08478675
Sequence 97, Application US/08478675
Patent No. 5773246
GENERAL INFORMATION:
PAPLICANT: KEDNE, JACK D.
APPLICANT: KING, PETER H.
APPLICANT: LEVINE, TODD
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE
TITLE OF INVENTION: PECOGNITION, BINDING AND EXPRESSION OF PIBONUCLET: ACIDS
TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGILATION
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                      ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.2%; Score 38; DB 3; Length 85; Best Local Similarity 88.0%; Pred. No. 1.98e-07; Matches 44; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,675
FILING DATE: 07-JUN-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/120,827
ATONEY/AGENT INFORMATION:
ANAMERICATION NUMBER: US 08/120,827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: CDNA
SEQUENCE 85 BP; 50 A; 5 C; 10 G; 20 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Oblon, No. 5773246man F.
PEGISTRATION NUMBER 24,618
REFERENCE/DOCKET NUMBER: 714-158-0 CIP
TELECOMMINICATION INFORMATION:
TELEPHONE: (703)413-3000
   JT 15
US-08-478-675-97 STANDARD; DNA; UNC; 85 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: Sat Oct 23 22:10:49 1999 Job time: 131 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 85 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                    STREET: 1755 Jeffe
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
                                       XXXXXX
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	(ME)
Release 3. Copyright Di	3.1A John F. Collins, Biocomputing Research Unit. htt (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd
MPsrch_nn n.a.	- n.a. database search, using Smith-Waterman algorithm
Tabular output n	not generated.
Title: Description: Perfect Score: N.A. Sequence: Comp:	>US-08-702-718-5 (1-1747) from US08702718.seq 1747 1 GCTCTTGGGATCTATTTCCTAAAAAAAAAAAAAA
Scoring table:	TABLE default Gap 6
Nmatch STD:	Dbase 0; Query 0
Searched:	2883791 seqs, 1171580779 bases x 2
Post-processing:	Minimum Match 0% Listing first 45 summaries
Database:	t58 est10
Database:	b:em_esty /:em_gss1 genbank-est111 genbank-est111 13:gb_est12 12:gb_est13 13:gb_est14 14:gb_est15 15:gb_est16 16:gb_est17 17:gb_est14 14:gb_est15 15:gb_est16 16:gb_est17 17:gb_est12 18:gb_est19 19:gb_est2 20:gb_est20 21:gb_est21 22:gb_est22 23:gb_est23 24:gb_est24 25:gb_est25 26:gb_est26 27:gb_est27 28:gb_est28 29:gb_est25 36:gb_est3 31:gb_est4 32:gb_est5 33:gb_est6 34:gb_est29 30:gb_est3 31:gb_est4 32:gb_est5 33:gb_est6 34:gb_est7 35:gb_est8 36:gb_est6 32:gb_est5 33:gb_est6
Statistics:	12.404; Variance 6.933; scale 1.789

	s the number of results predicted by chance to have a	score greater than or equal to the score of the result being printed,	and is derived by analysis of the total score distribution.	SUMMARIES		: 5
	. NO. 1S the hu	greater than	is derived by a		æ	
1	Pred.	score	andi			4

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Result No.	ult No.	Score	!	% Query Match Length DB	B ID	Description	Pred. No.
	7	247	14.1			L30-386T3 Ice plant La	9.20e-150
	7	210	12.0		7 T44185	7448 Lambda-FRL2 Arabi	
	m	190	10.9	417 24		_	6.97e-108
	4	187	10.7		1 R90544		1.07e-105
	Ŋ	187	10.7			~	1.07e-105
υ	9	174	10.0			EST220465 Normalized r	2.94e-96
	7	172	8.6		14		8.24e-95
	ω	163	6.6		α,	_	2.50e-88
	σ	155	8.9		2 AI054878	coau0002G14 Cotton Bol	1.48e-82
	10	152	8.7	307 1	0 AA231705		2.10e-80

11 12 13 14 15 16 17 17 19 19 20 21 22 23 23 23 24 44 44 44 44 44 44 44 44 44	143 8.2 522 10 AA237580 mx11d01.rl Soares mous 5.69e-74 7.7 501 11 AA313713 BTT185581 COLOn carcin 1.42e-67 122 12 13 12.2 13 BTT185581 COLOn carcin 1.42e-65 12.2 13 AA298291 vh38911.rl Barstead mo 2.18e-58 112 6.9 473 14 AA498291 vh38911.rl Barstead mo 3.27e-54 114 6.5 466 36 AA112941 zn59b06.rl Stratagene 1.63e-53 115 6.6 3 AA112941 zn59b06.rl Stratagene 1.63e-53 110 6.3 503 9 AA177425 mt59b06.rl Soares mous 9.83e-51 110 6.3 503 9 AA177425 mt59b01.rl Soares mous 9.83e-51 110 6.3 503 9 AA177425 mt59b01.rl Soares mous 9.83e-51 110 6.3 503 9 AA177425 mt59b01.rl Soares mous 9.83e-51 110 6.3 37 14 C38571 C28571 Rice callus cDN 1.18e-48 110 2.8 489 23 A1168709 occ6601.rl Soares mous 9.83e-51 110 5.8 566 15 AA58724 nnc1f09.rl Soares mous 9.83e-51 110 5.8 566 15 AA58724 nnc1f09.rl Soares mous 9.83e-51 110 5.8 566 15 AA32355 Nouse early bla 1.60e-44 110 5.7 506 26 AA901227 UI-R-A1-dp q-06-0-UI.S 7.77e-44 110 752 21 30 AA196933 26 AB908.rl Stratagene 4.22e-41 110 752 23 AA177950 200900.rl Stratagene 4.53e-36 37 AA177950 200900.rl Stratagene 7.52e-36 AA196934 24550 Mount pt 2.35e-36 37 AA196934 24550 Mount pt 2.35e-36 37 AA196934 24550 Mount pt 2.75e-36 26 26 26 26 26 26 26 26 26 26 26 26 26	AA896953 471 bp mRNA L30-36673 Lee plant Lambda Un Nacl treatment Mesembryanthem similar to Citrate synthase, sequence. AA8969533 9303346 EST. common ice plant. Mesembryanthemum crystallinum Eukaryota; Viridiplantae; Str euphyllophytes; Spermatophyta Caryophyllophytes; Spermatophyta Caryophyllophytes; Spermatophyta Caryophyllophytes; Garyophyllale Caryophyllophytes; Spermatophyta Caryophyllophytes; Spermatophyta Caryophyllophytes; Spermatophyta Caryophyllophytes; Spermatophyta Caryophyllophytes; Spermatophyta Caryophyllophytes; Spermatophyta Caryophyllophytes; Sperman JC On Jan 19, 1998 this sequence Contact: Cushman JC Department of Biochemistry an On Jan 19, 1998 this sequence Contact: Cushman JC Department of Biochemistry an Oklahoma State University 350 Noble Research Center, St Fax: 405-744-7799 Email: jcushman@biochem.oksta PCR PRIMERS FORWARD: T3 Plate: L30-4 row: H column: Seq primer: T3
		RESULT LOCUS DEFINITION ACCESSION NID VERSION VERYWORDS SOURCE ORGANISM TITLE JOURNAL COMMENT

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1 (bases 1 to 502)
Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C. Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones 95148729
                                                                                           /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1093 TTGAAAAGTGGCAAGGTTGTCCCTGGTTTCGGACATGGAGTTCTGCGCAAGACTGATCCA 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1153 AGATACACATGCCAGAGAGAGTTCGCTTTGAAGCATTTGCCTGAAGATCCACTGTTTCAA 1212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 TTAAAAAGTGGCAAGGTTGTACCTGGATATGGCCATGGAGTTCTGCGCAAGACGGATCCA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303 CTGGTTTCGAAGCTGTATGAATGGTGCCTCCAATTCTGACAGAGCTTGGGAAGGTAAAGA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCUS T44185 502 bp mRNA EST 07-JAN-1998
DEFINITION 7448 Lambda-PRL2 Arabidopsis thaliana cDNA clone 123C9T7, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 TTGGCTGGCCCACTTCATGGATTAGCCAATCAGGAAGTGTTGCTGTGGATCAAGTCAGTT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 AGATACTCTTGCCAGAGGGACTTTGCCCTTAAGCACTTACCTAATGATCCACTATTTCAA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                363 ACCATGGCCGAATGTTGATGCCCACAGTGGGTGTATTGCTGAACTACTATGGTTTGACAA 422
                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CATTIGGIGGIAGCGCACTITCAGATCCTIACCTITCATITGCAGCTGCACTGAATGGG 62
                                                                                                                                                                                                                                                                                                                                                                                              4; Gaps
                                                                                                                                    db_xref="taxon:3544"
/dclone="Laxon:3544"
/clone="Laxon:386"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 30 hours NaCl treatment"
/tissue_type="Leaf, 30 h 0.4M NaCl"
/tissue_type="Leaf, 30 h 0.4M NaCl"
/essue_type="Six we 127 t
7 52 9 127 t
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                                                                                                                                                                                                                                                                                                                                                Score 247; DB 20; Length 471; Pred. No. 9.20e-150;
                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 83; Indels
                                                                     /organism="Mesembryanthemum crystallinum"
High quality sequence stop: 320.
Location/Qualifiers
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Arabidopsis thaliana
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Best Local Similarity 80.3%;
Matches 354; Conservative
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/octail and columnia zip-Lox; Site_1: Sal; Site_2: Not: lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 quantities of 6 4 pools of mRNA. The mRNA sources were 1) 7 quantities of 6 4 pools of mRNA sources were 1) 7 quown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dr primed CDNA. [Ab_xref="faxon:3702"]
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euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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                                                                                  MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg.,E.
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DEFINITION C96653 Rice callus Oryza sativa cDNA clone C10531_5A, mRNA
On Jan 7, 1998 this sequence version replaced gi:948518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 210; DB 17; Length 502;
Pred. No. 1.67e-122;
0; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                       /organism="Arabidopsis thaliana"
/strain="var columbia"
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/clone_lib="Lambda-PRL2"
90 c 118 g 149
                                                                                                                                                                                               Tel: 517.353-0854
Fax: 517-353-9168
Email: 22313tcn@lbm.cl.msu.edu
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                                                          Contact: Thomas Newman
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Best Local Similarity 79.1%;
Matches 284; Conservative
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Poaceae; Oryza.

MEDLINE

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Score 187; DB 31; I
Pred. No. 1.07e-105;
0; Mismatches 67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Lambda-PRL2"
90 c 113 q 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="var columbia"
                                                                                                                                                                                                                                                                                                                                                      Tel: 577-353-0854
Fax: 517-353-9168
Email: 22313ten@ibm.cl.msu.edu
Seq primer: 17 dye primer.
Location/Qualifiers
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                                                                                                                                                                                                                                                                 Contact: Thomas Newman
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1 Similarity 79.3%;
265; Conservative
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Best Local 3
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                                                                                                                                                                                                                                                                                                                                                  /strain="cultivar Nipponbare, sub_species Japonica"
/note="Vector: pBluescript II SX+; Site_1: Sall; Site_2:
Not1: cDNA prepared from rice callus mRNAs by using
oligo(dT) as a primer and ligating to the Sall-NotI site
of pBluescript II SK+ phagemid. "
/db_xref="taxon:4530"
/map="ll"
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16899 Lambda-PRL2 Arabidopsis thaliana cDNA clone 189D15T7, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 ITAGCIGGACCATIGCACGGCCIGGCIAAICAGGAAGIGCIGIIGIGGAICAAAICIGIA 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 417;
1 (bases 1 to 417)
Sasaki,T. and Minobe,Y.
Rice cDNA from callus
Unpublished (1994)
On Aug 21, 1998 this sequence version replaced.
                                                                                                              Contact: Takuji Sasaki
National Institute of Agrobiological Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 190; DB 24; Pred. No. 6.97e-108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="C10531_5A"
/clone_lib="Rice callus"
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                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa"
                                                                                                                                                                                                                                                           Email: tsasaki@abr.affrc.go.jp
                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                 Rice Genome Research Program 2-1-2 Kannondai, Tsukuba
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Matches 306; Conservative
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R90544.1 GI:958084
                                                                                                                                                                                                   Japan 305
Tel: 0298-38-7441
Fax: 0298-38-7468
                                                                                                                                                                                                                                                                                                                 .417
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/note-"vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a CDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and sliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA.

/db.xref="taxon:3702"
Arabidopsis thaliana
Eukaryota, Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Rosidae; Capparales; Brasslaceae; Arabidopsis.

1 (bases 1 to 478)
Nowman,T., deBruijn,F.J., Green,F., Keegstra,K., Kende,H.,
McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M.,
Retzel,E. and Somerville,C.
Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.
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A1176862.1 GI:3727500
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Best Local Similarity 67.0%;
Matches 370; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1998)
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                    AU002699 Bombyx mori p50(Daizo) Bombyx mori cDNA clone n0357, mRNA
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  15-JAN-1999
                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Petryota; Lepidoptera; Bombycoidea; Bombycidae; Bombyx. 1 (bases 1 to 620)
Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S. Establishment of cDNA database of Bombyx mori on Unpublished (1999) on Sep 1, 1995 this sequence version replaced.
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141 c 146 g 171 t
                                                                                                                                                                                                                                                                                                                                                             Contact: Mita K
Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmita@uexs64.nirs.go.jp
PROJECT = 'CREST project by JST'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Bombyx mori"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="p50(Daizo)"
/db_xref="taxon:7091"
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                                                                                                         AU002699.1 GI:4159092
620 bp
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Best Local Similarity 67.1%;
Matches 396; Conservative
                                                                                                                                                   domestic silkworm.
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                                            sequence.
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All76862 676 bp mRNA EST 20-JAN-1999
S721220465 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
ROYBX80 3' end, mRNA sequence.
All76862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1434 CTTTGGCCTCTCTAGTGGCAATCCAAGAGCTCGGTCCCAAATTAGCTGAGAGCAAATGCC 1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1374 AAGAGCTCTTGATACACCAAAGAGGACCGTATAATATCTTGCTTCAGTTAAACCATAATA 1315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1256 TTCTGTAAGAATTGGAGGAACACT-TCGTAGAGTTTTGCAACCAGTTGAAACAGTGGATC 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1137 CAGAACTCCATGTCCGAAACCAGGGACAACCTTGCCACTTTTCAATGTTTTCCAAGCGTA 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1314 GTTCAACAACACCACTGTGGGCATCAACATTTGGCCAAGGGTT--TAACTTTGCCAAG 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 CTGGAGCAGCACCCCACTGTGAGCATCTACGTTGGGCCAGGGGTTCTTAGCCTTTCCTTG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303 CTCTAAGAGGATATTGGGCACAATCTTGTACAGCTGAGCAACCAGCTTAAACATGGGATC 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363 CTTGGGCAGATGTTTCAGAGCAAACTCTCGCTGACAGGAATATCGTGGATCAGTCTTCCT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423 TAGGACTGCATGACCATATCCTGGGACAACCCGTCCCGAGTTGAGTGTGTTTCCAGATGTA 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: ovary; Vector: p1713Pac; Site_1: ECORI; Site_2: Not1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 CTIGGGCCTTTCTAGAGGGAAGCCTAGGGCTCTGCTCCAGATAAGCTGGGCCAACACACC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 CAGTGCCCTCGACACTCCGAACAGGACTGTGTAGTAATTCATCTCCGTCATGCCATAGTA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 174; DB 23; Length 676;
Pred. No. 2.94e-96;
0; Mismatches 179; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 676)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
Kerlavage, A.R. and Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Jan 19, 1998 this sequence version replaced gi:2152042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Normalized rat ovary, Bento Soares"
188 c 150 g 181 t 1 others
The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA Tel: (301)-838-3529 Fax: (301)-838-0208 Email: nhlee@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref-"ATCC (inhost):2031570"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus sp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10118"
/clone="ROVBX80"
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Contact Terminal Term
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
Rosidae; Capparales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 527)
Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H.,
McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R90561 527 bp mRNA EST 30-DEC-1997
16916 Lambda-PRL2 Arabidopsis thaliana cDNA clone 18943T7, mRNA
                                                                          1077 GICTITICAACTGCTCTTTGGAAATGTTCTCCCCACACCTCTTACAACAGATTTGATCCA 1018
                                                                                                                                                                  543 GACAAGCACCTCCTGGTTTGCTAGTCCATGCAGAGGCCCTGCCAGCCCATTCATAGCTGC 602
                                                                                                                                                                                                          603 IGCANAGGACAGGIAAGGGICIGAAAGGGCGCIGCCCACCAAGIGGCTIGIGIGGGCACT 662
                                                                                                                                                                                                                                                                                                                                                                                 483 GICTCGTAACTICTCATCIGACACGICTIIGCCGACTICCTICTGIAGCIGCGICAGCCA 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       results from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg.,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Apr 14, 1993 this sequence version replaced gi:693674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Retzel, E. and Somerville, C. Genes galore: a summary of methods for accessing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Arabidopsis thaliana"
/strain="var columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /map="873F09; 1q21.3-1q23.2; 9"
/clone="189H3T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 t
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106 c 122 q 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oligo dT primed cDNA./db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: T7 dye primer.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 9.8%;
Best Local Similarity 76.7%;
Matches 247; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   663 TACATIGCCACC 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  897 GACGITACCACC 886
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MEDLINE
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KEYWORDS
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cloned into the Not1/Sall sites of a pSPORT vector (Life Technologies). Two different size selections: B1 (larger
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Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="B6D2 F1/J"
/note="Organ: embryo; Vector: pSPORT; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally from mRNA prepared
from 800 blastcoysts. Primer: Sall(dT):
5'-CGGTCGACCGTCTTTTTTTTTTTTTTT"3'. cDNAs were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA606966 657 bp mrNA EST 30-SEP-1997 vm94h09.rl knowles Solter mouse blastocyst B1 Mus musculus CDNA clone IMAGE:1005953 5' similar to SW:CISY_BIG P00889 CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR ;, mrNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:570169
                             188 ITCCACAGCTCATCCAATGACTCAATTTGCTAGCGGTGTTATGGCCCTCCAGGTGCAAAG 247
                                                                                                                                                                                                                                                                                                                                                                                              567 AGICACAGCICATCCAATGACTCAGTTTGCTACTGGAGTCATGGCTCTTCAGGTTCAAAG 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGAGTTTCAAAAGGCATATGAGAATGGAATTCATAAGTCAAAGTTCTGGGAGCCAACATA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 TITGIGGCTICITIAACIGGAAAGGIACCIAGCAAAGAGCAAGITGAAGCACIGICGAA 127
                                                                                                                                                                   447 ICICIGGCIICITITAACAGGAAAGGIGCCAICAAAAGAGCAAGIGGAIICAIIGICICA 506
                                                                                                                                                                                                                           128 AGACTTGGCGAACCGTGCTGCTGTGTGCAGATTATGTGTACAATGCCATCGATGCTCTGCC 187
                                                                                                                                                                                                                                                                                507 GGAATIGCGAAGTCGIGCTACTGICCCCGATCAIGIATACAAAACTAIIGAIGCCIIACC 566
8 IGAGIGCCAGAAAGIAIIACCIACIGCCCAGICIGGAGCIGAACCAIIACCGGAGGGICI 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1328460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washu'HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 473.
Location/Qualifiers
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                   308 TGAGGATIGCCICAACCIGATI 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          687 IGAGGATICCAIGAGTIIGATI 708
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/clone="IMAGE:1005953"

Clemson University Genomics Institute

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1 (bases 1 to 585)
Wan,C.-H., Yu,Y., Sasinowski,M. and Wing,R.A.
Cotton EST Database: Sequence Analysis of 2000 cDNA Clones from an
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euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
Rosidae; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1203 ACTGTTTCAA-CTGGTTGCAAAACTCTACGA-AGTGTTCCTCCAATTCTTACAGAACTTG 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1024 AAATCTGTTGTAGAGGAGTGTGGGGAGAACATTTCCAAAGAGCGGTTGAAAGACTACGCT 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1084 TGGAAAACATTGAAAAGTGGCAAGGTTGTCCCTGGTTTCGGACATGGAGTTCTGCGCAAG 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1144 ACTGATCCAAGATACACATGCCAGAGAGTTCGCTTTGAAGCATTTGCCTGAAG-ATCC 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1319 ATGGTTTAACTGAAGCAAGATATTATACGGTCCTCTTTGGTGTATCAAGAGCTCTTGGCA 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    964 TIGAAIGGITIAGCIGGACCACIICAIGGIIIAGCCAAICAGGAAGIIIIGCIAIGGAIC 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIOS4878 585 bp mRNA EST 16-JUL-1998 coau00002614 Cotton Boll Abscission Zone cDNA Library Gossypium hirsutum cDNA clone coau0002614 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 ATGAATGGGCTGGCGGGGCT-CTACATGGACTAGCAAATCAGGAGGTGCTTGTCTGGCTG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 ACACAGCTACAGAAGGAAGTTGGCAAAGACGTGTCAGATGAGAAGTTACGAGACTACATC 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGAACACACTCAATTCAGGACGGGTGGTCCCAGGATACGGTCATGCAGTACTGAGGAAG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 ACTGACCCTCGCTATTCCTGTCAGCGAGAGTTTGCTCTGAAACAICTGCCTAAGGGATTC 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         377 CCATGTTCAAGCTGGTGGCTCAGCTGTACAAGATTGTGCCCAATATCCTCTTAGAGCAAG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          437 GGAAGGCTAAGAACCCTTGGCCCAACGTAGACGCTCACAGTGGGGTGCTGCTCCAGTACT 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGCCATGACGGAGATGAACTACTACACGTCCTGTTTGGAGTGTCTCGGGCACTGGGTG 556
                                                                                                                                                                                                                                                                                             904 CACACAGGICACITGGITGCIAGIGCITIGICAGACCCITACCICICCITCGCIGCI 963
                                                                                                                                                                                                                                                                                                                                                                    79 CACACAAGCCATTTGGTGGGCAGCGCATT-TCAGACCCTTACCTGTCCTTTGCAGCAGCC 137
                                                                                                                                                                                                                                                                      19 GAGCTCATGCGTTTGTACCTCACCATCCATAGTGACCATGAGGGTGGTAATGTAAGTGCC 78
                                                                                                                                                                  Score 163; DB 15; Length 657;
Pred. No. 2.60e-88;
0; Mismatches 192; Indels 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1379 TITGCTCTCAGCTAATITGGGACCGAGCTCTTGGATTGCCACTAGAGAGGSCAAAG 1434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            557 TGCTAGCCCAGCTCATCTGGAGCAGAGCCCTAGGCTTCCCCCTGGAAAGGCCCAAG 612
/clone_lib="Knowles Solter mouse blastocyst B1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On Jan 9, 1998 this sequence version replaced gi:930638.
             /tissue_type="blastocyst"
/dev_stage="embryo" (pre-implantation)"
/lab_host="bH10B" 148 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Abscission Zone Library
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l Similarity 66.6%;
397; Conservative
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Gossypium hirsutum
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                                                                                                                                                                     Query Match
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Contact: Wing RA

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida: Poales; Poaceae; Avena.
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                                                                                                                                                                                                                                                     /note="Vector: Uni-ZAP XR; Site_1: EcoRI, Site_2: XhoI; This is a Uni-ZAP XR custom cDNA library made by Stratagene (U.S.A.: 1-800-424-5444): Stratagene cat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 TCAGAGCATGGAAAGGTTCAATTGGGAAACATCACAGTTGATGTTGTTCTTGGTGGAATG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 GCCATGGTGTTCTATCGCGGCGTTTCTCTGCTGTCAAAGCTGCGTTCTCGAGGGGGGGTCCAA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 CATICCAGICICAGCAAIICIGIIAGAIGCTICAAAIGCAGICCICITCCGAICIIGAI 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 CAGACAAATCTTAGCAACTCTGTGCGGTGGCTTCAAGTCCAAACCTCTTCTGGTCTTGAT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 CIGCGIICIGAGCIGCAAGAAIIGAIICCAGAACAACAGGAICGCCIAAAGAAGCICAAG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290 AGAGGGATGACAGNGGTTGCTTTGGGAAACCTCATTACTTG-CCCAGATGGGGGAATTTCG 348
                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Cotton Boll Abscission Zone cDNA Library"
/lab.host="XLI-Blue MRF" | 120 c 141 q 172 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-FEB-1997
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VanDeynze, A.E., Sorrells, M.E., Park, W.D., Ayres, N.M., Fu, H., Cartinhour, S.W. and McCouch, S.R.
Anchor Probes for Comparative Mapping of Grass Genera Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA231705 307 bp mRNA EST 27-FEB-199
CDO534.R cDNA from oat Avena sativa cDNA clone CDO534, mRNA
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 GCAGAACTGGNAAAAGTGCAACTTGGGAATATTACTGTTGATATGGTCATTGGTGGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        349 CTTTGGGGCCTTGTCATTCCGN-AGTGTCAAAAACTATTACCAGCTGCAAA-CCTGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 CTTCATTCGCAGTTGAAGGAATTGATTCCTGAACAACAGGAGCGCCTGAAGAAACTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 97; Indels
                                                                                            Email: rwing@clemson.edu
Seq primer: SP030 (AACAGCTATGACCATGATTA)
High quality sequence stop: 239.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.9%; Score 155; DB 22;
Best Local Similarity 73.7%; Pred. No. 1.48e-82;
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Trel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                /organism="Gossypium hirsutum"
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                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:3635"
                                                                                                                                                                                                                                                                                                                                                                                 /clone-"coau0002G14"
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AA231705.1 GI:1854091
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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p1713 vector. Library constructed and normalized by Bento Soares and M.Fatina
1 (bases 1 to 522)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                          Washington University School of Medicinep Washington University School of Medicinep 4444 Forest Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@mage.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1001 ATCAGGAAGTTTTGCTATGGATCAAATCTGTTGTAGAGGAGTGTGGGGGAGACATTTCCA 1060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1181 TGAAGCATTTGCCTGAAGATCCACTGTTTCAACTGGTTGCAAAACTCTACGA-AGTGTTC 1239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 CITACCTGTCCTTTGCAGCCAGGCCATGAATGGGCTGGCGGGGCT-CTACATGGACTAGCAA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAATATCCTCTTAGAGCAAGGGAAGGCTAAGAACCCTTGGCCCAACGTAGACGCTCACA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGAGGGTGGTAATGTAAGTGCCCACACACACATTTGGTGGG-AGCGCTGT-TCAGACC 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 ATGAGAAGTTACGAGACTACATCTGGAACACACTCCAATTCAGGACGGGTGGTCCCAGGAT
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On Sep 12, 1996 this sequence version replaced gi:1392879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 168; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 143; DB 10;
Pred. No. 5.69e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seg primer: -28ml3 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares mouse NML"
/tissue_type="Liver"
/lab_host="DH10B" 118 t
                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
                                                                                                                                                               The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 453.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
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1 Similarity 66.6%;
347; Conservative
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                                                                                                                                           Waterston, R.
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Best Local S
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     REFERENCE
                                 AUTHORS
                                                                                                                                                                                        JOURNAL
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Similar to SW:CISY_PIG P00889 CITRATE SYNTHASE, MITOCHONDRIAL
AA237580
                                                                                                                                                                                                                                                                                                                                                                                               //note="Vector: Uni-ZAP XR/pBluescript; Site_1: EcoRI; Site_2: XhOI; A Uni-ZAP XR CDNA library was constructed from etiolated leaf mRNA from the oat cultivar 'Brooks' and converted to pBluescript (amp resistant) as described in Heun et al. (1991) Genome 34:437-447. For insert amplification, use Ml3 forward and reverse primers. Clones from this library are designated with the prefix 'CDO'. *Note: Clone CDO1081 was recloned into the TA cloning vector and carries kanamycin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  958 GCTGCTTTGAATGGTTTAGCTGGACCACTTCATGGTTTAGCCAATCAGGAAGTTTTGCTA 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1018 TGGATCAAATCTGTTGTAGAGGAGTGTGGGGGAGAACATTTCCAAAGAGCAGTTGAAAGAC 10777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1078 TACGCTIGGAAAACATIGAAAAGIGGCAAGGTIGTCCCIGGIIICGGACAIGGAGIICIG 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1138 CGCAAGACTGATCCAAGATACACATGCCAGAGAGATTCGCTTTGAAGCATTTGCCTGAA 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1198 GATCCACTGTTTCAACTGGTTGCAAAACTCTACGAAGT-GTTCCTCCAATTCTTACAGAA 1256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TACGIAIGGAAGACACIGAAGAGIGGAAAGGIIGIICCIGGCIAIGGICAIGGAGIICIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TGGATCAAATCTGTGATGGAAGAACCGGGAGTAACATTACAACTGATCAGCTTAAAGAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 CGTAATACAGATCCACGATACTCGTGCCAAAGGGAGTTTGCACTTAAGTATTTACCCGAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 GACCCACTTTTCCAACTGGTCTCCAAGTTGTACGAAGTTGTGCCTCCTTACTGAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GCGGCACTGAACGGTTTAGCTGGGCCACTGCATGGCCTGGCTAATCAGGAAGTGTTGCTA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
                                                                                                                                                                                                            Email: srm4@cornell.edu
CDNA from oat (Avena sativa); reverse sequence of RFLP probe
CDO534. Sequence determined by Nicola M. Ayres.
  On Nov 29, 1993 this sequence version replaced gi:634857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 152; DB 10; Length 30°
Pred. No. 2.10e-80;
0; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="cDNA from oat"
/tissue_type="etiolated leaf"
64 c 79 g 80 t
                                                                                                                                                                                                                                                                                                                                                  /organism="Avena sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:4498"
/clone="CDO534"
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              /cultivar="Brooks"
                                                                        Dept Plant Breeding
Cornell University
Ithaca, W 14833-1901, USA
Tel: 607 255 6683
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AA237580.1 GI:1861602
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Best Local Similarity 75.6%;
Matches 232; Conservative
                                                       Contact: McCouch SR
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Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult.C.J., Lee, N.H., Kirkness, E.F., Wentstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Flizgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nquyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P. S., Olsen, H.,
Raymond, L., Welly, T.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Crose, J., Ruben, S.M.,
Frasc, C.M., and Venter, J.C., Rose, L.C., Haseltine, W.A., Fields, C.,
                                                                                                                                                                                                                                                                                                          EST185581 Colon carcinoma (HCC) cell line Homo sapiens CDNA 5' end similar to similar to citrate synthase, mRNA sequence. AA313713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.html)
Seq primer: M13 Reverse.
                                                                           1298 GIGGIGIGITGIIGAACTAITAIGGIITAACIGAAGCAAGATAITATACGGICCICIIIG 1357
1240 CTCCAATTCTTACAGAACTTGGCAAAGTTAA--ACCCTTGGCCAAATGTTGATGCCCACA 1297
                                               418 GTGGGGTGCTGCTCCAGTACTATGGCATGACGGAGATGAACTACTACACAGTCCTGTTTG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/note="Organ: colon; Vector: pBluescript SK-; Site_1:
EcoR1; Site_2: XhoI"
/db_xref="ATCC (inhost):109839"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                         19-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Apr 14, 1993 this sequence version replaced gi:693326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                         1358 GIGTATCAAGAGCTCTIGGCATTIGCTCTCAGCTAATTIGG 1398
                                                                                                                                                                                                                                                                                           EST
                                                                                                                                            478 GAGTGTCTCGGGCACTGGGTGTGCTAGCCCAGCTCATCTGG 518
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/cell_type="KM12C"
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Contact: Kerlavage, AR
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217455 213 bp mRNA EST 10-NOV-1992 ATTS0029 AC16H Arabidopsis thaliana cDNA clone TAT2B1 5' similar to CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR. Swiss-Prot entry P00889,
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/strain-"ecotype Columbia
/note-"vector: Lambda ZAPI; tissue-cell suspension
culture of ecotype columbia; clone_library-AC16H; Cloning
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euphyllophytes: Spermatophyta: Magnollophyta; eudicotyledons;
Rosidae: Capparales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                        1015 CTATGGATCAAAICTGTTGTAGAGGAGTGTGGGGAGAACATTTCCAAAGAGCAGTTGAAA 1074
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                                                                                                                                                                                                                                                                                     62 GTCTGGCTAACACAGCTGCAGAAGGAAGTTGGCAAAGATGTGTCAGATGAGAAGATTACGA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                   122 GACTACATCTGGAACACACTCAACTCAGGACGGGTTGTTCCAGGCTATGGCCATGCAGTA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 CTAAGGAAGACTGATCCGCGATATACCTGTCAGCGAGAGTTTGCTCTGAAACACCTGCCT 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 CAGTATTATGGCATGACGGAGATGAATTACTACGGGTCCTGTTTGGGGTGTCACGAGCA 421
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                                                                                                                                          2 GCAGCAGCCATGAACGGGCTGGCAGGGCCTCTCCATGGACTGGCAAATCAGGAAGTGCTT 61
                                                                          Gaps
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DB 11; Length 501;
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BP 27,31326 Castanet-Tolosan cedex,France
Email: lescuredtoulouse.inra.fr.
Location/Qualifiers
                                     Pred. No. 1.42e-67;
   Score 134;
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                             Best Local Similarity 65.4%;
Matches 316; Conservative
7.78;
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UMR05 CNRS/INRA
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Contact: Marra M/Mouse EST Project
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Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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The WashU-HHMI Mouse EST Project
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 Best Local Similarity 63.7%;
Matches 283; Conservative
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/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI: Sized fractionated cDNAs were directly ligated into
                                                                                                                                                                                         7
vector: Lambda ZAPII; Physiological condition: cycling
                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION GH15054.5prime GH Drosophila melanogaster head pOT2 Drosophila ACCESSION AI238915
                                                                                                                                                                                                                                                                                                                     923 CTAGIGCITIGICAGACCCTTACCTCTCCTTCGCTGCTGCTTTGAATGGTTTAGCTGGAC 982
                                                                                                                                                                                                                                                                                                                                                                            125 CACTCCATGGTTTGGCTAATCAGGAAGTTTTGCTTTGGATCAA-TCAGTCGTAGAGGAAT 183
                                                                                                                                                                                                                                                              863 TCACGATACACAGTGATCATGAAGGTGGTAACGTCAGTGCTCACACAGGTCACTTGGTTG 922
                                                                                                                                                                                                                                                                                                   65 GTAGIGCACTITCAGACCCATAICIGICALIIGCAGCIGCAITAAAIGGITIAGCIGGGC 124
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( Chases: 1 to 540.

Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C., Brokstein, P., Lewis, S. and Rubin, G.M.

BDGP/HHMI Drosophila EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Exa: 510 643 9947
Exa: 510 643 9947
Exa: 510 cov. E column: 6
Plate: 150 row: E column: 6
High quality sequence stop: 419.
Location/Qualifiers
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/db_xref="taxon:7227"

/clone="GH15054"

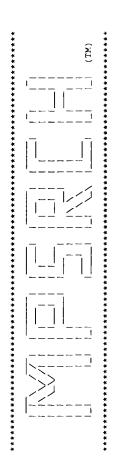
/clone=lib-="GH Drosophila melanogaster head poT2"

/sex="male and female"
                                                                                                                                                                                       2;
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                                                                                                                                                                                       0; Mismatches 33; Indels
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                                                                                                                                                 Score 131; DB 8; 1
Pred. No. 1.89e-65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="adult"
/lab_host="DH5 - alpha"
183 c 156 g
                                   /db_xref="taxon:3702"
/clone="TAT2B1"
/clone_lib="AC16H"
40 c 52 g
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                                                                                                                                               Query Match 7.5%;
Best Local Similarity 83.4%;
Matches 176; Conservative
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Eukaryota: Metazoa, Chordata, Craniata, Vertebrata, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus. 1 (bases I to 473)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA498291 473 bp mRNA EST 01-JUL-1997 VAS8491:11 Barstead mouse pooled organs MPLRB4 Mus musculus CDNA Clone IMAGE:889316 5' similar to SW:CISY_PIG P00889 CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1087 AAAACATTGAAAAGTGGCAAGGTTGTCCCTGGTTTCGGACATGGAGTTCTGCGCAAGACT 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1147 GATCCAAGATACACATGCCAGAGAGTTCGCTTTGAAGCATTTGCCTGAAGATCCACTG 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                        337 AAGCTGCAGAAGGAGGCCGGCAACAACCCGTCGGAGGAGCAGCTCAAGGAGTACATCTGG 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             397 AAGACCCTCAAGTCCGGACAGGTGGTTCCCGGCTACGGACACGCCGTGCTCCGCAAGACC 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                457 GATCCCCGCTACACCTGCCAGCGTGAGTTCGCGCTGAAGCACCTGCCCGAGGACGAGACG 516
                                                                                                           CTGGATTGGTCGCCGAACTTTGTGAAGATGCTCGGCTACGACAACGCCCCTTCACCGAG 156
                                                                                                                                                                                                                                                          157 CTGATGCGTCTCTATCTGACCATCCACAGTGACCACGAGGGTGGCAACGTGTCTGCCCAC 216
                                                                                                                                                                                                                                                                                                                                     847 CITATGAAGCICIATGICACGATACACAGIGAICAIGAAGGIGGIAACGICAGIGCICAC 906
                                                                                                                                                                                                                                                                                                                                                                                                             217 ACCGTICACTIGGIGGGCTCCGCCCTCAGCGATCCCTACCTCTCCTTTGCCGCCGGCCTG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277 AACGGICIGGCTGGTCCCCTGCACGGCCTGGCCAACCAGGAGGTGCTCGTGTGGGCTGCGC 336
                                                                                                                                                                                  787 CIGGAITAIGGIGCAAAITITGCICACAIGCIIGGIIICAGIAGCICIGACAIGCAIGAG 846
                                   0; Gaps
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On Sep 12, 1996 this sequence version replaced gi:1402331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washu-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Pred. No. 4.14e-59;
0; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seg primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 472.
Location/Qualifiers
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964 TIGAATGGTTTAGCTGGACCACTTCATGGTTTAGCCAATCAGGAACTTTTGCTATGGATC 1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1144 ACTGATCCAAGATACACATGCCAGAGAGTTCGCTTTGAAGCATTTGCCTGAAGATCCA 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       275 IGGAACACACTCAATTCAGGACGGGTGGTCCA-GGATACGGTCATGCAGTACTGAGGAAG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                             156 ATGAATGGCCTGGCGGGCT-CTACATGGACTAGCAAATCAGGAGGTGCTTGTCTGGCTG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215 ACACAGCTACAGAAGGAAGTTGGCAAAGACGTGTCAGATGAGAAGTTACGAGACTACATC 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 ACTGACCCTCGCTATTCCTGTCAGCGAGAGTTTGCTCTGAAACATCTGCCTAAAGATCCC 393
                                                                                                                                                                                                                                                                                                                                                                                                                       38 GAGCTCATGCGTTTGTACCTCACCATCCATAGTGACCATGAGGGTGGTAATGTAAGTGC- 96
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                  /clone="IMAGE:889316"
/clone_lib="Barstead mouse pooled organs MPLRB4"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                  Ouery Match 6.9%; Score 121; DB 14; Length 473; Best Local Similarity 68.2%; Pred. No. 2.08e-58; Matches 264; Conservative 0; Mismatches 119, Indels
                                                                                                                                                                                                                                           /tissue_type="pooled organs"
/dev_stage="7 day"
/lab_host="DHIOB"
122 124 g 107 t
/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: Sat Oct 23 22:01:18 1999 Job time : 2983 secs.
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                                                                                                                                                                                                                                                                                               124 g
                  /strain-"FVB/N"
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ORIGIN
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Oct 22 16:59:48 1999; MasPar time 18.52 Seconds 538.628 Million cell updates/sec Run on:

Tabular output not generated.

Description: Perfect Score:

>US-08-702-718-6 (1-469) from US08702718.pep 3443 1 MVFYRGVSLLSKLFSFAVQQ .......PLERPKSVIMEWLENHCKKA 469 Sednence.

PAM 150 Gap 11 Scoring table:

170751 seqs, 21266608 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-geneseg35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11.part11 12:part12 13.part13 13.part14 15:part14 15:part16 17:part17 18:part18 19:part14 20:part20 21:part21 22:part27 23:part28 24:part24 25:part25 25:part26 27:part27 28:part28 29:part29 30:part29 30:part30 31:part31 32:part32 33:part38 39:part39 Database:

Mean 35.933; Variance 168.408; scale 0.213 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result		<b>*</b>					
Sc	Score	Match	Match Length DB	DB	qi	Description	Pred. No.
	3443	100.0	469	14	R82840	Tobacco citrate synth	7.69e-299
	3098	0.06	471	15	R86383	Potato citrate syntha	3.55e-267
	3098	0.06	471	14	R82838	Potato citrate syntha	3.55e-267
	2800	81.3	437	14	R82839	Sugar beet citrate sy	7.44e-240
	313	9.1	436	m	R14357	Citrate synthase enco	1.06e-15
	116	3.4	456	34	W38570	Methyl tetrahydropter	3.08e+00
	106	3.1	220	σ	R47340	Fragment of chromaffi	1.47e+01
	103	3.0	329	58	W55330	H. pylori ORF hp3e110	2.33e+01
	103	3.0	329	53	W55574	H. pylori ORF 06ep302	2.33e+01
	102	3.0	355	24	W29179	Rat CC chemokine rece	2.71e+01
	101	2.9	3084	35	W50891	Mouse laminin A chain	3.15e+01
	86	2.8	355	Ξ	R52749	C-C chemokine recepto	4.95e+01
	86	2.8	355	24	W25751	Human MIP-lalpha/RANT	4.95e+01
	86	2.8	355	25	W26588	Human MIP-1 alpha/RAN	4.95e+01
	95	2.8	2164	7	P81045	Sequence of the viral	7.73e+01
	95	2.8	2164	Н	P80131	Peptides translated f	7.73e+01

1.04 e e + 0.02 e e +	)
Peptide encoded by pl pSCM525-derived pepti M. vaccae poth homolo Arabidopsis chloropla Klebsiella pneumoniae Acetobacter xylinum b QB ethylene response A. thaliana ethylene Human placenta G-prot T-lymphocyte TLISA An Human placenta G-prot T-lymphocyte TLISA An Human placenta G-prot T-lymphocyte TLISA An Human placenta G-prot Prostaglandin-Ep3-21 Prostaglandin-Ep3-21 Prostaglandin-Ep3-21 Prostaglandin-Ep3-3-1 Prostaglandin-Ep3-3-1 Human Ep3-V receptor. Salmonella secreted or H. pylori secreted or H. pylori secreted or Mature Penicillin V a Soluble type I insuli Full length Penicilli Human CLOCK protein. Sequence of beta-chai CF-5 pathogen resista IGF-1 receptor.	ac clibe t tugartu t
R85655 WW60133 WW60133 WW60133 WW60133 WW60125 WW60125 WW71228 WW71228 WW71228 WW71229 WW71229 WW71229 WW71229 WW71229 WW71229 WW71229 WW71229 WW71229 WW71229 WW71229 WW71229 WW71229 WW71229 WW71229 WW71229 WW71229 WW71229	
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1
LUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU	) *

## ALIGNMENTS

RESULT IN THE SULT	182840 standard; protein; 469 AA. 822840; 822840; 823840; 8-3AN-1996 (first entry) 10cotiana tabacum 10cotiana tabacum 4.SEP-1995; 10cotiana tabacum 4.SEP-1995; 10cotiana tabacum 4.SEP-1995; 10cotiana tabacum 4.SEP-1995; 10cotiana tabacum 4.SEP-1996; 10cotiana tabacum 4.SEP-1996; 10cotiana tabacum 4.SEP-1996; 10cotiana tabacum 4.SEP-1996; 10cotiana tabacum 10cotiana tab
ŭ	82840 standard; Protein; 469
A S	•
. Ta	25-JAN-1996 (first entrv)
DE	Tobacco citrate synthase.
ΚW	Citrate synthase; flower formation.
SO	Nicotiana tabacum
Nd	W09524487-A.
PD	14-SEP-1995.
PF	
PR	
PR	
PR	19-OCT-1994; DE-438821.
ΡA	-SCHERING AGREVO GMBH.
ΡΙ	ndschutze V, Muller-rober B, Landschuetze
ΡΙ	Mueller-roeber B;
DR	WPI; 95-328278/42.
DR	N-PSDB; T04201.
Еd	DNA encoding plant citrate synthase - used to regulate flower formation
Еd	to improve storage of tubers, etc. and to reduce sprouting
bS	Disclosure; Page 60-63; 87pp; English.
ပ္ပ	To identify a cDNA from tobacco which codes for citrate
ပ္ပ	synthase, a cDNA bank of leaf tissue from tobacco was prepd.
ပ္ပ	Plaques of this cDNA bank were screened using a radioactive DNA
ပ္ပ	probe which comprises Solanum tuberosum citrate synthase cDNA
ပ္ပ	(T04199). One of the clones was sequenced. The nt. sequence is
S	given in T04201.
S	
ō	Score 3443; DB 14; Length
Æ	Pred. No. 7.69e-299;
×	0; Mismatches 0; Indels 0;
qq	
è	MAPARGAST JSKT RSRANOOMNI SNSVRWI ONOORSSGI DI RSEI OEI I DECODRI KKI KS
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qq	ehgkvqlgnitvdmvlggmrgmtgllwetslldpdegirfrglsiyecqkvlpaakpgge
č	61 BHCKVOLONITADAWIGENEGELIMENGELINDORGIPERGISTRERG
Ś	ESCANQUOLITADEN ESCENTION DE LE CONTRACTOR DE LA CONTRACT

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Inhibiting citrate synthase (CS) activity in plants - to inhibit Inhibiting citrate synthase (CS) activity in plants - to inhibit also new CS sense and anti-sense DNA sequences.

The flower formation and improve storage capacity, e.g. in potatoes, also new CS sense and anti-sense DNA sequences.

Claim 5; Page 15-19; 35pp; German.

The potato citrate synthase (CS) gene or CDNA sequence encoding CS (T03410) may be used to produce antisense CS sequences. CS DNA sequences are useful for altering CS activity in plants. Antisense CS sequences are be used to inhibit CS expression in plants and has the effect of inhibiting flower formation and by doing so improves the plant's storage capacity. This is partic. useful in crop plants of any kind but esp. useful in potatoes. In addition to altering CS activity the DNA sequences can also be used to identify similar sequences in the genomes of other plants and in the production of transgenic plants with altered CS activity. This sequence in represents the amino acid sequence of potato citrate synthase.
                      181 ALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLIAQVPLVAAYVYRRMYKNGNTIPKDDSL 240
                                                                                                                                                                      241 dyganfahmlgfsssdmhelmklyvtihsdheggnvsahtghlvasalsdpylsfaaaln 300
                                                                                                                                                                                                 241 DYGANFAHMLGFSSDMHELMKLYVTIHSDHEGGNVSAHTGHLIHIHIHIHIHIHIHIHIHIH
                                                                                                                                                                                                                                                             301~{
m glagplhglangevllwiksvveecgeniskeqlkdyawktlksgkvvpgfghgvlrktd} 360~{
m glagplhglangevlrktd}
                                                                                                                                                                                                                                                                                                                                                   361 prytcgrefalkhlpedplfqlvaklyevflgflgnlaklnpwpnvdahsgvllnyyglt 420
                                                                                                                                                                                                                                                                                                                                                                          121 plpegllwllltgkvpskegvdslsgelrsratvpdhvyktidalpvtahpmtgfatgvm 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 4; Gaps
                                                                                      181 alqvqsefqkayekgihksklweptyedsmsliaqvplvaayvyrrmykngntipkddsl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Citrate synthase; inhibitor; increased storage capacity; potato;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Landschuetze V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 3098; DB 15; Length 471; Pred. No. 3.55e-267;
                                                                                                                                                                                                                                                                                                                                                                                                                                      421 earyytvlfgvsralgicsgliwdralglplerpksvtmewlenhckka 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 EARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENHCKKA 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Landschutze V, Muller-Roeber B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23; Mismatches
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(AGRE ) HOECHST-SCHERING AGREVO GMBH.
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R86383 standard; Protein; 471 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-APR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 89.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           423; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Potato citrate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-MAR-1994; 408629.
09-MAP-1994; DE-408629
22-SEP-1994; DE-435366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Solanum tuberosum.
DE4408629-A1.
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WPI, 95-321536/42.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antisense DNA.
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DNA encoding plant citrate synthase - used to regulate flower formation,
                       180 vmalqvqsefqkayekgihkskyweptyedsmnliaqvplvaayvyrrmykngdtipkde 239
                                                                                                        240 sldyganfahmlgfsssemhellmrlyvtihsdheggnvsahtghlvasalsdpylsfaa 299
                                                                                                                                                                                      300 alnglagplhglangevllwiksvveecgeniskeqlkdyvwktlnsgkvvpgfghgvlr 359
                                                                                                                                                                                                                                                                                                                                360 ktvprytcqrefamkhlpedplfqlvsklyevfllflqnlaklkpwpnvdahsgvllnyy 419
                                                                                                                                                                                                                                                                                                                                                                         358 KIDPRYTCOREFALKHLPEDPLFQLVAKLYEVFLQFLQNLAKLNPWPNVDAHSGVLLNYY 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 SEHGKVQLGNITVDMVLGGMRGMTGLLWETSLLDPDEGIRFRGLSIYECQKVLPAAKPGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 eplpegllwllltgkvpskeqvnsivsgiaesgiisliimyttidalpvtahpmtgfatg 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eplpegllwllltgkvpskegvnsivsgiaesgiisliimyttidalpvtahpmtgfatg 179
                                                                                                                                                                                                                                                                                         298 ALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYAWKTLKSGKVVPGFGHGVLR 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      firstly amplified using A thaliana cDNA and oligos T04202 and T04203 which are complementary to the 5' or 3' end of the coding region of A. thaliana cDNA for citrate synthase. The oligos additionally introduce BamHI cleavage sites at both ends of the amplified cDNA fragment. a CDNA library was prepd. from potato leaves and screened with A. thaliana citrate synthase cDNA. Positive clones were purified and sequenced. The nt sequence is given in T04199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 mvfyrsvsllsklrsravgqsnvsnsvrwlqvqtssgldlrselvqelipeggdrlkkik 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to improve storage of tubers, etc. and to reduce sprouting Disclosure; Page 53-56; 87pp; English. To identify a cDNA from potato which codes for citrate synthase, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Landschutze V, Muller-rober B, Landschuetze V;
                                                                                                                                                                                                                                                                                                                                                                                                                                      418 GLTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTWEWLENHCKKA 469
                                                                                                                                                                                                                                                                                                                                                                                                                   420 gltearyytvlfgvsralgicsqliwdralglplerpksvtmewlengckka 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 90.0%; Score 3098; DB 14; Length 471; Local Similarity 89.6%; Pred. No. 3.55e-267; Local Similarity 83; Mismatches 22; Indels 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potato citrate synthase.
Citrate synthase; flower formation; tuber storage.
Solanum tuberosum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-SEP-1995.
07-MAR-1995; E00859.
09-MAR-1994; DE-408629.
22-SEP-1994; DE-45366.
19-CCT-1994; DE-488821.
(AGRE ) HOECHST-SCHERING AGREVO GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R82838 standard; Protein; 471 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JAN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mueller-roeber B;
WPI; 95-328278/42.
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06-NOV-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding plant citrate synthase - used to regulate flower formation, to improve storage of tubers, etc. and to reduce sprouting Disclosure; Page 57-60; B7pp; English.

To identify a cDNA from sugar beet which codes for citrate synthase, a cDNA bank of leaf tissue from sugar beet was prepd. Plaques of this cDNA bank were screened using radioactive DNA probes which comprise a mixture of Solanum tuberosum citrate synthase cDNA (104199) and Micotian tabacum citrate synthase cDNA (see 10420)). One of the clones was sequenced. The nt. sequence is
121 pdhvyktidalpitahpmtqfctgvmalqtrsefqkayekgihkskfweptyedclslia 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qvpvvaayvyrrmykngqviplddsldyggnfahmlgfdspqmlelmrlyvtihsdhegg 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 QVPLVAAYVYRRMYKNGNTIPKDDSLDYGANFAHMLGFSSSDMHELMKLYVTIHSDHEGG 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 nvsahtghlvgsplsdpylsfaaalnglagplhglangevllwiksvvdecgenistegl 300
                                                               240 sldyganfahmlgfsssemhellmrlyvtihsdheggnvsahtghlvasalsdpylsfaa 299
                                                                              139 SLDYGANFAHMLGFSSSDMHEL-MKLYVIHSDHEGGNVSAHTGHLUHHHHHHHHHHHH
                                                                                                                           300 alnglagplhglangevllwiksvveecgeniskeqlkdyvwktlnsgkvvpgfghgvlr 359
                                                                                                                                                                                       360 ktvprytcgrefamkhlpedplfglvsklyevfllflgnlaklkpwpnvdahsgvllnyy 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 DEGIRFRGLSIYECQKVLPAAKPGGEPLPEGLLWLLLTGKVPSKEQVDSLSQELFSPATV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 PDHVYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLIA 214
                                                                                                                                                        298 ALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYAWKTLKSGKVVPGFGHGVLR 357
                                                                                                                                                                                                                       358 KTDPRYTCQREFALKHLPEDPLFQLVAKLYEVFLQFLQNLAKLNPWPNVDAHSGVLLNYY 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ssnldlrselgelipeggerlkkikkefgsfglgninvdmvlggmrgmtgllwetslldp 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35 SSGLDLRSELQELIFEQDDRLKKLKSEHGKVQLGNITVDMVLGGMRGMTGLLWETSLLDP 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Landschutze V, Muller-rober B, Landschuetze V;
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                                                                                                                                                                                                                                                       420 gltearyytvlfgvsralgicsgliwdralglplerpksvtmewlengckka 471
                                                                                                                                                                                                                                                                                      418 GLTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENHCKKA 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 81.3%; Score 2800; DB 14; Length 437; Local Similarity 85.7%; Pred. No. 7.44e-240; Les 373; Conservative 34; Mismatches 27; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                              Sugar beet citrate synthase.
Citrate synthase; flower formation.
Beta vulgaris strain Zuchtlinie 5S 0026
W09524487-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-MAR-1994; DE-408629.
22-SEP-1994; DE-433366.
19-OCT-1994; DE-438821.
(AGRE ) HOECHST-SCHERING AGREVO GMBH.
                                                                                                                                                                                                                                                                                                                                                 R82839 standard; Protein; 437 AA.
                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-1996 (first entry)
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07-MAR-1995; E00859.
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WPI; 95-328278/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      437 AA;
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87; Mismatches 109; Indels 32; Gaps 28;
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                                                                                                                                                                                                                                                                                    395 QNLAKL-NPWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALGLPLER 453
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275 NVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQL 334
                                                                                                                                                                                                            Disclosure; Fig 5; 12pp; Japanese.

The aarA gene encodes the citrate synthase and is part of an acetic acid resistance operon comprising aarA, aarB and aarC.

The DNA can be used to prepare an acetic acid resistant strain of bacteria for use in acetic acid fermentation.

See also R14358 and 59.
                                                                                                                                    335 KDYAWKTLKSGKVVPGFGHGVLRKTDPRYTCQREFALKHLPEDPLFQLVAKLYEVFLQFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acetic acid resistant gene with in plasmid and transformed acetobacter - improves yield of acetic acid fermentation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 5
R14357 standard; Protein; 436 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W38570 standard; Protein; 456 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Citrate synthase encoded by aarA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JAN-1992 (first entry)
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WPI; 91-329112/45.
                                                                                                                                                                                                                                                                                                                                                            421 pksvtmewlekfckr 435
                                                                                                                                                                                                                                                                                                                                                                                                                                454 PKSVTMEWLENHCKK 468
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05-FEB-1990; JP-024395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acetic acid resistance.
Acetobacter sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-1991.
05-FEB-1990; 024395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 436 AA;
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Con homology with an E. coli protein, is a methyl tetrahydropteroyltri glubarder-homocysteine methyltransferase, and is encoded by a DNA of the glubarder-homocysteine methyltransferase, and is encoded by a DNA of the invention. The DNA sequences were isolated from S. pneumoniae strain invention. The DNA sequences were isolated from S. pneumoniae strain 0100993 (NCIMB 40794). The Streptococus pneumoniae proteins of the invention can be used to identify compounds which interact with and inhibit or activate the activity of the proteins. Antagonists can be used to treat diseases caused by S. pneumoniae proteins, through genetic immunisation. They can also be used to induce an immunological response in a mammal by inoculation with the S. pneumoniae proteins of delivery of the encoding nucleic acids in a vector adequate to produce antibody and/or I cell immune responses to protect the animal from disease. The proteins can also be used to identify antimicrobial compounds which are capable of inhibiting their bloactivity. In particular the proteins of the invention can be used to prevent adhesion of bacteria to mammalian compounds. The proteins of proteins and produce antibody antimicrobial compounds which are capable of inhibiting their bloactivity. In particular the proteins of progression of pathogenesis in infections initiated other than by the compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 lavleqip-aenivltsscsllh-vpfttaneefepallnhfafavekldeirdl-dair 360
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                             Streptococcus pneumoniae protein; genetic immunisation; antagonist; immunological response; inoculation; antibody production; inhibitor; T cell immune response; antimicrobial compound; bacterial adhesion; extracellular matrix protein; protein-mediated cell invasion; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel Streptococcus pneumoniae proteins and related DNA - useful for diagnosing anti-microbial agents for treatment of bacterial
Methyl tetrahydropteroyltriglutamate-homocysteine methyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 11;
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22.3%; Pred. No. 3.08e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
Black MI, Hodgson JE, Knowles DJC, Nicholas RO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 ngqgsealaank-elfatervgenaelrariagltda 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 SDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGP 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; Pages 342-344; 483pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R47340 standard; Protein; 220 AA.
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Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1994 (first entry)
                                                                                                                                                                                                                                          Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-DEC-1993.
11-JUN-1993; U05704.
11-JUN-1992; US-899074.
30-JUL-1992; US-923096.
                                                                                                                                                                                                                                                                                                                                                                                                            14-MAY-1996; US-017670.
                                                                                                                                                                                                                                                                                                                                                             14-MAY-1997; U07950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98-008793/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; T98621.
                                                                                                                                                                                                                                                                                         WO9743303-A1.
                                                                                                                                                                                                    pathogenesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stodola RK;
                                                                                                                                                                                                                                                                                                                           20-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infections
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    $\text{P}$ 
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Mriobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The DNA and probes derived from it may be used for the identification of H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and used to prevent the translation of H. pylori mRNA. Antibodies against the protein can be used in immunoassays to evaluate the abundance and distribution of H. pylori specific antigens. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                      DNA, vectors, transformed cells and antibodies, for diagnosis and treatment of neurological disorders, e.g. Parkinson disease Example 2: page 114-115; 181pp; English.

The CDNA encoding the chromaffin granule amine transporter protein is useful in gene therapy and as a probe for detecting genomic sequences. The protein is used for screening cytoroxic compounds implicated in Parkinsons disease, diseases associated with activity of neurotoxins or psychiatric disorders and to identify compounds which selectively inhibit or activate its action. Antibodies raised against this protein are useful as immunoassay reagents for detecting the protein and as affinity reagents for purification. This fragment of the transporter protein shares homology with the Neternial domains of the methlenomycin; tetracycline and multi-drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 DSMSLIAQVPLVAAYVYRRMYKNGNT-IPKDDSLDYGANFAHM-LGFSSSD-MHELMKLY 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 dnmlltvvvpjvptflyatefkdsnsslhrgpsvssqeenvrigilfaskalmqllvnpf 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-1998 (first entry)
H. pylori ORF hp3el1024orf49 protein.
H. pylori ORF hp3el1024orf49 protein.
Gytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
                                                                 New mammalian vesicle membrane transport protein - and corresp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.1%; Score 106; DB 9; Length 220; 21.1%; Pred. No. 1.47e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 vgpltnrigyhipmfvgfmimf-lstlmfafsgtyallfvartlggigs 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265 VIIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGL-AG-PLHGLAN 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W55330 standard; Protein; 329 AA.
                                                                                                                                                                                                                                                                                                                                                                                                           resistance transporter proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 21.1%;
les 23; Conservative
(REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-MAR-1996; US-625811.
02-APR-1996; US-758731.
25-OCT-1996; US-736905.
28-OCT-1996; US-738859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-001-1997.
27-MAR-1997; U05223.
06-DEC-1996; US-761318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori. W09737044-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ASTR ) ASTRA AB.
Alm RA, Smith D;
WPI; 97-503122/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                    220 AA;
                                           WPI: 94-007556/01
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                         Edwards
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W29179 standard; Protein; 355 AA.
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                       membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           24-507-1998 (first entry)
24-507-1998 (first entry)
4. pylori ORF O6ep30223_23557202_c2_130 cytoplasmic protein.
Cytoplasmic; vaccine; prevention; treatment; infection; envelope;
identification; binding compound; bacteria; life cycle; activator;
inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
were analysed for significant homology to other known or exported
                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
                                                                                                                                                     Match 3.0%; Score 103; DB 29; Length 329; Local Similarity 30.6%; Pred. No. 2.33e+01; les 11; Conservative 15; Mismatches 8; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 329;
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Pred. No. 2.33e+01;
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                                                                                                                                                                                                                                                                                           213 IAQVPLVAAYVYRRMYKNGNTIPKDDSLDYGANFAH 248
                                                                                                                                                                                                                                                  218 veempliasvifnrl-kkgmplqmdgalny-qefsh 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218 veempliasvifnrl-kkgmplqmdgalny-qefsh 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       W55574 standard; Protein; 329 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.0%;
Best Local Similarity 30.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAR-1997; U05223.

06-DEC-1996; US-761318.

29-MAR-1995; US-761318.

22-ARR-1996; US-758731.

25-OCT-1996; US-736905.

28-OCT-1996; US-738859.

(ASTR) ASTRA AB.

AIM RA, SMILL D:

WPI; 97-503122/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori.
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                                                                                                               Sequence 329 AA;
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RESULT

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Claim 1: Page 20-21; 26pp; Japanese.
This sequence is a rat CC chemokine receptor. The receptor can be used to screen for novel binding compounds and for preparation of antibodies or antiserum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              379 LFQL-VAKLYEVF-LQFLQNLAKL-NPWPNVDAHSGVLLN-YY-GLTEARYYTVLFGVSR 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 lfnlavsdlvflftlpfwidy-klkdnwvfgdamckllsgfyylglyseiffiilltidr 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 15; Page 74-79; 132pp; English.

This is the amino acid sequence of the mouse laminin A chain. The primary object of the invention is to use laminin, laminin-derived protein fragments and/or laminin-derived polypeptides as potent inhibitors of amyloid formation, deposition, accumulation and/or persistence in Alzheimer's disease and other amyloidoses. The laminin products (see W50888-98) may include mouse or human laminin A or Al chain, laminin Bl or B2 chain, laminin A2 chain (merosin), laminin G1 chain, the globular repeats of the laminin A1 chain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wouse laminin A chain.

Mouse laminin A chain.

Laminin; mouse; beta-amyloid; amyloidosis; Alzheimer's disease;

Down's syndrome; hereditary cerebral haemornhage; inflammation;

malignancy; Familial Mediterranean Fever; multiple myeloma;

malignancy; Familial Mediterranean, Tever; multiple myeloma;

Gertsfamin-Straussler syndrome; Kutu; scrapie; haemodialysis;

carpal tunnel syndrome; senile cardiac amyloid polymeuropathy;

Familial Amyloidotic Polymeuropathy; thyroid carcinoma; diagnosis;
                                                                                                                                                                                                                                                    CC chemokine receptor protein - useful to screen for novel binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Castilio G, Snow AD;
WPI; 98-240534/21.
Use of laminin and fragments - for developing products for use in
the diagnosis and treatment of amyloid disease, e.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2746..2922
//note= "fourth globular domain repeat (Claim 13)"
2690..2700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "beta-amyloid protein binding region
(Claim 12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                    7. Match 3.0%; Score 102; DB 24; Length 355; Local Similarity 29.5%; Pred. No. 2.71e+01; nes 26; Conservative 17; Mismatches 38; Indels 7;
                     Rat CC chemokine receptor. rat; CC chemokine receptor; screen; binding; ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 ylaivhavfslrartvtfgiitsiii-w 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        434 ALGICSQLIWDRALGLPLERPKSVTMEW 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W50891 standard; Protein; 3084 AA.
                                                                                                                                                   22-FEB-1996; JP-035192.
(TAKE ) TAKEDA CHEM IND LTD.
WPI; 97-486426/45.
19-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-APR-1998.
08-OCT-1997; U18145.
08-OCT-1996; US-027981.
(UNIW ) UNIV WASHINGTON.
                                                                                                       02-SEP-1997.
22-FEB-1996; 035192.
                                                                                                                                                                                                                                                                                                                                                                                           355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease or CJD
                                                                      rattus.
                                                                                                                                                                                                                                N-PSDB; T86839
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                                                                                                                                                                                                                                                                              compounds
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 lknmtsiyllnlaisdllflftlpfwidy-klkddwvfgdamckilsgfyytglyseiff 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26; Mismatches 33; Indels 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 SKLRSRA-VQQTNLSNSVRWLQVQTSSGLDLRSELQELIPEQQDRLKKLKSEHGKVQLGN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence is that of the C-C chemokine receptor. The sequence can
be used in therapeutic or diagnostic compsns. for inflammation and
                                                                                                                                                                                                                                                                                            amyloid or inflammation-association amyloidosis), the amyloidosis associated with multiple myeloma and other B-cell abnormalities (AL amyloid), the amyloidosis associated with type II diabetes (amylin or islet amyloid), the amyloidosis associated with prion diseases including Creutzfeldt-Jacob diseases, Gertstmann-Straussler syndrome, kuru and animal scrapie (Prb amyloid), the amyloidosis associated with long-term haemodialysis and carpal tunnel syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Gaps
the beta-amyloid binding domain of the laminin A chain. A claimed method for treating an amyloid disease comprises administering a polypeptide having a conformational similarity to a fragment of a laminin protein. A method for diagnosing an amyloid disease laminin protein. A method for diagnosing an amyloid disease in hoolves determining levels of laminin in a sample. Production of laminin or its fourth globular repeat in vivo provides a method for in vivo inhibition of beta-amyloid amyloidosis. The products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; 062695.
New C-C chemokine receptor and nucleic acid - are used to develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prods. for use in diagnosis and therapy of inflammation and other cytokine-mediated disorders
                                                                                                                                                       and methods can be used for the diagnosis, prognosis, monitoring and treatment of amyloidoses such as Alzheimer's disease, Down's syndrome and hereditary cerebral haemorrhage with amyloidosis of the Dutch type (where the specific amyloid is the beta-amyloid protein), the amyloidosis associated with chronic inflammation, various forms of malignancy and Familial Mediterranean Fever (AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (prealbumin or transthyretin amyloid), and the amyloidosis associated with endocrine tumours such as medullary carcinoma of the thyroid (variant of procalcitonin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (beta 2-microglobulin amyloid), the amyloidosis associated with senile cardiac amyloid and Familial Amyloidotic Polyneuropathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 101; DB 35; Length 3084; Pred. No. 3.15e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred No. 4.95e+01;
15; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1940 lise-slas-rqkavlqrssrflkesvqtr 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITVDMVLGGMRGMTGLLWETSLLDPDEGIR 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.8%; Score 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-C chemokine receptor.

C-C CKR-1; cytokine; inflammation.
Homo sapiens.
W09411504-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   other cytokine mediated disorders.
See also R52750-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R52749 standard; Protein; 355 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 9; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schall T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 2.9%;
Best Local Similarity 26.7%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 30.6%;
ses 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-NOV-1993; U10672.
10-NOV-1992; US-974025.
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Disclosure: Page 15-16; 19pp; Japanese.

This sequence represents human MIP-1 alpha/RANTES receptor (macrophage inflammatory protein 1 alpha/regulated on activation, normal T cell expressed and secreted). The human MIP-1 alpha/RANTES receptor protein may be used in a method for the screening of human MIP-1 alpha/RANTES receptor receptor affinity compounds. The MIP-1 alpha/RANTES receptor coding sequence may be included in an expression vector, preferably pCCR, and used to transform a CHO cell for use in the same method. The receptor protein can provide a preventive and treating agent for viral diseases, infectious diseases, tumours, allergy, diabetes, central diseases, hyperlipidaemia, hypercholesterolaemia, osteoporosis, digestive ulcers,
                                                                                                                   20-NOV-1997 (first entry)
Human MIP-lalpha/RANTES receptor protein.
Human MIP-1 alpha/RANTES receptor; osteoporosis; pcCR; digestive ulcer;
                                                                                                                                                                             macrophage inflammatory protein 1 alpha; diabetes; central disease; regulated on activation, normal 7 cell expressed and secreted; allergy; affinity compound; expression vector; CHO cell; viral disease; infectious disease; tumour; hyperlipidaemia; hypercholesterolaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 lknmtsiyllnlaisdllflftlpfwidy-klkddwvfgdamckilsgfyytglyseiff 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               371 LKHLPEDPLFQL-VAKLYEVF-LQFLQNLAKL-NPWPNVDAHSGVLLN-YY-GLTEARYY 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 4.95e+01;
15; Mismatches 29; Indels 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIP-1-appa and RANTES receptor nucleic acid - used to develop products for the detection of these cytokine(s) and their receptors, particularly in inflammatory processes
                                                                                                                                                                                                                                                                                                                                                                                                                      Preparation of human MIP-1-alpha/RANIES receptor protein - used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human MIP-1 alpha/RATES receptor.

Macrophage inflammatory protein-1 alpha; MIP-1 alpha;

reduced upon activation normal T expressed and secreted; RANTES;

receptor; cytokine; antiinflammatory; inflammation; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                             the treatment of viral diseases, tumours, allergy, diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 24; Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 98;
                                                                             W25751 standard; Protein; 355 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W26588 standard; Protein; 355 AA.
                                                                                                                                                                                                                                                                                                08-JUL-1997.
28-DEC-1995; 342130.
28-DEC-1995; JP-342130.
(TAKE ) TAKEDA CHEM IND LTD.
WPI: 97-399449/37.
N-PSDB; T86154.
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Local Similarity 30.6%;
les 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JAN-1993; US-012988.
426 TVLFGVSRALGI 437
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28-JAN-1993; 012988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 97-392945/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteoporosis etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; T90384
                                                                                                                                                                                                                                                               Homo sapiens.
J09176048-A.
                                                                                                W25751;
20-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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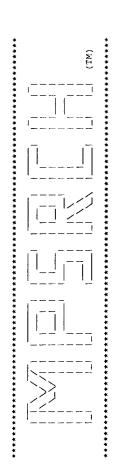
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9
            This polypeptide comprises a claimed receptor for human macrophage inflammatory protein-1 alpha (MIP-1 alpha) and regulated upon activation normal T expressed and secreted (RANTES) protein. Also claimed are: a nucleic acid (see T90384) that encodes the receptor: a subsequence of the nucleic acid, having at least 12 contiguous nucleotides: a cell transformed or transfected with the nucleic acid; and purified MIP-1 alpha/RANTES receptor polypeptide. The products can be used for detecting the MIP-1 alpha/RANTES receptor and polymorphisms in physiological samples. In addition, the receptor can be expressed and used to assay for MIP-1a/RANTES in useful for monitoring the levels of these cytckines in a patient. Such measurements are useful in following the antiinflammatory effects of drugs and prospective usefulness of new antiinflammatory
                                                                                                                                                                                                                                                                                                                           65 lknmtsiyllnlaisdllflftlpfwidy-klkddwvfgdamckilsgfyytglyseiff 123
                                                                                                                                                                                                                                                                                                                                                       371 LKHLPEDPLFQL-VAKLYEVF-LQFLQNLAKL-NPWPNVDAHSGVLLN-YY-GLTEARYY 425
                                                                                                                                                                                                                                                                  / Match 2.8%; Score 98; DB 25; Length 355;
Local Similarity 30.6%; Pred. No. 4.95e+01;
les 22; Conservative 15; Mismatches 29; Indels 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence of the viral proteins VP1-VP4, P2A-P2C, PCA-P3C encoded by the genomic RNA of rhinovirus strain HRV89 Vaccine; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BOEH) Beehringer Ingelheim.
Duechler M, Skern T, Sommergruber W, Neubauer C, Grundler P, Blaas,
Kuchler E, Frasel L, Zorn M;
Claim 2; Column 15-18; 12pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                             JT 15
P81045 standard; Protein; 2164 AA.
P81045;
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1679..2163
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/label- P2-A
1008..1101
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/label= PC-2
1422..1496
/label= P3-A
1497..1517
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/label= VP3
576..872
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/label= VP2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= VP4
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17-JAN-1987; DE-701301.
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426 TVLFGVSRALGI 437
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30-MAR-1988.
20-AUG-1987; 112104.
                                                                                                                                                                                                                                        355 AA;
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corresponding to viral RNA of rhino-virus HRV89 - useful for

New DNA

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2;
                                                                                                                                                                                                                                                           Gaps
prodn. of polypeptide(s) for stimulating immune system against HRV
                                                               The viral proteins are used for stimulating a protective immune response and for blocking cellular receptors. Abs against them are useful for assay and purificn. of the corresp. antigen, and can also be used for the therapeutic and diagnostic applications. Sequence 2164 AA;
                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                             Length 2164;
                                                                                                                                                                                                          Query Match 2.8%; Score 95; DB 2; Length 2164 Best Local Similarity 40.5%; Pred. No. 7.73e+01; Matches 15; Conservative 11; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                       1538 vvttdkg-kftglgiydqvmvlpthsdpgseilvdgv 1573
                                                                                                                                                                                                                                                                                                                           Search completed: Fri Oct 22 17:04:01 1999 Job time: 253 secs.
                                              Claim 8; Fig 4; 66pp; German..
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Oct 22 17:10:16 1999; MasPar time 7.25 Seconds 758.239 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-702-718-6 (1-469) from USO8702718.pep 3443 I MVFYRGVSLLSKLRSRAVQQ......PLERPKSVIMEWLENHCKKA 469 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

119857 seqs, 11713122 residues Searched: a-issued 1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1 Database:

Minimum Match 0% Listing first 45 summaries

Post-processing:

Mean 33.542; Variance 164.918; scale 0.203 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		a			SUMMARIES		
Result		Ouerv					
No.	Score	Match	Match Length	DB	ID	Description	Pred. No.
1	106	3.1	220	-	US-08-063-	Sequence 10, Applicati	7.81e+00
7	106	3.1	220	٣	PCT-US93-0	10,	7.81e+00
m	100		361	Н	US-08-415-	37, Applicat	1.92e+01
4	9.6		355	Н	US-08-450-	Ŋ,	2.58e+01
ß	86	2.8	355	Н	US-08-012-	Sequence 2, Applicatio	2.58e+01
9	86	2.8	355	ĸ	PCT-US95-0	'n	2.5
7	46		624	C a	US-08-756-	6	7
80	63		80	7	US-08-465-	14,	δ.
o,	93	2.7	80	7	US-09-119-	14,	5.37e+01
10	93	2.7	80	7	US-08-336-	14,	5.37e+01
11	93	2.7	80	Н	US-07-971-	14,	5.37e+01
12	94	2.7	773	7	US-08-484-	Sequence 44, Applicati	4.64e+01
13	76		773	C1	US-08-484-	42,	4.64e+01
14	88	5.6	253	~	us-08-685-	20,	9.53e+01
15	68		253	C a	US-09-144-	ñ	9.53e+01
16	88		268	4	5320958-6	Patent No. 5320958.	~
17	91		342	Н	US-08-499-	Sequence 5, Applicatio	7
18	91	5.6	507	-	us-08-363-	٦	7.16e+01
19	91		532	٦	-08-36	Sequence 22, Applicati	7.
20	68		897	Н	us-04-960-	ď	9.53e+01
21	68		1548	~	US-08-460-	7	9.53e+01
22	89		1548	C1	US-08-463-	Sequence 7, Applicatio	9.53e+01
23	88		3031	٦	US-07-689-	Sequence 2, Applicatio	1.10e + 02

86 2.5 112 3 PCT-US93-0 Sequence 3, Applicatio 1.466+02 87 2.5 230 2 US-08-301- Sequence 457, Applicatio 1.466+02 88 2.5 380 2 US-08-472- Sequence 34, Applicati 1.466+02 88 2.5 380 2 US-08-472- Sequence 34, Applicati 1.466+02 85 2.5 380 1 US-08-149- Sequence 7, Applicatio 1.688+02 85 2.5 434 2 US-08-911- Sequence 7, Applicatio 1.688+02 85 2.5 436 2 US-08-911- Sequence 3, Applicatio 1.688+02 85 2.5 436 2 US-08-870- Sequence 3, Applicatio 1.688+02 85 2.5 500 1 US-08-86-05 Sequence 4, Applicatio 1.688+02 85 2.5 500 1 US-08-849- Sequence 5, Applicatio 1.686+02 85 2.5 13 2 US-08-849- Sequence 2, Applicatio 1.466+02 86 2.5 879 1 US-08-413- Sequence 3, Applicatio 1.466+02 86 2.5 879 1 US-08-413- Sequence 3, Applicatio 1.466+02 86 2.5 879 1 US-08-413- Sequence 3, Applicatio 1.466+02 86 2.5 879 1 US-08-413- Sequence 3, Applicatio 1.466+02 86 2.5 879 1 US-08-413- Sequence 2, Applicatio 1.276+02 86 2.5 879 1 US-08-413- Sequence 2, Applicatio 1.276+02 86 2.5 336 2 US-08-430- Sequence 2, Applicatio 1.276+02 86 2.5 336 2 US-08-480- Sequence 10, Applicatio 1.276+02 86 2.5 336 2 US-08-405- Sequence 10, Applicatio 1.276+02 86 2.5 2366 2 US-08-405- Sequence 10, Applicatio 1.276+02 86 2.5 2366 2 US-08-405- Sequence 10, Applicatio 1.276+02 86 2.5 2366 2 US-08-405- Sequence 10, Applicatio 1.276+02 86 2.5 2366 2 US-08-405- Sequence 10, Applicatio 1.276+02 86 2.5 2366 2 US-08-405- Sequence 10, Applicatio 1.276+02 86 2.5 2366 2 US-08-405- Sequence 10, Applicatio 1.276+02 86 2.5 2366 2 US-08-80-80-80-80-80-80-80-80-80-80-80-80-	ALIGNMENTS 1 38-063-552-10 STANDARD; PRT; 220 AA.	Sequence 10, Application US/08063552 Patent No. 568836 GENERAL INFORMATION: GENERAL INFORMATION: TITLE OF INVENTION: Vesicle Membrane Transport Proteins NUMBER OF SECUENCES: 17 CORRESPONDENCE ADDRESS: ADDRESSED: Sheldon & Mak STREE: 225 South Lake Avenue, Ninth Floor CITY: Pasadena STARE: California COUNTRY: USA COUNTRY: POSADBLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READBLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READBLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/063,552 FILING DATE: 19930514 CLASSIFICATION NUMBER: 32,612 REFERENCE/DOCKET NUMBER: 9067-1 TELEPHONE: (818) 796-4000 TELEPHONE: (818) 796-4000 TELEPHONE: (818) 796-4000 TELEPHONE: 220 amino acids TYPE: ALINO ACID TOPOLOGY: linear MOLECULE TYPE: 100 FRAGMENT TYPE: internal ORIGINAL SOURCE:
224524 2254 226524 2274 2274 23333 2444 2444 2444 2444 2	S-08-053	Sequence 1 GENERAL 1 APPLICATION TITLE OF TITLE
44444466666666666666666	RESULT ID U XX AC X XX DT DT XX	×8888888888888888888888888888888888888

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84 VGPLTNRIGYHIPMFVGFMIMF-LSTLMFAFSGTYALLFVARTLQGIGS 131
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                                                                                    208 DSMSLIAQVPLVAAYVYRRMYKNGNT-IPKDDSLDYGANFAHM-LGFSSSD-MHELMKLY 264
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                                                                   24 DNMLLTVVVPIVPTFLYATEFKDSNSSLHRGPSVSSQEENVRIGILFASKALMQLLVNPF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 DNMLLTVVVPIVPTFLYATEFKDSNSSLHRGPSVSSQEENVRIGILFASKALMQLLVNPF 83
                                                 Gaps
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TITLE OF INVENTION: Vesicle Membrane Transport Proteins
NUMBER OF SEQUENCES: 17
                          Ouery Match 3.1%; Score 106; DB 1; Length 220; Best Local Similarity 21.1%; Pred. No. 7.81e+00; Matches 23; Conservative 40; Mismatches 40; Indels
                                                                                                        84 VGPLINRIGYHIPMFVGFMIMF-LSTLMFAFSGTYALLFVARTLQGIGS 131
                                                                                                                          265 VIIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGL-AG-PLHGLAN 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.1%; Score 106; DB 3; Length 220;
21.1%; Pred. No. 7.81e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: PCT/US93/05704
                                                                                                                                                                  220 AA
                                                                                                                                                                                                                                                                                                      E: Sheldon & Mak
225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                    UMBER: PCT/US93/05704
19930611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 9067-1PCT TELECOMOUNICATION: TELEPHONE: (818) 796-4000 TELEPHONE: (818) 795-6321
                                                                                                                                                                  PRT;
NISM: Rattus rattus
220 AA; 23695 MW; 270630 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Rattus rattus
ICE 220 AA; 23695 MW; 270630 CN;
                                                                                                                                                                                                                                             Sequence 10, Application PC/TUS9305704
                                                                                                                                                                                                                           Sequence 10, Application PC/TUS9305704
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Farber, Michael B
PEGISTRATION NUMBER: 32,512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10:
                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 220 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           internal
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Matches 23; Conservative
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California
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HYPOTHERMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                 PCT-US93-05704-10
                                                                                                                                                                                                                                                                                                                                          COUNTRY: UC
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 ORGANISM:
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         SEQUENCE
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265 VIIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGL-AG-PLHGLAN 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND RNA ENCODING THEM, HYBRID VECTOR AND TRANSFORMED HOST AND METHODS FOR IMMUNOTHERAPY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
STARE: California
CCUNTRY: United States of America
ZIP: 94306-1840
CMEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRYPTOSPORIDIUM ANTIBODIES, DNA
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CE 361 AA; 39600 MW; 808936 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLYPEPTIDES BINDING ANTI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COPPESPONDENCE ADDRESS:
ADDRESSEE: PHILLIPS, MOORE, LEMPIO & FINLEY
STREET: 385 Sherman Avenue, Suite 6
                                                                                                361 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       480.19-2 (HHD)
                                                                                                                                                                                                                                          Sequence 37, Application US/08415751
Patent No. 5643772
GENERAL INFORMATION:
APPLICANT: BETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: NELSON, RICHARD, C.
APPLICANT: OUT, JIRI POLYPEPTIDES BINDIN
TITLE OF INVENTION: POLYPEPTIDES BINDIN
TITLE OF INVENTION: CRYPTOSPORTIOU ANT.
TITLE OF INVENTION: WETHODS FOR IMMUNOTH
TITLE OF INVENTION: METHODS FOR IMMUNOTH
TITLE OF INVENTION: METHODS FOR IMMUNOTH
TITLE OF INVENTION: DIAGNOSIS AND XIT
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUFTWARE SISTEM: DOS
SUFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,751
FILING DATE: 03-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Cryptosporidium parvum
                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/071,880
FILING DATE: June 1, 1993
APPLICATION NUMBER: 07/891,301
FILING DATE: MAY 29, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-1677
TELEFAX: (415) 324-1678
INFORMATION FOR SEQ ID NO: 37:
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REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
                                                                                                STANDARD;
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                                                                                                US-08-415-751-37
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JENCE 355 AA; 41172 MW; 710742 CN;
                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                               Sequence 2, Application US/08012988A Patent No. 5652133 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application PC/TUS9500476
                                           Sequence 2, Application US/08012988A
                                                                                                                                                                                                                                                                                                                                                                 NAME: Weber,, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 1528
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 antho acids
                                                                                                                                                                                                                                                           Floppy disk
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                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                      STREET: One Market P
CIIY: San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Gaps
       240 SVLLKNGPEFECSYQNVLQDLPQDEMQDLILYNLVDMYWDFLTQNIPIMD 289
                   APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
IIILE OF INVENTION: MAMMALIAN MONOCYTE CHEMOAITRACTANT
IIILE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                              Cooley Godward Castro Huddleson & Tatum
                                                                                                                                                                                                                                                                                                  CITY: Palo Alto
CITY: Palo Alto
COUTRY: California
COMPUTER: California
ZIP: 94306-215
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IB PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,393A
FILING DATE: May 25, 1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 98; DB 1; Length 355;
Pred. No. 2.58e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Mismatches 29; Indels
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                                                                            355 AA
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                                                                            PRT;
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                                                                                                                                                                        Sequence 5, Application US/08450393A
Patent No. 5707815
                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CSET', LUANN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5165
TELEFAX: 415-843-5165
TELEFAX: 380816CO2102PA
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                 Sequence 5, Application US/08450393A
                                                                                                                                                                                                                                                                               ADDRESSEE: Cooley Godward C
STREET: 5 Palo Alto Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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Best Local Similarity 30.6%;
Matches 22; Conservative
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                                                                          US-08-450-393A-5
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                                                                                                    XXXXXX
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APPLICANT: Murphy, Philip M.

APPLICANT: Murphy, Philip M.

TITLE OF INVENTION: Cloning and Expression of Human

TITLE OF INVENTION: Macrophage Inflammatory Protein-1 alpha (MIP-1

TITLE OF INVENTION: alpha)/RANTES Receptor

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSE: Townsend and Townsend Khourie and Crew

STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 LKNMTSIYLLNLAISDLLFLFTLPFWIDY-KLKDDWVFGDAMCKILSGFYYTGLYSEIFF 123
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GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 2.8%; Score 98; DB 1; Length 355; Local Similarity 30.6%; Pred. No. 2.58e+01; es 22; Conservative 15; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/012,988A
FILING DATE: 19930128
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                     65 LKNMTSIYLLNLAISDLLFLFTLPFWIDY-KLKDDWVFGDAMCKILSGFYYTGLYSEIFF 123
                                                                                                                                                                                                                                                                                                              APPLICANT: Clemente, Thomas E.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Mitsky, Timothy A.
APPLICANT: Stark, David M.
TITLE OF INVENTION: Improved Rhodospirillum Rubrum
TITLE OF INVENTION: Poly-B-Hydroxyalkonoate Synthase
CORRESPONDENCE: 15
                                                                                                                                                                                                                                                                    Score 98; DB 3; Length 355;
Pred. No. 2.58e+01;
15; Mismatches 29; Indels
                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00476
 SSEE: Robbins, Berliner & Carson
1: 201 N. Figueroa Street, 5th Floor
Los Angeles
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                  5555-291
                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                     355 AA; 41172 MW; 710742 CN;
                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08756317
Patent No. 5849894
GENERAL INFORMATION:
                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/POCKET NUMBER: 5555
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-977-1001
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/08756317
                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                               MOLECULE TYPE: protein HYPOTHETICAL: NO
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                    Match 2.8%;
Local Similarity 30.6%;
les 22; Conservative
                                                                                                                                                                                                                         linear
                                    COUNTRY: USA
ZIP: 90012-2628
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                                                                                                                                                                                                                                                                                                                                    124 IILLTIDRYLAI 135
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                                                                                                                   CLASSIFICATION:
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                                                                                                            FILING DATE:
       ADDRESSEE:
                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                               ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                   XXXXXX
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90 WIKLLAEQ-PERVIGOQV-SY-WGETLRHFAEAQAAFARGTVIPPPSEGPRDRRFA-NPL 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/08465273
Patent No. 5866361
GENERAL INFORMATION:
APPLICANT: Choulika, Andre
APPLICANT: Dujon, Bernard
APPLICANT: Dujon, Bernard
APPLICANT: Nicolas, Jean-Francois
TITLE OF INVENTION: Nucleotide Sequence Encoding the Enzyme Patent No. 5866361
TITLE OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.8%; Score 97; DB 2; Length 624; 27.1%; Pred. No. 2.99e+01; ative 22; Mismatches 33; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NOWER: US/08/756,317
FILING DATE: 25-NOV-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/007,693
FILING DATE: 29-NOV-1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET UNMBER: 33,062
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET UNMBER: 33,062
RECOMMULICATION INFORMATION:
TELEPHONE: (713) 787-1440
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 624 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: Z0005-3315
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
CE 624 AA; 69538 MW; 1929028 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/08465273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 WEAHPFFNFIKROYQINAQALQEAA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           375 -PEDPLFQLVAKLYEVFLQFLQNLA 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.8%;
Best Local Similarity 27.1%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-465-273-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Gaps
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APPLICANT: Perrin, Arnaud
APPLICANT: Dujon, Bernard
APPLICANT: Nicolas, Jean-Francois
TITLE OF INVENTION: Nucleotide Sequence Encoding the Enzyme
tent No. 5792632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | | : : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKSNNALIVILGTVTLDAVGIGLVMPVLPGLLRDIPLMPERDGPNHPDMCV 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.7%; Score 93; DB 2; Length 80;
Best Local Similarity 31.4%; Pred. No. 5.37e+01;
Matches 16, Conservative 14; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,241
FILLING DATE: 07-NOV-1994
CLASSIFICATION: 800
PRIOR APPLICATION: DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: I-SCEI and the Uses Thereof NUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                             03495-0111-03000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 AA.
                                                                                                         FILING DATE: 05-NOV-1992
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/879,689
FILING DATE: 05-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: POLICE, Jane E.R.
REGISTRATION NUMBER: E.R.
                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/336,241
FILING DATE: 07-NOV-1994
                                                                                       UMBER: US 07/971,160
05-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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Patent No. 5792632
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peotide
JENCE 80 AA, 8936 MW; 32220 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/08336241
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IBM PC compatible
                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1300 I Street, N.W.
                                                                                                                                                                                                                                                                              TELEPAONE: 202-408-4000
TELEPAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington
 FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
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Patent No. 5948678
GENERAL INFORMATION:
APPLICANT: Choulika, Andre
APPLICANT: Dujon, Bernard
APPLICANT: Nicolas, Jean-Francois
ITILE OF INVENTION: Nucleotide Sequence Encoding the Enzyme Patent No. 5948678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Mismatches 18; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKSNNALIVILGTVTLDAVGIGLVMPVLPGLLRDIRLMRERDGRNHRDMCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 93; DB 2; Length 80; Pred. No. 5.37e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER PEADABLE FORM.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: I-SCEI and the Uses Thereof
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                   03495-0111-06000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 AA
                                                                                     APPLICATION NUMBER: US 07/879,689
FILING DATE: 05-MAY-1992
ATTORNEY/AGENT INFORMATION:
                 APPLICATION NUMBER: US/08/465,273
FILING DATE: 06-MAY-1995
                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/336,241
FILING DATE: 07-NOV-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/09/119,024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
JENCE 80 AA; 8936 MW; 32220 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/09119024
                                                                                                                                                                                                                                                                            NAME: Potter, Jane E.R. PEGISTRATION NUMBER: 33,332 REFERENCE/DOCKET NUMBER: 03, TELECOMMUNICATION INFORMATION: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1300 I Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.7%;
Local Similarity 31.4%;
les 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 80 am....
TVDE: amino acid
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20005-3315
                                     FILING DATE: 06 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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TOPOLOGY:
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APPLICANT: Plessis, Anne
APPLICANT: Thiers, Anne
APPLICANT: Thiers, Agnes
TITLE OF INVENTION: Nucleotide Sequence Encoding the Enzyme
TITLE OF INVENTION: I-SCEI and the Uses Thereof
CORRESPONDENCE 52
                                                                                                                                                                                       3;
                                                                                                                                                                                                                    58 LKSEHG-KVQLGNITVDMV-LG-GMRGMIGLLWETSLLDPDEGIRFRGLSI 105
                                                                                                                                                                                                        1 MKSNNALIVILGTVTLDAVGIGLVMPVLPGLLRDIRLMRERDGRNHRDMCV 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
                                                                                                                                                                                      14; Mismatches 18; Indels
                                                                                                                                                                    Query Match 2.7%; Score 93; DB 2; Length 80; Best Local Similarity 31.4%; Pred. No. 5.37e+01; Matches 16; Conservative 14; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/971,160
FILING DATE: 19921105
CLASSIFICATION: 435
     ATCALICATION NUMBER: US 07/879,689
FILING DATE: 05-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 03495-0111-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4000
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
TOPOLOGY: 1:0---
                                                                                                                                                                                                                                                              80 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/879,689
FILING DATE: 05-AMX-1992
ATTORNEY/AGENT INFORMATION:
NAME: Ogden, Stasia L.
                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/07971160
Patent No. 544896
GENERAL INFORMATION:
APPLICANT: Dujon, Bernard
APPLICANT: Choulika, Andre
APPLICANT: Choulika, Andre
                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                         MOLECULE TYPE: peptide
JENCE 80 AA; 8936 MW; 32220 CN;
                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/07971160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36,228
FILING DATE: 05-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20005-3315
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.0
                                                                                                                                                                                                                                                             US-07-971-160-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                    SEQUENCE
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 44, Application US/08484101B
Patent No. 5824868
GENERAL INFORMATION:
APPLICANT: California Institute of Technology
TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO
TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO
WUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                Score 93; DB 1; Length 80;
Pred. No. 5.37e+01;
14; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                           1 MKSNNALIVILGTVTLDAVGIGLVMPVLPGLLRDIRLMRERDGRNHRDMCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,101B
FILING DATE: 07-JUN-1995
CLASSIFCATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Richard F. Trecartin
STREET: 3400 Embarcadero Center, Suite 3400
REFERENCE/DOCKET NUMBER: 03495-0111-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-57515-2/RFT
TRIEDUMNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: POT/US94/
FILING DATE: 01-3U1-1994
CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: US 08/086,555
FILING DATE: 01-3U1-1993
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                         TELEPHONE: 202-408-4000
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHRACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE 80 AA; 8936 MW; 32220 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 44, Application US/08484101B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 773 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 773 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                Query Match 2.7%;
Best Local Similarity 31.4%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J 12
US-08-484-101B-44
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635 AHPHSNSLLRGLQVLLVDINDSNRAVTRKLLEKLGCDVTAVSSGFDCLTAIAPGSSSPST 694
                                                                                                                    115 AKPGGEPLPEGLLWILLTGKVPSKEQVDSLSQELRSRATVPDHVYKTIDAL-PVTAHPMT 173
                                                                   4; Gaps
                                                                                                                                                                                                                                                                                                                                Sequence 42, Application US/08484101B
Patent No. 5824868
GENERAL INFORMATION:
APPLICANT: California Institute of Technology
TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO
                                      Score 94; DB 2; Length 773; Pred. No. 4.64e+01; 28; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,101B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
                                                                                                                                             695 SFQVVVLDLQM-AEMD-GYEVAMRIRSRSWPLIVATTVSLDEEM 736
                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard F. Irecartin
STREET: 3400 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                           773 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A-57515-2/RFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/
FILING DATE: 01-0101-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/086,555
FILING DATE: 01-01-1993
CLASSIFICATION: 800
                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
JENCE 773 AA; 85689 MW; 3085314 CN;
MOLECULE TYPE: protein
JENCE 773 AA; 85689 MW; 3085314 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                        Sequence 42, Application US/08484101B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Trecartin, Richard F. REGISTRATION NUMBER: 31,801 REFERENCE/DOCKET NUMBER: A-1 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHAPACTERISTICS:
LENGTH: 773 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 50
                                        Query Match
Best Local Similarity 24.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 3400 Embarca
CITY: San Francisco
STATE: California
                                                                  25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94111
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             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                  Matches
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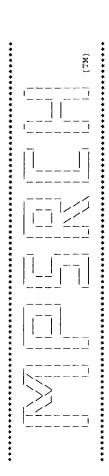
2.7%; Score 94; DB 2; Length 773; 24.0%; Pred. No. 4.64e+01;

Query Match Best Local Similarity

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635 AHPHSNSLLRGLQVLLVDINDSNRAVIRKLLEKLGCDVIAVSSGFDCLTAIAPGSSSPST 694
                                                  115 AKPGGEPLPEGLLWLLLTGKVPSKEQVDSLSQELRSRATVPDHVYKTIDAL-PVTAHPMT 173
4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 DYTWNLLKAGKIPEEFNVFNLIQEMRTQRHSAVQTKEQYELVHRAIAQLFEKQLQLY 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       336 DYAWKILKSGKVVPGFG-HGVLR--KTDPRYTCQ-RE-FALKHLPEDPLFQLVAKLY 387
25; Conservative 28; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20; Indels
                                                                                                                                                                                                                                                                                                       APPLICANT: TONKS, Nicholas
APPLICANT: Flint, Andrew J.
IIILE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
IIILE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON BROOK, SMITH & REYNOLDS, P.C.
STREET: TWO Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 253;
                                                                             695 SFQVVVLDLQM-AEMD-GYEVAMRIRSRSWPLIVATTVSLDEEM 736
                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
ODERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 89; DB 2; L
Pred. No. 9.53e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSHL96-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/685,992 FILING DATE: 25-JUL-1996 CLASSIFICATION: 435
                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
JENCE 253 AA; 29778 MW; 320375 CN;
                                                                                                                                                                                                                                                                Sequence 20, Application US/08685992 Patent No. 5912138 GENERAL INFORMATION:
                                                                                                                                                                                                                                          Seguence 20, Application US/08685992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Grandhan, Patritaia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER:
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Best Local Similarity 29.8%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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US-08-585-992-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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Matches
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Best Local Similarity 29.8%; Pred. No. 9.53e+01;
Matches 17; Conservative 15; Mismatches 20; Indels 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 DYTWNLLKAGKIPEEFNVFNLIQEMRTQRHSAVQTKEQYELVHRAIAQLFEKQLQLY 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  336 DYAWKTLKSGKVVPGFG-HGVLR--KIDPRYTCQ-RE-FALKHLPEDPLFQLVAKLY 387
                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BPOOK, SMITH & REYNOLDS, P.C. STREET: Two Militia Drive CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: Windows 95
SOFTWARE: FASTEM: Windows 95
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/144,925
FILING DATE:
PRIOR APPLICATION:
PRIOR PAPLICATION:
APPLICATION NUMBER: 08/685,992
FILING DATE: July 25, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                Sequence 20, Application US/09144925
Patent No. 5951979
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
            253 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL96-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
JENCE 253 AA; 29778 MW; 320375 CN;
                                                                                          Sequence 20, Application US/09144925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 20;
                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
            STANDARD;
                                                                                                                                                                                                                36
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                              STATE: MA
COUNTRY: USA
ZIP: 02421-4799
LT 15
US-09-144-925-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                       XXXXXX
RESULT
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Search completed: Fri Oct 22 17:10:33 1999 Job time : 17 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Oct 22 17:04:20 1999; MasPar time 20.94 Seconds 897.479 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-702-718-6 (1-469) from US08702718.pep 3443

Description: Perfect Score:

1 MVFYRGVSLLSKLRSRAVQQ.....PLERPKSVTMEWLENHCKKA 469 Scoring table: Sequence:

122810 seqs, 40068593 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

pir60 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Mean 50.451; Variance 107.716; scale 0.468 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	8	00e+00	00e+00	00e+00	00e+00	00e+00	00e+00	58e-29	00e-29	29e-23	61e-203	58e-4(	35-3	9-3	-3		e-2	~ >	e-2	$\sim$	3-25	e-2	e ::	ç.;
	Pred.	.00	00	00	00.	00	00	586	.00	236	.616	586	.98e-3	.33e-3	.59e-3	.46e-3	12	.45	.756	196	.79e-2	586	.62	8
	Pre	0	0	0	0	0	0	H	H	- 1	9	~	4	H	6	ø	-1	ci	H	H	m	Ŋ	C4	۳.
	ion	ethanolamine ammonia-	citr		(3)	(Si)	(81)	(3;)-	(81)-	filament protei	(si)-synthase		٠,				(si)-synthase	~	_			synthase		
	ipt	nol	abl	ate	ate	ate	ate	ate	ate		ate.	ate	ate	ate.	ate	ate	ate	ate	ate	apl	ate	ate	ate	ate
	Description	etha	probable	citrate	citrate	citrate	citrate	citrate	citrate	14 - nm	citrate	citrate	citrate	citrate	citrate	citrate	citrate	citrate	citrate	probable	citrate	citrate	citrate	citrate
IES																								
SUMMARIES	DI CI	S44316	T02390	YKMUM	YKPG	S42370	YKBY	YKBYC	S41563	JC5625	S52814	140717	A43936	YKQPC	E69628	S74344	139506	YKFSCA	JQ1392	E70782	C69417	S53007	D71982	009699
	DB	7	C4	Н	Н	C1	_	Н	7	<b>ر</b> ا	7	7	7	٦	~	C1	C4	٦	C a	7	7	C1	C1	C)
	Query Match Length	471	474	472	464	458	479	9	469	9	$\infty$	437	~	3	$\sim$	397	$\sim$	4.28	3	3	~	516	C1	372
	ch	0.0	6.8	.3	8.7	6.	7	8.	8.	۲.	₹.	.5	.1	0.	6.	8.9		<u>د</u> .				7.9	ري - ا	. 2
de	Query Match	96	86	7.	55	Ŋ	5	4	₹	4	3.	7	10	٠,	w	w	ω	~	w	w				
	Score	3098	2987	2454	2021	1820	1763	1679	1680	1385	1218	360	347	310	305	306	287	285	274	275	272	271	S	248
	Result No.		C1	e	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	Cį.	C1	23

360 KIVPRYICQREFAMKHLPEDPLFQLVSKLYEVFLLFLQNLAKLKPWPNVDAHSGVLLNYY 419

300 ALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYVWKTLNSGKVVPGFGHGVLR 359

Db õ

0.7

11.1 13.045.3 14.1 15.045.3 16.05.3 17.05.3	c.change B. B.	Gaps 4: KKIK 60   :    :    :    :    :    :    :
citrate synthase - He citrate (si)-synthase probable citrate synt citrate (si)-synthase probable citrate probable citrate citrate (si)-synthase probable citrate probable citrate probable citrate probable citrate probable citrate probable citrate citrate (si)-synthase probable citrate probable probable citrate probable prob	(EC 4.3.1.7) - potato sum #common_name potaticion 10-Nov-1995 #text_ion 10-Nov-1995 #text_ir, L.; Mueller-Roeber, Library, September 1997 #3509; PID:9483510 ynthase gen 1yase gen 1yase	998; DB 2; Length 471; 5. 0.00e+00; 5. matches 22; Indels 4; 9VQTSSGLDLRSELVOELIPEOODRL [
B64523 YKRECC YKRECC 140044 140044 1604760 YKRY YKRY YKRY YKRY YKRY YKRY YKRY YKR	ALIGNMENTS  type complete e ammonia-lyase solanum tuberce #sequence_revis  v.; willmitze tv.; willmitze the EMBL Data #label LAN ::X75082; NID:94 ::X75082; NID:94 ::A75082; NID	08; Score 306 08; Pred. No ve 23; Miss 00SNVSNSVRMLO)   :             00TINLSNSVRMLO)   :
000000000000000000000000000000000000000	#ty] ne an	08; 08; 000; 001; 002; 003; 004; 005; 006; 007; 007; 007; 008; 00
44448888488888888888888888888888888888	16 nolami nal_na nal_na sep-19 Sep-19 16 schuet itted itted itted 1-471 1-471 nia-1y	imilarity 89.6%; Pr. 89.0%; Sc. Conservative 23 RSVSLLSKLRSRAVQOSNVSN 19:11111111111111111111111111111111111
40204066480448000000000	S44316 ethano % forma % forma % forma % of S % of S	larity Conse SLLSKL          SLLSKL         CONITY         WLLLT 
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#length 474 #molecular-weight 52782 #checksum 6960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, May 1998
Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence.
                      417
                                                                                                                                                                                                                    probable citrate (si)-synthase (EC 4.1.3.7) - Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17/3; 39/3; 53/3; 75/3; 97/3; 135/3; 157/1; 184/3; 201/2; 22//2; 270/2; 284/3; 313/3; 347/3; 383/3; 400/3; 425/2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 MALQVQSEFQKAYENGIHKSKFWEPTYEDCLNLIARVPVVAAYVYRRMYKNGDSIPSDKS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 LDYGANFSHMLGFDDEKVKELMRLYITIHSDHEGGNVSAHTGHLVGSALSDPYLSFAAAL 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NGLAGPLHGLANQEVLLWIKSVVEECGEDISKEQLKEYVWKTLNSGKVIPGYGHGVLRNT 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Brandon, R.C.; Sykes, S.M.; Kaul, S.; Mason, T.M.;
Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MVFFRSVSAFTRLRSRVQGQQSSLSNSVRWIQMQSSTDLDLKSQLQELIPEQQDRLKKLK 60
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                                                                                                                                                                                                                                                                                   #formal_name Arabidopsis thaliana #common_name mouse-ear
                                                                                                                                                                                                                                                                                                                            05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change
Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
                                                                                        418 GLTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTWEWLENHCKKA 469
                                                               420 GLTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENQCKKA 471
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Pred. No. 0.00e+00;
53; Mismatches 27;
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citrate (si) synthase (EC 4.1.3.7) precursor, mitochondrial - Arabidopsis thallana
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*#note the sequence from Fig. 2 is inconsistent with that from
Fig. 1 in having 47-G1y, 125-Trp, 14-Leu, 151.Ser,
185-Asn, 187-Asn, 191-Asn, 348-Leu, an additional G1y
after 89-Trp, an additional Val after 393-Cys and two
additional Arg after 228-Arg, in lacking 114-Leu and
residues 333 to 241
                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant Mol. Biol. (1989) 13:411-418
Isolation of a cDNA encoding mitochondrial citrate synthase
from Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                 Unger, E.A.; Hand, J.M.; Cashmore, A.R.; Vasconcelos, A.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SEHGKVQLGNITVDMVIGGMRGMTGLLWETSLLDPEEVFALGDCRLPECQKALLPTAQSG 120
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                                                                                                                                                                                                                            #formal_name Arabidopsis thaliana #common_name mouse-ear
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#length 472 #molecular-weight 52941 #checksum 9626
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419 LTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENHCKKA 469
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carbon-carbon lyase; homodimer; mitochondrion;
oxo-acid-lyase; tricarboxylic acid cycle
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                                                                                                                               *type complete
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*authors Evans, C.T.; Owens, D.D.; Sumegi, B.; Kispal, G.; Srere, P.A. #journal Biochemistry (1988) 27:4680-4686
#title Isolation, nucleotide sequence, and expression of a cDNA encoding pig citrate synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      It is synthesized in the cytoplasm but functions in the mitochondrion of eukaryote cells. This molecule is a dimer of identical chains. Each dimer binds two molecules of acetyl-CoA and two molecules of oxaloacetate at two active sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ts annotation; X-ray crystallography, 2.7 and 1.7 angstroms citrate (si)-synthase is found in nearly all cells capable of oxidative metabolism. It catallyzes the condensation of oxaloacetate and acetyl-CoA to form citrate in the tricarboxylic
                                                                                                                              citrate (si)-synthase (EC 4.1.3.7) precursor - pig
#formal_name Sus scrofa domestica #common_name domestic pig
15.0ct-1982 #sequence_revision 30-Sep-1992 #text_change
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#modified_site N6,N6-trimethyllysine (Lys) #status
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#product citrate (si)-synthase #status experimental
#label MAT\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bloxham, D.P.; Parmelee, D.C.; Kumar, S.; Walsh, K.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bloxham, D.P.; Parmelee, D.C.; Kumar, S.; Wade, R.D.; Ericsson, L.H.; Neurath, H.; Walsh, K.A.; Iltani, K. Proc. Natl. Acad. Sci. U.S.A. (1981) 78:5381-5385 Primary structure of porcine heart citrate synthase. A61347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carbon-carbon lyase; homodimer; methylated amino acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochemistry (1982) 21:2028-2036
Complete amino acid sequence of porcine heart citrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *authors Remington, S.; Wiegand, G.; Huber, R.

*journal J. Mol. Biol. (1982) 158:111-152

*title Crystallographic refinement and atomic models of two different forms of citrate synthase at 2.7 and 1.7

*cross-references MUID:83010291
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417 YGLTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENHCKKA 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                          #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type protein
##residues 28-464 ##label BLO
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                                                                                                                                                                                                                                        A29966; A01109; A61347
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#accession A01109
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27 SASSINLKDILADLIPKEOARIKTFROOHGNIVVGOITVDMMYGGMRGMKGLVYEISVLD 86

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S42370 #type complete citrate (si)-synthase (EC 4.1.3.7) precursor - Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                387 VLLEQGKAKNPWPNVDAHSGVLLQYYGMTEMNYYTVLFGVSRALGVLAQLIWSRALGFPL 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 SLLDPDEGIRFRGLSIYECQKVLPAAKPGGEPLPEGLLWLLLTGKVPSKEQVDSLSQELR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 MDLLAKLPTVAAIIYRNLYRDGSAVSVIDPKKDWSANFSSMLGYDDPLFAELMRLYLVIH 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 MSLIAQVPLVAAYVYRRMYKNGNTIP-KDDSLDYGANFAHMLGFSSSDMHELMKLYVTIH 268
                                                                           87 PDEGIRFRGYSIPECQKMLPKAKGGEEPLPEGLFWLLVTGQIPTEEQVSWLSKEWAKRAA 146
                                                                                                                                                                                                                                154 VPDHVYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLI 213
                                                                                                                                                                                                                                                                                   207 AKLPCVAAKIYRNLYREGSSIGAIDSKLDWSHNFTNMLGYTDAQFTELMRLYLTIHSDHE 266
                                                                                                                                                                                                                                                                                                                                                                                                                        327 KLRDYIWNTLNSGRVVPGYGHAVLRKTDPRYTCQREFALKHLPHDPMFKLVAQLYKIVPN 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 ARADLPTHVVRMLDNFPDNLHPMAQFIAAIAALNNESKFAGAYARGVAKASYWEYAYEDS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 SRATVPDHVYKIIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKLWEPTYEDS 209
                                                                                                                            94 PDEGIPFPGLSIYECOKVLPAAKPGGEPLPEGLLWLLTGKVPSKEQVDSLSQELPSPAT 153
                                                                                                                                                                                                                                                                                                                                    214 AQVPLVAAYVYRRMYKNGNTI-PKDDSLDYGANFAHMLGFSSSDMHELMKLYVTIHSDHE 272
                                                                                                                                                                                                                                                                                                                                                                                          267 GGNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLVWLTQLQKEVGKDVSDE 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            333 QLKDYAWKTLKSGKVVPGFGHGVLRKTDPRYTCQREFALKHLPEDPLFQLVAKLYEVFLQ 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 393 FLQNLAKL-NPWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALGLPL 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 SVLDPEEGIRFRGYSIPECQKLLPKAKGGEEPLPEAIWWLLCTGDVPSEAQTAAITKEWN 144
34 ISSGLDLRSELQELIPPQQDRLKKLKSEHGKVQLGNITVDMVLGGMRGMTGLLWETSLLD 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 LQVQTSSGLDLRSELQELIPEQQDRLKKLKSEHGKVQLGNITVDMVLGGMRGMTGLLWET 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         elegans
#formal_name Caenorhabditis elegans
07-0ct-1994 #sequence_revision 10-Nov-1995 #text_change
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                                                                                                                                                                             147 LPSHVVTMLDNFPINLHPMSQLSAAITALNSESNFARAYAEGIHRTKYWELIYEDCMDLI
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carbon-carbon lyase; mitochondrion; oxo-acid-lyase
#length 468  #molecular-weight 51540  #checksum 26;
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Local Similarity 56.5%; Pred. No. 0.00e+00;
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452 ERPKSVTME 460
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EMBO J. (1984) 3:1773-1781
Isolation of the nuclear yeast genes for citrate synthase and
fifteen other mitochondrial proteins by a new screening
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Verhasselt, P.; Aert, R.; Voet, M.; Volckaert, G.
submitted to the EMBL Data Library, January 1994
Twelve open reading frames revealed on the 23.6 kbp segment
flanking the centromere on the Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                    YKBY *type complete citrate (si)-synthase (EC 41.3.7) precursor, mitochondrial yeast (Saccharomyces cerevisiae) protein N2019; protein YNR001c
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##note the nucleotide sequence was submitted to the EMBL Data
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Teast (1994) 10:1355-1361
Twelve open reading frames revealed in the 23.6 kb segment
flanking the centromere on the Saccharomyces cerevisiae
                                                                                                                                                                                                           389 VFLQFLQNLAKL-NPWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGIC-SQLIWDRA 446
                        269 SDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGEN 328
                                                                                                                                                                                     385 ITPCILLEQGKAKNPWPNVDSHSGVLLQYFGMTEMSFYTVLFGVSRALG-CLSQLIWARG 443
                                                                                          325 YTEEQLKEWVWKHLKSGQVVPGYGHAVLRKTDPRYECQREFALKHLPNDDLFKLVSTLYK 384
                                                                                                                                      329 ISKEQLKDYAWKTLKSGKVVPGFGHGVLRKTDPRYTCQREFALKHLPEDPLFQLVAKLYE 388
265 SDHEGGNVSAHTSHLVGSALSDPYLSFSAAMAGLAGPLHGLANQEVLVFLNKIVGEIGFN 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #formal_name Saccharomyces cerevisiae
25-Feb-1985 #sequence_revision 10-Feb-1995 #text_change
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#product citrate (si)-synthase #status predicted #label
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           219 GKLPVIASKIYRNVFKDGKITSTDPNADYGKNLAQLLGYENKDFIDLMRLYLTIHSDHEG 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                339 IEKYLWDILNAGRVVPGYGHAVLRKIDPRYIAQREFALKHFPDYELFKLVSIIYEVAPGV 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 VPDHVYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLI 213
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#length 479 #molecular-weight 53360 #checksum 4
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                                              P.A.; Guarente, L.P.
Mol. Cell. Biol. (1986) 6:4509-4515
Mitochondrial and nonmitochondrial citrate synthases in
Saccharomyces cerevisiae are encoded by distinct homologous
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The complete sequence of a 10.8kb fragment to the right of
the chromosome III centromere of Saccharomyces cerevisiae.
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                       Rosenkrantz, M.; Alam, T.; Kim, K.S.; Clark, B.J.; Srere
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submitted to the Protein Sequence Database, March 1992
8119474
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Intramitochondrial functions regulate nommitochondrial citrate synthase (CIT2) expression in Saccharomycos
                                                                                                                                                                                                                                                                   ##cross-references EMBL:211113, NID:93297; PID.93299, GB:M14685;
NID:9171226; PID:9171227
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#title Characterization of the cit-1 gene from Neurospora crassa encoding the mitochondrial form of citrate synthase.
#cross-references MUID:94104594
                                                        251 LIIHSDHEGGNVSAHTSHLVGSALSSPYLSLASGLNGLAGPLHGRANQEVLEWLFALKEE 310
                                                                                                                                                               311 VNDDYSKDTIEKYLWDTLNSGRVIPGYGHAVLRKTDPRYMAQRKFAMDHFPDYELFKLVS 370
                                                                                                                                                                                                                                                                                371 SIYEVAPGVLTEHGKTKNPWPNVDAHSGVLLQYYGLKESSFYTVLFGVSRAFGILAQLIT 430
                                                                                                                                                                                                                                                                                                             97 FFRGKTIPECQELLPKA-PGGKEPLPEGLFWLLLTGEVPSEQQVRDLSAEWAARSDVPKF 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 IEELIDRCPSDLHPMAQLSLAVTALEHTSSFARAYAKGINKKEYWGYTFEDSMDLIAKLP 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 TIAARIYQNVFKGGKVAAVQKDKDYSFNFANQLGFGDNKDFVELLRLYLTIHTDHEGGNV 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 LVAAYVYRRMYKNGNTIPKDDSLDYGANFAHMLGFSSS-DMHELMKLYVTIHSDHEGGNV 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    276 SAHTTHLVGSALSSPFLSVAAGLNGLAGPLHGLANQEVLNWLTEMKKVIGDDLSDEAITK 335
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                                                                                                                                                                                                   325 CGENISKEQLKDYAWKILKSGKVVPGFGHGVLRKIDPRYICQREFALKHLPEDPLFQLVA 384
205 TYEDSMSLIAQVPLVAAYVYRRMYKNGNTIPKDDSLDYGANFAHMLGFSSSDMHELMKLY 264
                                                                                                             265 VIIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEE 324
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20-May-1994 #sequence_revision 10-Nov-1995 #text_change
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Best Local Similarity 56.2%; Pred. No. 1.00e-293;
Matches 244; Conscrvative 78; Mismatches 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Numata, O.; Takemasa, T.; Takagi, I.; Hirono, M.; Hirano, H.;
Chiba, J.; Watanabe, Y.
Biochem. Biophys. Res. Commun. (1991) 174:1028-1034
Tetrahymena 14-nm filament-forming protein has citrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #domain transit peptide (mitochondrion) *status
predicted *label TNP\
#product 14-nm filament protein/citrate synthase *status
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**cross-references GB:D90117; NID-9217406; PID:d1014848; PID:g1588046

**note part of this sequence, including the amino end of the mature protein, was confirmed by protein sequencing mature protein, oral morphogenesis preceding binary fission, and in nuclear events during fertilization, such as formation of gametic pronuclei and zygote formation of gametic pronuclei and intochondrial enzyme, citrate
84 IIFRCYTIPQLKEFLPKADPKAADQANQEPLPEGIFWLLMTGQLPTHAQVDALKHEWQNR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 IRFRGLSTYECOKVLP-A-AKPG--G--EPLPEGLLWLLTGKVPSKEQVDSLSGELPSP 151
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                                                                                                                                                                                                                            14-nm filament protein/Citrate synthase (EC 4.1.3.-) -
Tetrahymena thermophila (SGC5)
49K filament-forning protein
#formal_name Tetrahymena thermophila
14-oct.1997 #sequence_revision 07-Nov-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                    Takeda, T.; Watanabe, Y.; Numata, O.
Biochem. Biophys. Res. Commun. (1997) 237:205-210
Direct demonstration of the bifunctional property of
Tetrahymena 14-nm filament protein/citrate synthase
following expression of the gene in Escherichia coli
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                                                                    456 SYSTDKWIEI-CKK 468
                                                                                                                456 SVTME-WLENHCKK 468
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                                                                                                                                                                                                           JC5625
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Wang, Y.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.;
Hall, J.; Storms, R.K.; Vo, D.H.; Winnett, E.
submitted to the EMBL Data Library, July 1995
The sequence of Saccharomyces cerevisiae chromosome XVI right
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##cross-references EMBL:248951; NID:q762999; PID.q763000, MIPS:YPR001w
##experimental_source strain AB972
**NCE S57724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 LDPDEGIRFRGLSIYECQKVLPAAKPGGEP-LPEGLLWLLLIGKVPSKEQVDSLSQELRS 150
                               211 SLIAQVPLVAAYVYRRMYKNGNTIPKDDSLDYGANFAHMLGFSSSDMHELMKLYVTIHSD 270
                                                                                   264 HEGGNVSAHTTHLVGSALSDPYLSYSAGVNGLAGPLHGLANQEVLKWLLQFIEEKGTKVS 323
                                                                                                                                           271 HEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENIS 330
                                                                                                                                                                                                         324 DKDIEDYVDHVISSGRVVPGYGHAVLRDTDPRFHHQVDFSKFHLKDDQMIKLLHQCADVI 383
                                                                                                                                                                                                                                                                                                                            384 PKKLLTYKKIANPYPNVDCHSGVLLYSLGLTEYQYYTVVFAVSRALG-CMANLIWSRAFG 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      citrate (si)-synthase (EC 4.1.3.7) - yeast (Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 LDPEHGIKFQGLTIEECQNRLPNTGIDGDNFLPESMLWLLMTGGVPTFQQAASFRKELAI 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #formal_name Saccharomyces cerevisiae
19-May-1995 #sequence_revision 01-Sep-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jia, Y.K.; Becam, A.M.; Slonimski, P.P.; Herbert, C.J.
submitted to the EMBL Data Library, June 1995
S57724
                                                                                                                                                                                                                                           331 KEQLKDYAWKTLKSGKVVPGFGHGVLRKTDPRYTCQREFALKHLPEDPLFQLVAKLYEVF
                                                                                                                                                                                                                                                                                                                                                           391 LQFLQNLAKL-NPWPNVDAHSGVLLNYGLTEARYYTVLFGVSRALGIC-SQLIWDRALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 VQTSSGLDLRSELQELIPEQQDRLKKLKSEHGKVQLGNITVDMVLGGMRGMTGLLWETSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carbon-carbon lyase; oxo-acid-lyase
#length 486 #molecular-weight 53811 #checksum 9998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein LPZ1w; protein YP9723.01; protein YPR001w
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S52814
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Best Local Similarity 45.0%; Pred. No. 6.61e-203;
Matches 205; Conservative 102; Mismatches 124;
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Pearson, D.; Bowman, S.
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##residues 1-486 ##label JIA
                                                                                                                                                                                                                                                                                                                                                                                                                                               443 LPIERPGSADLKWFHDKYR 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    449 LPLERPKSVTMEWLENHCK 467
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301 GLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYAWKTLKSGKVVPGFGHGVLRKTD 360

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324 PRAAIVKETAHEILEHLGGDDLLDLAIKLEEIALA-DDYFISRKLYPNVDFYTGLIYRAM 382

361 PRYTCQREFA---LKHLPEDPLFQLVAKLYEVFLQFLQNLAKLNPWPNVDAHSGVLLNYY 417

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Nucleotide Sequence, expression and transcriptional analysis of the Corynebacterium glutamicum gltA gene encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carbon-carbon lyase; oxo-acid-lyase; catalyzes synthesis of citrate from acetyl-CoA and oxaloacetic acid tricarboxylic acid cycle *superfamily citrate (si)-synthase carbon.carbon.carbon.lyase; hombhexamer; oxo-acid-lyase; tricarboxylic acid cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 LLINGELPTPDELHKFNDEIRHH-TLLDEDFKSQFNVFPRDAHPMATLASSVNILST-Y- 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 RMMFGYPTEPYEIDPIMVKALDKLILHADHEQ-NCSTSTVRMIGSAQANMFVSIAGGIN 266
141 PGRKLPHYTEKVLSSLPKDMHPMTQLAIGLASMNKGSLFATNYQKGLIGKMEFWKDTLED 200
                           201 SLNLIASLPLLTGRIYSNITNEGHPLGQYSEEVDWCTNICSLLGMTNGTNSSNTCNLTSQ 260
                                                                                                                   261 OSLDFINLMRLYTGIHVDHEGGNVSAHTTHLVGSALSDPYLSYSSGIMGLAGPLHGLAAQ 320
                                                                                                                                                                                                               258 H--E---LMKLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQ 312
                                                                                                                                                                                                                                                          321 EVVRFLIEMNSNIS-SIAREQEIKDYLWKILNSNRVIPGYGHAVLRKPDPRFTAMLEFAQ 379
                                                                                                                                                                                                                                                                                        380 KRPIEFENDKNVLLMQKLAEIAPKVLLEHGKSKNPFPNVDSASGILFYHYGIRELLFFTV 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 LLLTGKVPSKEQVDSLSQELRSRATVPDHVYKT-IDALPVTAHPMTQFATGVMALQVQSE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 YQDQLN-PLDEAQL-D-K--ATVRLMAKVPMLAAYAHRAR-KGAPYMYPDNSLNARENFL 207
                                                                                                                                                                                                                                                                                                                                                                                         372 KH-LP-E-DPLFQLVAKLYEVFLQFLQNLAKL-NPWPNVDAHSGVLLNYYGLTEARYYTV 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #formal_name Corynebacterium glutamicum
16_Aug-1996_#sequence_revision 16-Aug-1996 #text_change
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#length 437 #molecular-weight 48929 #checksum 2093
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Microbiology (1994) 140:1817-1828
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#authors Schendel, F.J.; August, P.R.; Anderson, C.R.; Hanson, R.S.;
Flickinger, M.C.
#journal Appl. Environ. Microbiol. (1992) 58:335-345
#title Cloning and nucleotide sequence of the gene coding for citrate synthase from a thermotolerant Bacillus sp.
#cross-references MUID:92171501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##note sequence inconsistent with the nucleotide translation sequence extracted from NOBI backbone (NCBIP:84047)
CLASSIFICATION #superfamily foliate foil-synthase #note feeth 373 #molecular-weight 41970 #checksum 2911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 LLLEGTIPNEAEKQHLEETLKQEYDVPDEIIQVLSLLPKTAHPMDALRTGVSVL-A-S-F 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 DTELLNREHSTNL-KRAYQ--L-L-GKIPNIVANSYHILHSEEPVQPLOD-LSYSANFLY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 QKAYEKGIHKSKLWEPTYEDSMSLIAQVPLVAAYVYRRMYKNGNTIPKDDSLDYGANFAH 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 MITGKKPTELEEKIFDRSLVLYSEHELPN-STFTARVIASTLSDLYGALTGAVASLKGHL 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 30.3%; Pred. No. 4.98e-38;
Matches 96; Conservative 80; Mismatches 117; Indels 24; Gaps
                                                                                                                                                                    A43936 *type complete
citrate synthase - Bacillus sp.
*formal_name Bacillus sp.
10-Mar-1993 *sequence_revision 18-Nov-1994 *text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##experimental_source strain C4, ATCC 55182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##status
##molecule_type nucleic acid; protein
##residues 1-373 ##label SCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     333 PIFFS-SRTVGLCAHVM 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             425 TVLFGVSRALGICSQLI 442
                                                                                                                                                                                                                                                                      21-Aug-1998
A43936
                                                       418 GLTEARYYTVLFGVSR 433
  383 GFPID-FFIVLFAIGR 397
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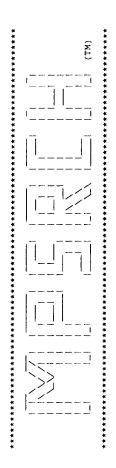
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Kunst, F.: Ogasawara, N.: Moszer, I.; Albertini, A.M.;
Alloni, G.: Azevedo, V.: Bertero, M.G.: Bessieres, P.:
Bolotin, A.: Borchert, S.: Boriss, R.: Boursier, L.: Brans,
A.: Braun, M.: Brignell, S.C.: Bron, S.: Brouillet, S.:
Bruschi, C.V.: Cadwell, B.: Capuano, V.: Curmings, N.M.;
Choi, S.K.: Codani, J.J.: Connerton, I.F.: Curmings, N.J.;
Daniel, R. A.: Denizot, F.: Devine, K. M.; Duesterhoeft, A.;
Ehrlich, S.D.: Emmerson, P.T.: Entian, K.D.: Errington, J.;
Fabret, C.: Ferrari, E.: Foulger, D.: Fritz, C.: Fujita,
M.: Fujita, Y.; Funa, S.; Galizzi, A.; Galleron, N.: Ghim,
S.Y.: Glaser, P.: Goffeau, A.: Golightly, E.J.; Grandi, G.;
                                                                                                                                                                                                                                                                                                                                                                                                                            of
                                                                                                                                                             Cloning of genes responsible for acetic acid resistance in Acetobacter aceti.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 A-F-YPDANDIAIP-AN-RDLA---AMPLIAKIPTIAAWAYK--YTQGEAFIYPRND-LN 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 EGLLWLLLTGKVPSKEQVDSLSQELRSRATVPDHVYKTIDALPVTAHPMTQFATGVMALQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 VQSEFQKAYEKGIHKSKLWEPTYEDSMSLIAQVPLVAAYVYRRMYKNGNT-I-PKDDSLD 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 YAENFLSMMFARMSEPYKVNPVLARAMNRILILHADHEQ-NASTSTVRLAGSTGANPFAC 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 IAAGIAALWGPAHGGANEAVLK-MLARIGK-KENIP-AFIAQ-V-KDKNSSVKLMGFGHR 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 FAAALNGLAGPLHGLANOEVLLWIKSVVEECGENISKEQLKDYAWKTLKSGKVVPGFGHG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315 VYKNFDPRAKIMQQTCHEVLTELGIKDDPLLDLAVELEKIALS-DDYFVQRKLYPNVDFY 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                355 VLRKTDPRYTC-QRE-FA-LKHLP--EDPLFQLVAKLYEVFLQFLQNLAKLNPWPNVDAH 409
                                                                                                                                                                                                                                                                                                                                                                                                                   carbon-carbon lyase; oxo-acid-lyase; catalyzes synthesis citrate from acetyl-CoA and oxaloacetic acid tricarboxylic acid cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 310; DB 1; Length 436;
Pred. No. 1.33e-31;
87; Mismatches 109; Indels 32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *superfamily citrate (si)-synthase
allosteric regulation; carbon-carbon lyase; homohexamer;
oxo-acid-lyase; tricarboxylic acid cycle
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05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #length 436 #molecular-weight 48196 #checksum 9071
                                                                                Fukaya, M.; Takemura, H.; Okumura, H.; Kawamura, Y.;
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                                                                                                                                                                                                                                                                                                     #active_site His #status predicted
                                                                                                          Horinouchi, S.; Beppu, T.
J. Bacteriol. (1990) 172:2096-2194
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Matches 99; Conservative
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17-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                homohexamer
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                    A35157
A35157
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Guiseppi, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Haramata, D.; Kasahara, F.; Klaerr-Blanchard, M.; Klein, C.; Kobayash, Y.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A., Lavine, A.; Liu, H.; Masuda, S.; Maueel, C.; Medique, C.; Medina, N.; Mellado, R.P.; Mizuno, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, D.; Porwolik, S.; Prescott, A.M.; Presecon, E.; Puijc, P.; Purnelle, B.; Rapoport, G.; Roche, B.; Rosce, M.; Sadaie, Y.; Sato, T.; Scanlon, E.; Schleich, S.; Schroeter, R.; Scoffone, F.; Sckjuchi, J.; Schleich, S.; Schroeter, R.; Scoffone, F.; Sckjuchi, J.; Sckwarka, A.; Tacconi, E.; Takadi, T.; Takahashi, H.; Tarkemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.; Tarkemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.; Tarkente, R.; Wedler, F.; Wedler, H.; Weitzenegger, T.; Wanbutt, R.; Wedler, A.; Yanane, K.; Yasumoto, K.; Yasa, H.; P.; Lata, K.; Yoshikawa, H.F.; Zumstein, E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99; Mismatches 118; Indels 27; Gaps 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
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##cross.references GB:299116; GB:AL009126, NID:q2634723; PID.e1185682:
##Cross.references PID:q2634848.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 GYDRQID-DRSPSANK--ERAYQ--L-L-GKMPALTAASYRIINKKEPILPLQ-TLSYSA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 QSEFQKAYEKGIHKSKLWEPTYEDSMSLIAQVPLVAAYVYRRMYKNGNTIPKDDSLDYGA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 NFLYMMIGKLPSSLEEQIFDRSLVLYSEHEMPN-STFAARVIASTHSDLYGALTGAVASL 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 LLWLLLIGKVPSKEQVDSLSQELRSRATVP-DHVYKTIDALPVTAHPMTQFATGVMALQV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary; nucleic acid sequence not shown;
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Pred. No. 9.59e-31;
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Nature (1997) 390:249-256
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8.9%;
Best Local Similarity 27.8%;
Matches 94; Conservative
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##molecule_type DNA
##residues 1-397 ##label KAN
##cross-references EMBL:D64001; GB:AB001339; NID:g1001102; PID:d1010913;
##cross-references EMBL:D64001.22
##note the nucleotide sequence was submitted to the EMBL Data
Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps 22;
                                                                                                                                                                                                                                                                                  #authors Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.; Sasamcto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Markaraki, A.; Nakazaki, N.; Natuo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Tabata, S. Yasuda, M.; Yasuda, M.; Tabata, S. Yasuda, M.; Tabata, S. Yasuda, M.; Yasuda, Yasuda, M.; Yasuda, M.; Yasuda, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 Y-A-RRALDDPK-YIRA--AVVRLLAKIPTMVA-AFH-MIREGNDPIQPNDKLDYASNFL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 YMLTEKEPDPFAAKVFDVCLTLHAEH-TMNASTFSARVTASTLTDPYAVVASAVGTLAGP 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 HMLGFSSSD-MHE-LMKLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGP 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 LHGGANEEVL----NMLEEIG-SV--ENVRPYVEKCLANKQRIMGFGHRVYKVKDPRAII 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279 LODLAEQLFAKMGHDEYYEIAVELEKVVEEYV-G-QK-GIYPNVDFYSG-LV-YRKLDIP 333
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25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change
21-Aug-1998
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hypothetical protein s110401 #formal_name Synechocystis sp.
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422 ARYYTVLFGVSRALG 436
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    ALTERNATE_NAMES
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Fri Oct 22 17:06:20 1999; MasPar time 14.51 Seconds 913.625 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-702-718-6 (1-469) from US08702718.pep 3443 Title:

Description: Perfect Score:

1 MVFYRGVSLLSKLRSRAVQQ......PLERPKSVTMEWLENHCKKA 469 Sequence:

PAM 150 Gap 11 Scoring table:

77977 seqs, 28268293 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot37 1:swissprot Database:

Mean 51.766; Variance 94.679; scale 0.547 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		o#						
Result No.	Score	Query Match	Length	DB	QI	Description		Pred. No.
	2932	85.2	471		CISY_CITMA	CITRATE SYNTHASE, M	MITO	0.00e+00
2	2454	71.3	472	٦	CISY_ARATH	SYNTHASE,	MITO	0.00e+00
m	2021	58.7	464	Н	CISY_PIG		MITO	
4	1944	56	433	٦	CISY_CHICK	CITRATE SYNTHASE, N	MITO	0.00e+00
'n	1820		468	-	CISY_CAEEL	PROBABLE CITRATE SY	SYNTH	0.00e+00
9	1782	51.	482	4	CISY_SCHPO	PROBABLE CITRATE SY	SYNTH	0.00e+00
7	1763	51.	479	Н	CISY_YEAST	CITRATE SYNTHASE, N	MITO	0.00e+00
00	1740	50.5	467	Н	CISY_CANTR		MITO	0.00e+00
σ	1725		474	Ч	CISY_EMENI		MITO	0.00e+00
10	1714	49.8	475	Ч	CISY_ASPNG		MITO	0.00e+00
11	1679	48.8	460	П	CISZ_YEAST	CITRATE SYNTHASE, F	PERO	0.00e+00
12	1680	4	469	Н	CISY_NEUCR		MITO	0.00e+00
13	1385	4	462	Н	CISY_TETTH	CITRATE SYNTHASE, N	MITO	1.50e-274
14	1218	35		Н	CISX_YEAST	CITRATE SYNTHASE 3	3 (EC	2.04e-236
15	360	7		Н	CISY_CORGL	CITRATE SYNTHASE (E	EC 4	4.32e-47
16	347	10.	373	Н	CISY_BACCO	CITRATE SYNTHASE (E	EC 4	1.95e-44
17	310	6	436	Н	CISY_ACEAC	CITRATE SYNTHASE (F	EC 4	5.58e-37
18	305	ω.	372	Н	CISW_BACSU	CITRATE SYNTHASE IN	) II	5.52e-36
19	306	œ.	397	Н	CISY_SYNY3	CITRATE SYNTHASE (F	EC 4	3.49e-36
20	287	ω.	423	Н	CISY_ACIAN	CITRATE SYNTHASE (E	EC 4	2.00e-32
21	282		428	Н	CISY_PSEAE	CITRATE SYNTHASE (F	EC 4	1.91e-31
22	280	8.1	376	Н	CISY_PYRFU	CITRATE SYNTHASE (F	EC 4	4.70e-31
	277		386	۲,	CISY_THIFE	CITRATE SYNTHASE (F	EC 4	1.81e-30

85.2%; Score 2932; DB 1; Length 471;

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SENCE FROM N.A.  INCV. SIAMESE SWEET 2240;  ENCOTA, VIRIDIPLANTAE; STREATOPHYTA; MACINICOPHYTA; NOALGAE; RETACARSOXILC ACID CYCLE; MATCARSOXILC ACID CYCLE; MATCARSOXILC ACID CYCLE; MITCCHOUDRIC ACID CONDUCTION CONDUCTED	8.0 430 1 CISY_COXBU CITRAT 7.9 516 1 CYSZ_CUCMA CITRAT 7.5 411 1 CISY_ENGLY CITRAT 7.5 411 1 CISY_ENGLY CITRAT 7.2 411 1 CISY_ENGLY CITRAT 7.1 411 1 CISY_ENGLY CISY_ENGLY CITRAT 7.1 411 1 CISY_ENGLY CISY_ENGL	10. 430   CISY_MYCTU CITRAT 19. 516   CYSZ_CUCMA CITRAT 19. 516   CYSZ_CUCMA CITRAT 19. 411   CISY_ETCJANU CITRAT 19. 411   CISY_ETCJANU CITRAT 19. 411   CISY_ETCJANU CITRAT 19. 411   CISY_RICHE 19. 412   CISY_RICHE 19. 411   CISY_RICHE 19. 412   CISY_RICHE 19. 411   CISY_RICHE 19. 411   CISY_RICHE 19. 411   CISY_RICHE 19. 427   CISY_RICHE 19.	430 1 CISY_MCTU CITRAT 431 1 CISY_MCTU CITRAT 431 1 CISY_MCTU CITRAT 431 1 CISY_CUCMA CITRAT 431 1 CISY_CICUMA CITRAT 431 1 CISY_RICHE 431 1 CISY_RICHE 431 1 CISY_RICHE CISY_RICHE 432 1 CISY_RICHE CISY_RICHE 433 1 CISY_RICHE 431 1 CISY_RICHE 433 1 CISY_RICHE 441 1 CISY_RICHE 441 1 CISY_RICHE 442 1 CISY_RICHE 444 1 CISY_RICHE 444 1 CISY_RICHE 445 1 CISY_RICHE 446 1 CISY_RICHE 447 1 CISY_RICHE 447 1 CISY_RICHE 647 1 CISY_RICHE 64 1 CISY_RICHE 65 1 CISY_RICHE 66 1 CISY_RICHE 66 1 CISY_RICHE 67	1 CISY_COXBU CITRAT 1 CISY_MYCTU CITRAT 1 CISY_SCUCMA CITRAT 1 CISY_SCUCMA CITRAT 1 CISY_SCUCMA CITRAT 1 CISY_STAND CITRAT 1 CISY_BATCHE CITRAT 1 CISY_BATCHE CITRAT 1 CISY_RACGE CITRAT 2 CISY_RACGE CITRAT 2 CISY_RACGE CITRAT 2 CISY_RACGE CITRAT 3 COPYTIGH. 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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION MITOCHONDPIAL MATRIX
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA, VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                             61 DLGKAQLGNITIDVVIGGMRGMTGLLWETSLLDPDEGIRFRGLSIPECQKLLPAAKPDGE 120
                                                                                                                                     61 EHGKVQLGNITVDMVLGGMRGMTGLLWETSLLDPDEGIRFRGLSIYECQKVLPAAKPGGE 120
                                                                                                                                                                 121 PLPEGLLWILLTGKVPSKEQVDGLSKELRDRATVPDYVYKAIDALPVSAHPMTQFASGVM 180
                                                                                                                                                                                 181 ALQVQSEFQEAYEKGIHKSKSWEPTSEDSLNLIARVPVVAAYVYQRIYKDGKIIPKDDSL 240
                                                                                                                                                                                                                                                                                        241 DYGGNFSHMLGFDDPKMLELMRLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFLAALN 300
                                                                                                                                                                                                                                                                                                      301 GLAGPLHGLANQEVLLWIKSVVDECGENVTTEQLKDYVWKTLNSGKVVPGFGHGVLRKTD 360
                                                                                                                                                                                                                                                                                                                                                                                                          361 PRYTCQREFALKHLPDDPLFQLVSKLYEVVPPILTKLGKVKNPWPNVDAHSGVLLNHFGL 420
                                                                                                                                                                                                                                                                                                                                                                                                                           1 MVEYRGVSLLSKLRSRAVQQTNLSNSVRWLQVQTSSGLDLRSBLQELIPEQQDRLKKLKS 50
                                             1 MASLRSATALSRAGOGSNLSNSVRWLQMQSSADLDLHSQLKEMIPEQQERLKKVKS 60
                 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                  UNGER E.A., HAND J.M., CASHMORE A.R., VASCONCELOS A.C.; "Isolation of a cDNA encoding mitochondrial citrate synthase from Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420 TEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENHCKKA 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 AEARYYTVLFGVSRSLGICSQLIWDRALGLPLERPKSVTLDWIEKNCKKA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLANT MOL. BIOL. 13:411-418(1989).
-!- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)0
                 51; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
Best Local Similarity 82.3%; Pred. No. 0.00e+00;
Matches 387; Conservative 51; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1991 (REL. 17, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SEHGKVQLGNITVDMVIGGMRGMTGLLWETSLLDPEEVFALGDCRLPECQKALLPTAQSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 G-EPLPEGLL-WLLLTGKVPSKEQVDSLSQELRSRATVPDHVYKTIDALPVTAHPMTQFA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGVMALQVQSEFQKAYENGIHKSKFWEPTYEDCLNLIARVPVVAAYVYRRMYKNGDSIPS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 IGVMALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLIAQVPLVAAYVYRRMYKNGNTIPK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 DKSLDYGANFSHMLGFDDERLKELMRLTSPSTVMHEGGNVSAHTGHLVGSALSDPYLSFA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 AALNGLAGPLHGLANQEVLLWIKSVVEECGEDISKEQLKEYVWKTLNSGKVIPGYGHGVL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   357 RKTDPRYTCQREFALKHLPEDPLFQLVAKLYEVFLQFLQNLAKLNPWPNVDAHSGVLLNY 416
                                                                                                                                                                                                                                                                                                                                                                                    1 MVFFRSVSAFTRLRSRVQGQQSSLSNSVRWIQMQSSTDLDLKSQLQELIPEHKDRLKKLK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MVFYRGVSLLSKLRSRA-VQQTNLSNSVRWLQVQTSSGLDLRSELQELIPEQQDRLKKLK 59
                                                                                                                                                                                                                                                                                                                                         8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVANS C.T., OWENS D.D., SUMEGI B., KISPAL G., SRERE P.A.; "Isolation, nucleotide sequence, and expression of a cDNA encoding pig citrate synthase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOXHAM D.P., PARMELEE D.C., KUMAR S., WALSH K.A., TITANI K.; "Complete amino acid sequence of porcine heart citrate synthase."; BIOCHEMISTRY 21:2028-2036(1982).
                                                               LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUS SCROFA (PIG).
EURARXOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                            Length 472;
                                                                                                                                                                                                                                                                                                             Pred. No. 0.00e+00;
62; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (REL. 01, CREATED)
01-CCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNORMION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                      CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
3: 954AFA81 CRC32;
                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 464 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARTIODACTYLA; SUIFORMES; SUINA; SUIDAE; SUS
                                                                                                                    MITOCHONDRION
                                                                                                                                                                                                                                                                                         Score 2454;
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                    PFAM; PF00285; citrate_synt; 1.
HSSP; P23007; 5CSC.
                                                                                                                                                                                                                                         52941 MW:
                                                                                                                                                                                                                                                                                    Query Match 71.3%;
Best Local Similarity 71.7%;
Matches 339; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                    472
309
355
407
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355 3
407 4
472 AA;
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                                                                                        MULTIGENE FAMILY.
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CISY_PIG
P00889;
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58.78;
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265; Conservative
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443
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461
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Best Local Similarity
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                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                       -:- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-:- SUBUNT: HOMODIMER.
-:- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
-:- CITRAIE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
         MEDLINE; 83010291.
REMINGTON S., WIEGAND G., HUBER R.;
"Crystallographic refinement and atomic models of two different forms of citrate synthase at 2.7 and 1.7-A resolution.";
J. Mol. BIOL. 158:111-152(1982).
                                            MUTAGENESIS.
MEDLINE: 91104711.
ALTER G.M., CASAZZA J.P., ZHI W., NEMETH P., SRERE P.A., EVANS C.T.;
ALTER G.M., CASAZZA J.P., ZHI W., NEMETH P., SRERE P.A., EVANS C.T.;
ALTERGON of essential catalytic residues in pig citrate synthase.";
BIOCHEMISTRY 29:7557-7563(1990).
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                   PROSITE; PS00480; CITRATE_SYNTHASE; 1.
PFAM: PF002B5; citrate_synt; 1.
LYASE; TRICARBOXLIC ACID CYCLE; MITOCHONDRION; 3D-SIRUCTURE; TRANSIT PEPTIDE: METHYLATION.
                                                                                                                    -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY
                                                                                                                                                                                                                                                  CITRATE SYNTHASE. METHYLATION (TRI-).
     X-RAY CRYSTALLOGRAPHY (2.7 AND 1.7 ANGSTROMS)
                                                                                                                                                                                                                                            NCINCHUCHIOLIM
                                                                                                                                                                                 EMBL; M21197; G164419; -.
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193
221
224
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157
161
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177
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PDB; 1CTS; 16-JUL-88.
PDB; 2CTS; 09-OCT-88.
PDB; 3CTS; 09-OCT-88.
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273 GGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLMIKSVVEEGGENISKE 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      387 VLLEQGKAKNPWPNVDAHSGVLLQYYGMTEMNYYTVLFGVSRALGVLAQLIWSRALGFPL 446
                                                                                                                                                                                                                                                                                     327 KLRDYIWNTLNSGRVVPGYGHAVLRKTDPRYTCQREFALKHLPHDPMFKLVAQLYKIVPN 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             393 FLQNLAKL-NPWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALGLPL 451
                                                                                                                                                                                                                                                     87 PDEGIRFRGYSIPECQKMLPKAKGGEEPLPEGLFWLLVTGQIPTEEQVSWLSKEWAKRAA 146
                                                                                                                                                                                 27 SASSINLKDILADLIPKEQARIKTFRQQHGNTVVGQITVDMMYGGMRGMKGLVYETSVLD 86
                                                                                                  2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                             154 VPDHVYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLI
                                           Score 2021; DB 1; Length 464;
Pred. No. 0.00e+00;
78; Mismatches 84; Indels
51629 MW; 3BC38D25 CRC32;
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-! SUBUNIT: HONODIMEN:
-! SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
-!- CUTTRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                             MEDLINE; 91255228.

LIAO D - I , KAPPUSAS M , PENINGTON S J ;

LIAO D - I , KAPPUSAS M , PENINGTON S J ;

"Crystal structure of an open conformation of citrate synthase from chicken heart at 2.8-A resolution.";

BIOCHEMISTRY 30:6031-6036(1991)

- : CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)C +
                                                                                                                                                                           "Proposed mechanism for the condensation reaction of citrate synthase: 1.9-A structure of the ternary complex with oxaloacetate and carboxymethyl coenzyme A."; BIOCHEMISTRY 29:2213-2219(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                         METABOLISM:
--- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
--- CAUTION: THIS IS AN X-RAY DETERMINED SEQUENCE WHICH WAS ESTABLISHED USING THE SEQUENCE OF PIG CITRATE SYNTHASE AND MODIFYING IT BASED ON THE OBSERVED ELECTRON DENSITY.
                                                                                                                EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES; NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF OPEN CONFORMATION
                                                         01-AUG-1991 (REL. 19, CREATED)
01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
01-SUU-1998 (REL. 35, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL (EC 4.1.3.7).
                                                                                                                                                 TISSUE-HEART MUSCLE;
MEDLINE; 90248434.
KAPPUSAS M., BPANCHAUD R., REMINGTON S J.;
                                                                                                                                         X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
                                          PRT;
                                          STANDARD;
                                                                                                      GALLUS GALLUS (CHICKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-APR-91.
15-APR-91.
15-APR-91.
15-APR-91.
24-DEC-97.
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2CSC; 15-APR-91.
3CSC; 15-APR-91.
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ERPKSVTME 460
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CISY_CHICK
P23007;
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5CSC;
6CSC;
5CTS;
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61 DEGIRFRGFSIPECOKLLPKGGXGGEPLPEGLFWLLVTGQIPTGAQVSWLSKEWAKRAAL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 PSHVVTMLDNFPTNLHPMSQLSAAITALNSESNFARAYAEGILRTKYWEMVYESAMDLIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 PDHVYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLIA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 QVPLVAAYVYRRMYKNGNTI-PKDDSLDYGANFAHMLGFSSSDMHELMKLYVTIHSDHEG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 GNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLGWLAQLQKAXXXAGADAS 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 56.5%: Score 1944; DB 1; Length 433; Best Local Similarity 60.3%; Pred. No. 0.00e+00; Matches 258; Conservative 73; Mismatches 95; Indels
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433 AA;
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SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
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larity 57.2%; Pred. No. 0.0
Conservative 83; Mismatch
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482
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482 AA;
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les 242; Conser
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                                                                                                                                                                                                                                                                                -:- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-: SUBUNIT: HOWDDIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: MITOGROUDERAL MATRIX (BY SIMILARITY).
-!- CUTRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 SRATVPDHVYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKLWEPTYEDS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 ARADLPTHVVRMLDNFPDNLHPMAQFIAAIAALNNESKFAGAYARGVAKASYWEYAYEDS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 MDLLAKLPIVAAIIYRNLYRDGSAVSVIDPKKDWSANFSSMLGYDDPLFAELMRLYLVIH 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 MSLIAQVPLVAAYVYRRMYKNGNTIP-KDDSLDYGANFAHMLGFSSSDMHELMKLYVTIH 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      265 SDHEGGNVSAHTSHLVGSALSDPYLSFSAAMAGLAGPLHGLANQEVLVFLNKIVGEIGFN 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P23007; 5CSC. HYPOTHETICAL PROTEIN: LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 SVLDPEEGIRFRGYSIPECQKLLPKAKGGEEPLPEAIWWLLCTGDVPSEAQTAAITKEWN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 LSTSAEGSTNLKEVLSKKIPAHNAKVKSFRTEHGSTVVQNVNIDMIYGGMRSMKGMVTET 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 LQVQTSSGLDLRSELQELIPEQQDRLKKLKSEHGKVQLGNITVDMVLGGMRGMTGLLWET 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.00e+00;
82; Mismatches 103; Indels 4; Gaps
                                                                                                                                                            EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA; RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                         01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
PROBABLE CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1820; DB 1; Length 458;
                                                                                                                                                                                                             STRAIN-ERISTOL N2;
BERKS M., SMITH A.:
SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: CITRAIE + COA = ACETYL-COA + H(2)O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

ADA3A630 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITRATE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WORMPEP; T20G5.2; CE00513.
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY
                                                                            01-FEB-1994 (REL. 28, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51540 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00285; citrate_synt;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 52.9%;
1 Similarity 56.5%;
245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z30423; G458482; -.
                                                     STANDARD;
                                                                                                                                               CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S42370; S42370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 468 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                   SEQUENCE FROM N.A.
453 RPKSVTME 460
                                                                                                                                                                                                                                                                      OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303
349
404
                                                                                                                                                                                                                                                                                                                                        METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSIT PEPTIDE
                                                 CISY_CAEEL P34575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
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                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-:- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (BY SIMILARITY).
-:- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                         389 VFLQFLQNLAKL-NPWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGIC-SQLIWDRA 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 LKDRLAELIPPEKQAEIKKFRAEHGQDVIGEVTINQMYGGARGVRSLIWEGSVLDPNEGIR 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 FRGYTIPECQKLLPSSPNGKQPLPESLFWLLVTGEIPTLSQVQALSADWAARSQLPKFVE 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP: P23007; SCSC.
HYPOTHETICAL PROTEIN: LYASE; TRICARPOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE.

1 44 MITOCHONDRION (BY SIMILARITY).
                                                                                                                         325 YTEEQLKEWVWKHLKSGQVVPGYGHAVLRKTDPRYECQREFALKHLPNDDLFKLVSTLYK 384
                                                                                                                                                                                                    329 ISKEQLKDYAWKTLKSGKVVPGFGHGVLRKTDPRYTCQREFALKHLPEDPLFQLVAKLYE 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 LRSELQELIPEQQDFLKKLKSEHGKVQLGNITVDMVLGGMRGMTGLLWETSLLDPDEGIR 99
                                                                                                                                                                                                                                                                               385 ITPGILLEQGKAKNPWPNVDSHSGVLLQYFGMTEMSFYTVLFGVSRALG-CLSQLIWARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-972;

BOYLIN K., CHURCHER C.M., BAPRELL B.G., RAJANDREAM M.A., WALSH S. SUBMITTED (FEB-1996) TO EMBL/GENBANK/DBJ DATA BANKS.

-I- CATALYIIC ACTIVITY: CITRAIE + COA - ACETYL-COA + H(2)O + OXALOACETAIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PROBABLE CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MITOCHONDRION (BY SIMILARITY).
CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W; 18145A7D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1782; DB 1; Length 482;
Pred. No. 0.00e+00;
83; Mismatches 96; Indole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
SCHIZOSACCHAROMYCES.
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PATHWAY: TRICARBOXYLIC ACID CYCLE.
SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                              160 KTIDALPVTAHPMTQFATGVWALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLIAQVPLV 219
                                                                 231 AGRIYRNLYRDGVVAPIQMDKDHSYNFANVLGFANNEEFVELMRLYLTIHADHEGGNVSA 290
                                                                                    291 HIGHLVGSALSSPFLSMAASLNGLAGPLHGLANQEVLNFLIIMKKEIGDDLSEETIKSYL 350
                                                                                                                                                351 WKLLNSGRVVPGYGHAVLRKTDPRYTAQREFALEHLPKDPMFQLVSRLYEIVPGVLTEHG 410
                                                                                                                                                                                                               411 KTKNPYPNVDSHSGVLLQYYGLKEQSFYTVLFGVSRTLGVASQLIWDRALGLPIERPKSF 470
171 ELIDRCPPTLHPMAQFSLAVTALEHDSAFAKAYERGMNKHDYWKYEYEDCMDLIAKTVPI 230
                                                                                                                                                                                                                                                                                 VERHASSELT P., AERT R., VOET M., VOLCKAERT G.; Twelve open reading frames revealed in the 23.6 kb segment flanking the centromere on the Saccharomyces cerevisiae chromosome XIV right
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUISSA M., SUDA K., SCHATZ G.;
"Isolation of the nuclear yeast genes for citrate synthase and
fifteen other mitochondrial proteins by a new screening method.";
EMBO J. 3:1773-1781(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LALO D., STETTLER S., MARIOTTE S., GENDREAU E., THURIAUX P., "Organization of the centromeric region of chromosome XIV in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae.";
YEAST 10:523-533(1994).
-!- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-D273-10B;
LINDNER P., PLUECKTHUN A :
SUBMITTED (JUL-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (REL. 01, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CITTALE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC
CITT OR LYS6 OR GLU3 OR YNROULC OR NZOL19.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
                                                                                                                                                                                                                                                                                                                                                                                                                             479 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TEAST 10:1355-1361(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-S288C / FY1679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 85003587.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 95028151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 95208356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-D273-10B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-GRE88;
                                                                                                                                                                                                                                                                                                                           471 STE 473
                                                                                                                                                                                                                                                                                                                                                              458 TME 460
                                                                                                                                                                                                                                                                                                                                                                                                                            CISY_YEAST
P00890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTA;
g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 IPEHVIQLLDSLPKDLHPMAQFSIAVTALESESKFAKAYAQGVSKKEYWSYTFEDSLDLL 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 VPDHVYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLI 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         279 GNVSAHTTHLVGSALSSPYLSLAAGLNGLAGPLHGRANQEVLEWLFKLREEVKGDYSKET 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339 IEKYLWDTLNAGRVVPGYGHAVLRKTDPRYTAQREFALKHFPDYELFKLVSTIYEVAPGV 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 LKDYAWKILKSGKVVPGFGHGVLRKIDPRYICQREFALKHLPEDPLFQLVAKLYEVFLQF 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      399 LIKHGKTKNPWPNVDSHSGVLLQYYGLTEASFYTVLFGVARAIGVLPQLIIDRAVGAPIE 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 PEEGIRFRGRTIPEIQRELPKAEGSTEPLPEALFWLLLTGEIPTDAQVKALSADLAARSE 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 SASEQTLKERFAEIIPAKAEEIKKFKKEHGKTVIGEVLLEQAYGGMRGIKGLVWEGSVLD 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 TSSGLDLRSELQELIPEQQDRLKKLKSEHGKVQLGNITVDMVLGGMRGMTGLLWETSLLD 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88; Mismatches 102; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKLPVIASKIYRNVFKDGKITSTDPNADYGKNLAQLLGYENKDFIDLMRLYLTIHSDHEG
                                                                                                                                                                                                                                                                                                                              TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 479;
-!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                             CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
E -> Q (IN REF. 2).
E -> E (IN REF. 2).
W; C6896385 CRC32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    467 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                               MITOCHONDRION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1763;
                                                                                                                                                                                                                                                          SGD; L0000341; CIT1.
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
PFAM; PF00285; citrate_synt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         479 AA; 53360 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 55.4%;
hes 237; Conservative
                                                                                                                                                             EMBL; Z23259; G313750; -.
                                                                                                                                                                              EMBL; X00782; G3603; -.
EMBL; X77395; G496718; -.
EMBL; Z71616; E239778; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                             37
479
312
358
413
58
78
                                                                                                                                                                                                                             PIR; A01110; YKBY.
PIR; S35390; S35390.
                                                                                                                                                                                                                                                                                                             HSSP; P23007; 5CSC
                                                                                                                                                                                                                                                                                                                             LYASE; TRICARBOXYI
MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       459 RPKSFSTE 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    453 RPKSVTME 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CISY_CANTR
P79024;
                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                             TRANSIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 GENKEFLELMRLYLTIHSDHEGGNVSAHTTHLVGSALSSPFLSLAAGLNGLAGPLHGPAN 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           306 QEVLEWLFKLREELNGDYSKEAIEKYLWDTLNAGRVGPGYGHAVLRKTDPRYTAQREFAL 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 QAYGGMRGIKGLVWEGSVLDPIEGIRFRGRTIPDIQKELPKAPGGEEPLPEALFWLLLTG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 MVLGGMRGMIGLLWEISLLDPDEGIRFRGLSIYECQKVLPAAKPGGEPLPEGLLWLLLIG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 EVPTEAQTRALSEEFAARSALPKHVEELIDRSPSHLHPMAQFSIAVTALESESQFAKAYA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 KVPSKEQVDSLSQELRSRATVPDHVYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 SSS-DMHELMKLYVIIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLAN 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312 QEVLLWIKSVVEECGENISKEQLKDYAWKTLKSGKVVPGFGHGVLRKTDPRYTCQREFAL 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         366 KHMPDYELFKLVSNIYEVAPGVFDQHGMTK-NPWPNVGSHSGVLLQYYGLTEESFYTVLF 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 RSRAVQQTNLSNSVRWLQVQTSSGLDLRSELQELIPEQQDRLKKLKSEHGKVQLGNITVD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82; Mismatches 111; Indels 8; Gaps
                                                                                                       CANDIDA TROPICALIS (YEAST).
EURARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE
                                                                                                                                                                                                                                                                                                                              UEDA M., SANUKI S., KAWACHI H., SHIMIZU K., ATOMI H , TANAKA A SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 467;
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CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W; FEE342A9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -! - SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1740; DB 1;
Pred. No. 0.00e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS00480; CITRATE SYNTHASE: 1.
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HSSP; P23007; 5CSC.
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Local Similarity 55.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250; Conservative
                                                                                                                                                                                CANDIDACEAE; CANDIDA.
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347
3402
467 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 AAKIYRNVFKDGKVAPIQKDKDYSYNLANQLGFADNKDFVELMRLYLTIHSDHEGGNVSA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 AAYVYRRMYKNGNTIPKDDSLDYGANFAHMLGFSSS-DMHELMKLYVTIHSDHEGGNVSA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTTHLVGSALSSPMLSLAAGLNGLAGPLHGLANQEVLNWLTEMKKVVGNDLSDQSIKDYL 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 LKETFADKLPGELEKVKKLPKEHGNKVIGELTIJDQAYGGAPGVKCLVWEGSVLDSEEGIP 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 FRGLTIPECQKLLPKAPGGEEPLPFGLFWLLLTGEVPSEQQVRDLSAEWAARSDLPKFIE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 LRSELQELIPEQQDRLKKLKSEHGKVQLGNITVDMVLGGMRGMTGLLWETSLLDPDEGIR 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 474;
                                                                                                                                                                                                                                           EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETĖS; PLECTOMYCETES;
EUROTIALES; TRICHOCOMACEAE; EMERICELLA.
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CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W; D97E1E91 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -:- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                            01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
CITPATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4 1.3.7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1725; DB 1;
Pred. No. 0.00e+00;
79; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
                               474 AA
                                                                                                                                                                                                                     EMERICELLA NIDULANS (ASPERGILLUS NIDULANS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00480; CIRKATE_SYNTHASE; 1. PFAM; PF00285; citrate_synt; 1. HSSP; P23007; 5CSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- PATHWAY: TRICAPBOXYLIC ACID CYCLE.
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Local Similarity 57.4%;
les 243; Conservative
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                               STANDARD;
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310
356
411
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MEDLINE; 97306446.
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411
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LT 9
CISY_EMENI
O00098;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-:- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (BY SIMILARITY).
-:- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                   402 KTKNPYPNVDAHSGVLLQYYGLTERNYYTVLFGVSRALGVLPQLIIDRAFGAPIERPKSF 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 DSEEGIRFRGRTIPECQELLPKA-PGGQEPLPEGLFWLLLTGEIPTEQQVRDLSAEWAAR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 DPDEGIRERGLSIYECQKVLPAAKPGG-EPLPEGLLWLLLTGKVPSKEQVDSLSQELRSR 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 SDLPKFIEELIDRCPSTLHPMSQFSLAVTALEHESAFAKAYAKGINKKDYWNYTFEDSMD 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 ATVPDHVYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKLWEPTYEDSMS 211
342 WSTLNAGRVVPGYGHAVLRKTDPRYTSQREFALRKLPDDPMFKLVSQVYKIAPGVLTEHG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 IGKAKSLKETFAEKLPAELEKVKKLRKEHGSKV-IGEVILDQAYGGARGVKCLVWEGSVL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 TSSGLDLRSELQELIPEQODPLKKLKSEHG-KVQLGNITVDMVLGGMRGMTGLLWETSLL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99; Indels 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PLECTOMYCETES;
EUROTIALES; TRICHOCOMACEAE; MITOSPORIC TRICHOCOMACEAE; ASPERGILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MITOCHONDRION (BY SIMILARITY).
CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W; 48D237BC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OSHIDA Y., MIYAKE K., KANAYAMA S., KIRIMURA K., USAMI S.;
SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1714; DB 1; Length 475; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                             01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
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                                                                                                                                                                                                                                                             475 AA.
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Local Similarity 57.1%;
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                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D63376; G927641; -.
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356 3
411 4
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                                                                                                                                                 462 STE 464
                                                                                                                                                                                    458 TME 460
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P51044;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: PEROXISOMAL CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                       274 HEGGNVSAHTTHLVGSALSSPMLSLAAGLNGLAGPLHGLANQEVLNWLTKMKAAIGNDLS 333
                                                                                                         334 DEAIKNYLWSTLNAGQVVPGYGHAVLRKTDPRYVSQREFALRKLPDDPMFKLVSQVYKIA 393
                                                                                                                                                                                                        331 KEQLKDYAWKTLKSGKVVPGFGHGVLRKTDPRYTCQREFALKHLPEDPLFQLVAKLYEVF 390
                                                                                                                                                                                                                                               394 PGVLTEHGKTKNPYPNVDAHSGVLLQYYGLTEANYYTVLFGVSRALGVLPQLIIDRALGA 453
                                                                                                                                                                                                                                                                  214 LIAKLPTIAAKIYRNVFKDGKVAPIQKDKDYSYNLANQLGYGDNNDFVELMRLYLTIHSD 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Mitochondrial and nonmitochondrial citrate synthases in Saccharomyces cerevisiae are encoded by distinct homologous genes."; MOL. CELL. BIOL. 6:4509-4515(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE, PEROXISOMAL (EC 4.1.3.7).
CITZ OR YCRODSC OR YCRSC OR YCRO43.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 92254505.
BITEAU N., FREMAUX C., HEBRARD S., MENARA A., AIGLE M., CROUZET "The complete sequence of a 10.8kb fragment to the right of the chromosome III centromere of Saccharomyces cerevisiae."; YEAST 8:61-70(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 91094853.
LIAO X., SMALL W.C., SRERE P.A., BUTOW R.A.;
LIAO X., SMALL W.C., SRERE P.A., BUTOW R.A.;
"Intramitochondrial functions regulate nonmitochondrial citrate synthase (CIT2) expression in Saccharomyces cerevistae.";
MOL. CELL. BIOL. 11:38-46(1991).
-!-CALLINIALYIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O + OXALOACETATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 87089811.
ROSENKRANTZ M., ALAM T., KIM K.-S., CLARK B.J., SRERE P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-24 FROM N.A.
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EMBL; M14586; G171227; -
                                                                                                                                                                                                                                                                                                                                                                     450 PLERPKSVTME 460
                                                                                                                                                                                                                                                                                                                              454 PIERPKSYSTE 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S5 LLWETSLLDPDEGIRFRGLSIYECQKVLPAAKPGGEPLPEGLLWLLLTGKVPSKEQVDSL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 SADLMSRSELPSHVVQLLDNLPKDLHPMAQFSIAVTALESESKFAKAYAQGISKQDYWSY 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 SQELRSRATVPDHVYKTIDALPVTAHPMIQFATGVMALQVQSEFQKAYEKGIHKSKLWEP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 TFEDSLDLLGKLPVIAAKIYRNVFKDGKMGEVDPNADYAKNLVNLIGSKDEDFVDLMRLY 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 LIIHSDHEGGNVSAHTSHLVGSALSSPYLSLASGLNGLAGPLHGRANQEVLEWLFALKEE 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 VNDDYSKOTIEKYLWDTLNSGRVIPGYGHAVLRKTDPRYMAQRKFAMDHFPDYELFKLVS 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          371 SIYEVAPGVLTEHGKTKNPWPNVDAHSGVLLQYYGLKESSFYTVLFGVSRAFGILAQLIT 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 VIIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEE 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 NVASYLQSNSSQEKTLKERFSEIYPIHAQDVRQFVKEHGKTKISDVLLEQVYGGMRGIPG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 NSVRWLQVQTSSGLDLRSELQELIPEQQDRLKKLKSEHGKVQLGNITVDMVLGGMRGMTG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                      92; Mismatches 115; Indels 1; Gaps
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"Characterization of the cit-1 gene from Neurospora crassa encoding
the mitochondrial form of citrate synthase.";
MOL. GENT. 242:105-110(1994).
--- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                 MICROBODY TARGETING SIGNAL (POTENTIAL) 9E93E2FD CRC32;
                                                                                                                                                                                                                   TRICARBOXYLIC ACID CYCLE; PEROXISOME; MULTIGENE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                         Length 460;
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SORDARIALES; SORDARIACEAE; NEUROSPORA.
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                                                                                                                                                                                                                                                                                                                                                                                      Score 1679; DB 1;
Pred. No. 0.00e+00;
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LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                 SIMILARITY.
                                                                                                                  PROSITE: PS00342; MICROBODIES_CTER; 1.
PROSITE: PS00480; CITRATE_SYNTHASE; 1.
PFAM; PF00285; Citrate_synt; 1.
HSSP; P23007; SCSC.
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01-FEB-1994 (REL. 28, LAST SEQI
01-NOV-1995 (REL. 32, LAST ANNO
                                                                                                                                                                                                                                                                                                                                        460 AA; 51413 MW;
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 52.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         229; Conservative
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EMBL; M54982; G171229;
EMBL; X59720; E264468;
PIR; A25393; YKBYC.
                                                                                                                                                                                                                                            293
                                                                       YEPD; 5440; -.
SGD; L0000342; CIT2.
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P34085;
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8
                                 FARMAN, TALCALLOLAR LOCATION: MITOCHONDRIAL MATRIX,
DEVELDULAR LOCATION: MITOCHONDRIAL MATRIX,
DEVELOPMENTAL STAGE: ABUNDANT AFTER 6-12 HRS OF GROWTH, IT IS
NOT SIGNIFICANTLY EXPRESSED AFTER 24 HRS, WHICH IS SEVERAL HRS
AFTER ENTERING THE STATIONARY PHASE OF GROWTH.
CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 RFRGKTIPECQELLPKA-PGGKEPLPEGLFWLLLTGEVPSEQQVRDLSAEWAARSDVPKF 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 IEELIDRCPSDLHPMAQLSLAVTALEHTSSFARAYAKGINKKEYWGYTFEDSMDLIAKLP 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158 VYKTIDALPVTAHPMIQFAIGVMALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLIAQVP 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 TIAARIYQNVFKGGKVAAVQKDKDYSFNFANQLGFGDNKDFVELLRLYLTIHTDHEGGNV 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276 SAHTTHLVGSALSSPFLSVAAGLNGLAGPLHGLANOEVLNWLTEMKKVIGDDLSDEAITK 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YLWDTLNAGRVVPGYAHAVLRKTDPRYSAQRKFAQEHLPEDPMFQLVSQVYKIAPKVLTE 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 396 HGKTKNPYPNVDAHSGVLLQHYGLTEANYYTVLFGVSRAIGVLPQLIIDRAVGAPIERPK 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 LKERFAELLPENIEKIKALRKEHGSKV-VDKVTLDQVYGGARGIKCLVWEGSVLDAEEGI 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 LRSELQELIPEQQDRLKKLKSEHG-KVQLGNITVDMVLGGMRGMTGLLWETSLLDPDEGI 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE; MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.8%; Score 1680; DB 1; Length 469; larity 56.2%; Pred. No. 0.00e+00; Conservative 78; Mismatches 104; Indels
                                                                                                                                                                            METABOLISM. SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITRATE SYNTHASE.
BY SIMILARITY.
E6281B97 CRC32;
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(REL. 21, LAST SEQUENCE UPDATE)
(REL. 28, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    462 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S41563; S41563.
PROSTIE; PSO0480; CITRATE_SYNTHASE; 1.
PFAM; PF00285; citrate_Synt; 1.
HSSP; P23007; SCSC.
                      PATHWAY: TRICARBOXYLIC ACID CYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 33 MI
34 469 CI
352 352 BY
469 AA; 52002 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M84187; G168775; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          456 SVTME-WLENHCKK 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CISY_TETTH
P24118;
01-MAR-1992 (
01-MAR-1992 (
01-FEB-1994 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          336
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21 IIKSSALTLKEALENVIPKKRDAVKKLKACYGSTFVGPITISSVLGGMRGNQSMFWQGTS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
SITE
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89; Mismatches 123; Indels 12; Gaps 10;
                                                                                                                                                                                                                                                                                                        CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 ATVPDHVYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKG-IHKSKLWEPTYEDSM 210
                                       EUKARYOTA; ALVEOLATA; CILIOPHORA; OLIGOHYMENOPHOREA; HYMENOSTOMATIDA;
TETRAHYMENINA; TETRAHYMENA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 IIFRGYIIPQLKEFLPKADPKAADQANQEPLPEGIFWLLMTGQLPTHAQVDALKHEWQNR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 IRFRGLSIYECQKVLP-A-AKPG--G--EPLPEGLLWLLLTGKVPSKEQVDSLSQELRSR 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 GTVNQDCVNFILNLPKDLHSMTMLSMALLYLQKDSKFAKLYDEGKISKKDYWEPFYEDSM 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 DLIAKIPRVAAIIYRHKYRDSKLIDSDSKLDWAGNYAHMMGFEQHVVKECIRGYLSIHCD 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 SLIAQVPLVAAYVYRRMYKNGNTIPKDDSLDYGANFAHMLGFSSSDMHELMKLYVTIHSD 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 HEGGNVSAHTTHLVGSALSDPYLSYSAGVNGLAGPLHGLANQEVLKWLLQFIEEKGTKVS 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               271 HEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENIS 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 DKDIEDYVDHVISSGRVVPGYGHAVLRDTDPRFHHQVDFSKFHLKDDQMIKLLHQCADVI 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 NLKKVIAEIIPQKQAELKEVĶEKYGDKV-VGQYTVKQVIGGMRGMKGLMSDLSRCDPYQG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 DLRSELQELIPEQQDRLKKLKSEHG-KVQLGNITVDMVLGGMRGMTGLLWETSLLDPDEG 97
                                                                                                                                                                     BIOCHEM. BIOPHYS. RES. COMMUN. 174:1028-1034(1991).
-!- FUNCTION: STRUCTURAL PROTEIN INVOLVED IN ORAL WORPHOGENESIS AND
IN PROUNDLEAR BEHAVIOR DUBING CONJUGATION. RESPIRATORY ENZYME.
-!- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)0 +
                                                                                                                NUMATA O., TAKEMASA T., TAKAGI I., HIRONO M., HIRANO H., CHIBA J.,
WATANABE Y.;
                                                                                                                                           "Tetrahymena 14-nm filament-forming protein has citrate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE;
                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX AND CYTOPLASMIC
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7) (14 NM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 462; 50e-274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
17. 7B6A39BC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MITOCHONDRION
                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 22-40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1385; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; JN0130; JN0130.
PROSTER: PSOOM40; CITRATE_SYNTHASE; 1.
PFAM; PF00285; Citrate_Synt; 1.
HSSP; P23007; 5CSC.
                                                                                                                                                                                                                                          PATHWAY: TRICARBOXYLIC ACID CYCLE. SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401 401 E
462 AA; 52575 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 40.2%;
Local Similarity 49.0%;
es 215; Conservative
             FILAMENT-FORMING PROTEIN). TETRAHYMENA THERMOPHILA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D90117; E33571; -.
                                                                                                   91128358
                                                                                                                                                                                                                                                                                            CYTOSKELETON.
                                                                                                                                                                                                                                 OXALOACETATE
                                                                                                                                                                                                                                                                                                                       METABOLISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOSKELETON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                            activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                          391 LQFLQNLAKL-NPWPNVDAHSGVLLNYGLTEARYYTVLFGVSRALGIC-SQLIWDRALG 448
331 KEQLKDYAWKTLKSGKVVPGFGHGVLRKTDPRYTCQREFALKHLPEDPLFQLVAKLYEVF 390
                                                                   384 PKKLLTYKKIANPYPNVDCHSGVLLYSLGLTEYQYYTVVFAVSRALG-CMANLIWSRAFG 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 315 315 BY SIMILARITY.
361 361 BY SIMILARITY.
419 BY SIMILARITY.
484 486 MICROBODY TRAGETING SIGNAL (POTENTIAL).
486 AA: 53811 MM; 806F987D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , WALSH S.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y., AHMED A., BUSSEY H., FORTIN N., FRIESEN J.D., HALL J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STORMS R.K., VO D.H., WINNETT E.;
SUBMITTED (XXX-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-S288C / AB972;
PEARSON D , ROWMAN S., BARPELL B G., RAJANDREAM M.A.,
SUBMITTED (APR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JIA Y.K., BECAM A.-M., SLONIMSKI P.P., HERBERT C.J.; SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRICARBOXYLIC ACID CYCLE; MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.4%; Score 1218; DB 1,
Similarity 45.0%; Pred. No. 2.04e-236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 32, LAST ANNOTATION UPDATE)
CITRALE SYNTHASE 3 (EC 4.1.3.7)
CIT3 OR YPROOIW OR YP9723.01.
                                                                                                                                                                                                                                                                                                                                                                                                           486 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: Z48951; G763000; -.
EMBL: Z71255; E236811; -.
EMBL: U31900; G939735; -.
SGD: L0002855; CIT3.
PROSITE: PS00342; MICROBODIES_CTER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00480; CITRATE_SYNTHASE;
                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SACCHAROMYCETACEAE; SACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00285; citrate_synt; 1.
HSSP; P23007; 5CSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (REL. 32, CREATED)
                                                                                                                                                                                                  443 LPIERPGSADLKWFHDKYR 461
                                                                                                                                                                                                                                                                     449 LPLERPKSVTMEWLENHCK 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X88846; G895889; -.
                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CW04
                                                                                                                                                                                                                                                                                                                                                                                                 CISX_YEAST
P43635;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED cutstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -:- ENZYME REGULATION: WEAKLY INHIBITED BY ATP (APPARENT KI = 10 MM).
-:- PATHWAY: FRICARBOXXLIC ACID CYCLE.
-:- SUBUNIT: HOMOHEXAMER (BY SIMILARITY).
-:- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                         81 LDPEHGIKFQGLTIEECQNRLPNTGIDGDNFLPESMLWLLMTGGVPTFQQAASFRKELAI 140
                                                                                           92 LDPDEGIRFRGLSIYECQKVLPAAKPGGEP-LPEGLLWLLLTGKVPSKEQVDSLSQELRS 150
                                                                                                                                                                                                                                                                                               261 QSLDFINLMRLYTGIHVDHEGGNVSAHTTHLVGSALSDPYLSYSSGIMGLAGPLHGLAAQ 320
                                                                                                                                                                                                                                                                                                                                                                            EVVRFLIEMNSNIS-SIAREQEIKDYLWKILNSNRVIPGYGHAVLRKPDPRFTAMLEFAQ 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                        380 KRPIEFENDKNVLLMQKLAEIAPKVLLEHGKSKNPFPNVDSASGILFYHYGIRELLFFTV 439
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE: 95005436.

EIKMANNS B.J., THUM-SCHMITZ N., EGGELING L., LUEDTKE K.U., SAHM H.;

"Nucleotide sequence, expression and transcriptional analysis of the
Corprehencerium glutamicum gltA gene encoding citrate synthase.";

MICROBIOLOGY 140:1817-1828(1994).

-: CATALYIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)0 +

OXALOACETATE.
: ||:| |: |:::|| :| :||||: | 32 VQTSSGLDLRSELQELIPEQQDRLKKLKSEHGKVQLGNITVDMVLGGMRGMTGLLMETSL 91
                                                                                                                                                                                                                                           RGRKLPHYTEKVLSSLPKDMHPMTQLAIGLASMNKGSLFATNYQKGLIGKMEFWKDTLED
                                                                                                                                                                             RA-TVPDHVYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKG-IHKSKLWEPTYED
                                                                                                                                                                                                                  SLNLIASLPLLIGRIYSNITNEGHPLGQYSEEVDWCTNICSLLGMTNGTNSSNTCNLTSQ
                                                                                                                                                                                                                                                                                                                                    H--E---LMKLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; CORYNEBACTERINEAB; CORYNEBACTERIACEAE;
CORYNEBACTERIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       440 IFGCSRAMGPLTQLVWDRILGLPIERPKSLNLEGLE 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL: X66112; G505581; -.
PROSITE: PS00480; CITRATE_SYNTHASE; 1.
PFAM: PF00285; citrate_synt; 1.
HSSP; Q53534; 1A.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CISY_CORGL STANDARD; PR. P42457; 01-NOV-1995 (REL. 32, LAST SEQUE 01-NOV-1995 (REL. 32, LAST SEQUE 01-NOV-1995 (REL. 32, LAST ANNOT CITRATE SYNTHASE (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORYNEBACTERIUM GLUTAMICUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=ATCC 13032;
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22;
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                                                                                                                                                                                                                                                       RMMFGYPTEPYEIDPIMVKALDKLLILHADHEQ-NCSTSTVRMIGSAQANMFVSIAGGIN 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 HML-GFSS-S-DMHELM-K-L--YVTIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALN 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 ALSGPLHGGANQAVLEMLEDIKSNHGGD-ATEFMNK-V-KNKEDGVRLMGFGHRVYKNYD 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324 PRAAIVKETAHEILEHLGGDDLLDLAIKLEEIALA-DDYFISRKLYPNVDFYTGLIYRAM 382
                                                                                                                                                                                                                                                                                                                        154 YQDQLN-PLDEAQL-D-K--ATVRLMAKVPMLAAYAHPAR-KGAPYMYPDNSLNARENFL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRYTCQREFA---LKHLPEDPLFQLVAKLYEVFLQFLQNLAKLNPWPNVDAHSGVLLNYY 417
                                                                                                                                                                          89; Mismatches 105; Indels 26; Gaps
                                                                                                                              Length 437;
LYASE; TRICARBOXYLIC ACID CYCLE; ALLOSTERIC ENZYME.
ACT_SITE 316 BY SIMILARITY.
ACT_SITE 372 BY SIMILARITY.
                                                                                                                                                   Pred. No. 4.32e-47;
                                                                        437 AA; 48929 MW; B408BFA5 CRC32;
                                                                                                                           Score 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: Fri Oct 22 17:07:24 1999 Job time : 64 secs.
                                                                                                                      10.5%;
Local Similarity 30.4%;
les 96; Conservative
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418 GLTEARYYTVLFGVSR 433
                                                                        SEQUENCE
                                                                                                                           Query Match
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Oct 22 17:07:42 1999; MasPar time 29.55 Seconds 866.114 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-702-718-6 (1-469) from US08702718.pep Title:

Description: Perfect Score:

3443 ........PLERPKSVTMEWLENHCKKA 469 Sequence:

PAM 150 Gap 11 Scoring table:

179066 segs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptremb19
1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle
9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified
13:sp\_vertebrate 14:sp\_virus

Mean 49.645; Variance 97.075; scale 0.511 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

No.	00	00	00	00	00	00	00	28	26	25	24	24	24	24	23	23	23	22	22	21
Pred. N	0.00e+00	0.00e+00	0.00e+0C	0.00e+00	0.00e+00	0.00e+00	0.00e+00	7.31e-28	2.12e-26	1.14e-25	2.11e-	4.83e-2	7.32e-2	3.19e-	2.54e-2	3.83e-2	5.80e-2	1.32e	3.01e-2	1.03e-2
1 1 1 1	(EC 4	NIA-L	(EC 4	(EC 4	HASE	HASE	(EC 4	(CITZ	(EC 4		(FRAG	(EC 4								
ion	CITRATE SYNTHASE	ETHANOLAMINE AMMONIA-L	SYNTHASE	SYNTHASE	(SI)-SYNTHASE	(SI)-SYNTHASE	SYNTHASE	SYNTHASE	SYNTHASE	SYNTHASE.	SYNTHASE									
Description	CITRATE	ETHANOL!	CITRATE	CITRATE	CITRATE	CITRATE	CITRATE	CITRATE	CITRATE	CITRATE	CITRATE	CITRATE	CITRATE	CITRATE	CITRATE	CITRATE	CITRATE	CITRATE	CITRATE	CITRATE
ID	024135	043175	080433	064869	096544	024259	075390	028929	032705	034002	053115	059777	P77936	033066	060047	059469	059779	059775	059769	054382
DB	10	10	10	10	10	10	4	-	Н	7	(1	7	~	C1	~	7	~	C 3	C1	7
ouery Match Length	469	471	472	474	437	339	466	372	379	379	411	411	411	431	411	411	411	411	410	356
Query Match	100.0	90.0	89.9	86.8	81.3	61.9	58.0	7.9	7.7	7.6	7.3	7.3	7.3	7.3	7.2	7.1	7.1	7.1	7.0	6.9
Score	3443	3098	3096	2987	2800	2131	1997	272	264	260	253	251	250	252	247	246	245	243	241	238
Result No.	н	2	ĸ	4	S	9	7	<b>0</b> 0	on	10	11	12	13	14	15	16	17	18	19	20

1.20e-20	1.80e-20	1.70e-17	4.42e-14	9.61e-13	6.43e - 12	6.43e-12	2.06e-12	2.06e-12	9.39e-12	2.91e-11	2.73e-10	1.81e-03	1.81e-03	1.42e-01	2.57e-01	6.19e - 01	8.26e-01	2.57e+00	1.94e+00	1.46e+00	•	2.57e+00	2.57e+00	1.10e+00
CITRATE SYNTHASE (EC 4	E SYNTHASE (	_	CITRATE SYNTHASE (EC 4	YOTIAO (FRAGMENT).	YOTIAO.	CITRATE SYNTHASE (FRAG	GOLGI COMPLEX AUTOANTI	F52C6.11 PROTEIN.	KIAA0378 (FRAGMENT).	SIMILAR TO BACILLUS SU	AMINODEOXYCHORISMATE L	CELL DIVISION PROTEIN	REVERSE TRANSCRIPTASE.	MCASK-A.	CASK.	CODED FOR BY C. ELEGAN								
068883	$\sim$	033915	059236	059234	059235	059238	030966	070008	008395	059237	P77822	966660	014869	045540	092805	044818	015083	098468	025309	085717	053751	070588	н	023081
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427	434	429	322	319	315	318	349	390	393	321	319	1620	1642	299	767	283	808	188	329	402	480	664	897	2288
•	6.7	6.2	٠	5.4		٠	5.3	•	•	5.5			3.7	3.3	3.2					3.0			3.0	
232	231	214	194	186	181	181	184	184	180	177	171	126	126	112	110	107	106	102	103	104	103	102	102	105
21	22	23	C1	25	56	27		53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

1 1 2 2.4135 2.4135 2.4135 2.4135 2.4135. 2.4135. 2.4135. 2.4135. 2.4135. 2.4135. 2.4135. 2.4136. 2.4136. 2.4136. 2.4136. 2.4136. 2.4136. 2.4136. 2.4136. 2.4136. 2.4136. 2.4136. 2.4136. 2.416. 2.4136. 2.4136. 2.4136. 2.4136. 2.4136. 2.4136. 2.4136. 2.4136. 2.4136. 2.4136. 2.4136. 2.4136. 2.4136. 2.4136. 2.4136. 2.4136. 2.4136. 2.416. 2.	NICOTIANA TABACUM (COMMON TOBACCO).  BUKARYOTA; VIRIDIPLANTAE: STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;  EUFRYLLOPHYTES; SPERNATOPHYTA; MAGNOLLOPHYTA; EUDICOTYLEDONS;  ASTERIDAE; SOLANANAE; SOLANALES; SOLANACEAE; NICOTIANA.  [1]  SEQUENCE FROM N.A.	LA COGNITO LANDSCHUETZE V., WILLMITZER L., MUELLER-ROEBER B.; PLANT CELL PHYSIOL. 0:0-0(0)!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O + OXAALOACEPRINE.	-:- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF -:- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF -:- SIMILARITY: TO OTHER CITRATE SYNTHASES. EMBL; X84226; E137432; PROSITE; PSO0440; CITRATE_SYNT; 1. PROSITE; PSO0480; CITRATE_SYNT; 1. LYASE; TRICARBOXYLIC ACID CYCLE. SEQUENCE 469 AA; 52492 MM; 6BE3C325 CRC32;	atch 100.0%; Score 3443; DB 10; Length 469; cal Similarity 100.0%; Pred. No. 0.00e+00; 469; Conservative 0; Mismatches 0; Indels 0; Gaps (	MVFYRGVSLLSKLRSRAVQQTNLSNSVRMLQVQTSSGLDLRSELQELIPEQQDRLKKLKS 60 	EHGKVQLGNITVDMVLGGMRGMTGLLWETSLLDPDEGIRFRGLSIYECQKVLPAAKPGGE 120 	PLPEGLIWILLTGKVPSKEQVDSLSQELRSRATVPDHVYKTIDALPVTAHPMTQFA1GVM 180 
LT 1 024135; 024135; 01-JAN-1998 01-JAN-1998 01-NOV-1998 CITRATE SYN	CILL: CILL: EUKARYOTA EUPHYLLOP ASTERIDAE [1] SEQUENCE STEATN	LA COGNATA PLANT CELL -!- CATALYI OXALOAC	-!- PATHW -!- CITRA -!- SIMIL EMBL; X84 PROSITE; PFAM; PFO LYASE; TR	Query Match Best Local S Matches 46	1 MVFY      1 MVFY	61 EHGK             51 EHGK	121 PLPE       21 PLPE
RESULT ID O AC O DT O DT O DT O DT O	2 0 0 0 0 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	888888	00000	Qu Be Ma	da Qy	Db	Db Qy

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120 EPLPEGLLWLLLTGKVPSKEQVDSLSQELRSRATVPDHV-YKTIDALPVTAHPWTQFATG 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 WALOVOSEFOKAYEKGIHKSKLWEPTYEDSMSLIAQVPLVAAYVYRRYKNGNTIPKDD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 SLDYGANFAHMLGFSSSEMHELLMRLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFAA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 ALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLIAQVPLVAAYVYRRMYKNGNTIPKDDSL 240
                                                                                                      241 DYGANFAHMLGESSSDMHELMKLYVT1HSDHEGGNVSAHTGHLVASALSDFYLSFAAALN 300
                                                                                                                                                               GLAGPLHGLANOEVLLWIKSVVEECGENISKEOLKDYAWKTLKSGKVVPGFGHGVLRKTD 360
                                                                                                                                                                                                   301 GLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYAWKTLKSGKVVPGFGHGVLRKTD 360
                                                                                                                                                                                                                                            361 PRYTCQREFALKHLPEDPLFQLVAKLYEVFLQFLQNLAKLNPWPNVDAHSGVLLNYYGLT 420
                                                                                                                                                                                                                                                                   61 SDM-KGSIGNITVDMVLGGMRGMTGLLWKPHYLDPDEGIRFRGLSIPECQKVLPAAKPGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 SEHGKVQLGNITVDMVLGGMRGMTGLLWETSLLDPDEGIRFRGLSIYECQKVLPAAKPGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 EPLPEGLLWLLLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MVFYPSVSLLSKLRSRAVQQSNVSNSVPWLQVQTSSGLDLPSELVQELIPEQQDPLKKIK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LANDSCHUETZE V . WILLMITZEP L , MUELLER-ROEBER B .: "Micochondrial citrate synthase from potato: predominant expression in mature leaves and young flower buds."; PLANTA 196:756-764(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOLANUM TUBEROSUM (POTATO).
URDIDILANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERWATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
ASTERIDAE; SOLANANAE; SOLANALES; SOLANACEAE; SOLANUM.
ALGVĢSEFGKAYEKGIHKSKLWEPTYEDSMSLIAQVPLVAAYVYRMYKNGNTIPKDDSL
                                                                                DYGANFAHMLGFSSSDMHELMKLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.0%; Score 3098; DB 10; Length 471; 89.6%; Pred. No. 0.00e+00;

    :- CATALYTIC ACTIVITY: ETHANOLAMINE - ACETALDEHYDE + NH(3).

                                                                                                                                                                                                                                                                                                                                               421 EARYYTVLFGVSRALGICSQLIMDRALGLPLERPKSVTMEWLENHCKKA 469
                                                                                                                                                                                                                                                                                                                            EARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENHCKKA 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
ETHANOLAMINE AMMONIA-LYASE (EC 4.3.1.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     471 AA; 52612 MW; BC96A65C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0.00e+1
23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 471 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (11, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- COFACTOR: COBALAMIN.

###L: X75082; 6483510; -

PFAM. FF00285, citrate_synt, 1.

#ENDEL; 15200; SOLtu;2977;mn15200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               larity 89.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TPEMBLPEL.
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01-JAN-1999
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                                                                               KIVPRYICQREFAMKHLPEDPLFQLVSKLYEVFLLFLQNLAKLKPWPNVDAHSGVLLNYY 419
                                                                                                                     358 KTDPRYTCQREFALKHLPEDPLFQLVAKLYEVFLQFLQNLAKLNPWPNVDAHSGVLLNYY 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPLPEGLLWLLITGKVPTKEQVDALSAELRSRAAVPEHVYKTIDALPVTAHPMTQFATGV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 EPLPEGLLWLLLTGKVPSKEQVDSLSQELRSRATVPDHVYKTIDALPVTAHPMTQFATGV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 MALQVQSEFQKAYEKGIHKTKYWEPTYEDSITLIAQLPVVAAYIYRRMYKNGQSISTDDS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 LDYGANFAHMLGYDSPSMQELMRLYVTIHTDHEGGNVSAHTGHLVASALSDPYLSFAAAL 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 NGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYAWKTLKSGKVVPGFGHGVLRKT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 DPRYICOREFALKHLPDDPLFQLVSNLFEVVPPILTELGKVKNPWPNVDAHSGVLLNHYG 420
ALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYVWKTLNSGKVVPGFGHGVLR 359
                                     298 ALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYAWKTLKSGKVVPGFGHGVLR 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59
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                                                                                                                                                                                                                                                                                                                                                                                                                                           EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MVFYRGVSLLSKLRSRAVQQTNLSNSVRWLQVQTS-SGLDLRSELQELIPEQQDRLKKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 LDYGANFAHMLGFSSSDMHELMKLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFAAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AEHGKVQLGNITVDMVLGGMRGMIGLLWETSLLDPEEGIRFRGLSIPECQKLLPGAKPGG
                                                                                                                                                                                 418 GLTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENHCKKA 469
                                                                                                                                                             GLIEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENQCKKA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- PATHWAY: TRICARBOXYLIC ACID CYCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.9%; Score 3096; DB 10; Length 472; 86.2%; Pred. No. 0.00e+00; ative 46; Mismatches 17; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CV. MS YONSUN;
TAKITA E., KOYAMA H., SHIRANO Y., SHIBATA D., HARA T.;
CDNA encoding carrot mitochondrial citrate synthase.";
SUBNITIED (AUG-1998) TO EMBL/CBBANK/DBU DATA BANKS.
-:- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)0
                                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- SIMILARITY: TO OTHER CITRATE SYNTHASES.
EMBL; AB017159; D1033521; -.
LYASE; TECARBOXYLIC ACID CYCLE.
SEQUENCE 472 AA; 52656 MW; D46C38CC CRC32;
                                                                                                                                                                                                                                                                                472 AA
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                                                                                                                                                                                                                                                                                                                     01-NOV-1998 (TREMBLREL. 08, CREATED)
                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                              CITRATE SYNTHASE (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 86.2%;
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                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                        DAUCUS CAROTA (CARROT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPRYVCQREFALKHLPDDPLFQLVSKLYEVVPPVLTELGKVKNPWPNVDAHSGVLLNHYG 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MVFFRSVSAFTRLRSRVQGQOSSLSNSVRWIQMQSSTDLDLKSQLQELIPEQQDRLKKLK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Gaps
                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CV. COLUMBIA;
ROUNSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
SOMEBVILLE C.R., VENTER J.C.,
SUBMITTED (MAY-1999) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
  421 LTEARYYTVLFGVSRAIGICSQLVWDRALGLPLERPKSVTMEWLENHCKKS 471
                      419 LIEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENHCKKA 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-:- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 474;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53; Mismatches 27; Indels
                                                                                                                                                   01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10;
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Pred. No. 0.00e+00;
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EMBL; AC004521; G3128180; -.
LYASE; TE: PS00480: CITRATE_SYNTHASE; 1.
LYASE; TRICARBOXIC ACID CYCLE.
SEQUENCE 474 AA; 52782 MW; 64FF2AC6 CRC32;
                                                                                                                  474 AA
                                                                                                                                                                                                                                 F411.16.
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
                                                                                                                  PRT;
                                                                                                                                                                                                                 CITRATE SYNTHASE (EC 4.1.3.7).
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Best Local Similarity 82.6%;
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                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
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064869
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215 QVPLVAAYVYRRYKKNGNTIPKDDSLDYGANFAHMLGFSSSDMHELMKLYVTIHSDHEGG 274
                                                                       01-FED-1997 (TREMBLEEL. 02, LAST SEQUENCE UPDATE)
01-AAN-1999 (TREMBLEEL. 09, LAST ANNOTATION UPDATE)
01-AAN-1999 (TREMBLEEL. 09, LAST ANNOTATION UPDATE)
(CITRATE (SI)-SYNTHASE (EC. 4.1.3.7) (COMBENSING ENZWE)
(CITRATE CONDENSING ENZWE) (CITROGENASE) (OXALOACETATE TRANSACETASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 EEGIRFRGFSIPECQKLLPAASAGAEPLPEGLLWLLLTGKVPSKEQVDALSADLRKRASI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 PDHVYKTIDALPITAHPMTQFCTGVMALQTRSEFQKAYEKGIHKSKFWEPTYEDCLSLIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 PDHVYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLIA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 NVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       275 NVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 KDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYEVVPPIL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 LELGKVKNPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRALGLPLER 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SSNLDLRSELQELIPEQQERLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLDP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Gaps
                                                                                                                                                                                        BETA VULGARIS (SUGAR BEET).
URAPUTA, VIRDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEDPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
CARYOPHYLLIDAE; CARYOPHYLLALES; CHENOPODIACEAE; BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 SSGLDLRSELQELIPEQQDRLKKLKSEHGKVQLGNITVDMVLGGMRGMTGLLWETSLLDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 QVPVVAAYVYRRMYKNGQVIPLDDSLDYGGNFAHMLGFDSPQMLELMRLYVTIHSDHEGG
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                                                                                                                                                                                                                                                                                                          LA COGNATA U., LANDSCHUETZE V., WILLMITZER L., MUELLER-ROEBER
PLANT CELL PHYSIOL. 0:0-0(0).
--- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 81.3%; Score 2800; DB 10; Length 4 Local Similarity 85.7%; Pred. No. 0.00e+00; nes 373; Conservative 34; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE (21)-SYNTHASE (EC 4 1.3.7) (CONDENSING ENZYME)
(CITRATE CONDENSING ENZYME) (CITROGENASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          437 AA; 48881 MW; 003688CE CRC32;
                      437 AA
                                                          CREATED)
                    PPT;
                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X84228; E137433; -.
PFAM; PF00285; citrate_synt; 1.
MENDEL; 15201; BETvu;2977;mn15201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (OXALOACETATE TRANSACETASE)
JUT 5
Q96544,
Q96544,
016549,
01-FEB-1997 (TREMBLREL, 0
01-FEB-1997 (TREMBLREL, 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      454 PKSVIMEWLENHCKK 468
                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 PKSVIMEWLEKFCKR 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       OXALOACETATE
                                                                                                                                                        (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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024259
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYASE
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
              POPULUS DELTOIDES X POPULUS BALSAMIFERA SUBSP. TRICHOCARPA.
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUFHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255 SDMHELMKLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANOEV 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 LLWIKSVVEECGENITTEQLKDYVWKTLNSGKVVPGFGHGVLRKTVPRYTCQREFALKHL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 VPSKEQVDSLSQELRSRATVPDHVYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEK 194
                                                                                                                                                                                                                                                                                                                                                                                                                              61 GIHKSKYWEPTYEDSLSLIARVPIVASYIYRRIYKDGKVIPMNDSLVIGGNFSHMLGFDS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 GIHKSKLWEPTYEDSMSLIAQVPLVAAYVYRRMYKNGNTIPKDDSLDYGANFAHMLGFSS 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 PEMQELMRLYVTNHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANOEV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 PDDPLFQLVSKLYEVVPPVLTQLGKVKNPWPNVDAHSGVLLNYYGLTEARYYTVLFGVSR 300
                                                                                                                                                                                                                                                                                                                                                       1 MPTKEQVGALSKELRDRALVHDYVFKAIDALPVTAHPMTQFATGVMALQVQSEFQKAYEK 60
                                                                                                                      LA COGNATA U., LANDSCHUETZE V., WILLMITZER L., MUELLER-ROEBER R.; PLANT CELL PHYSIOL. 0:0-0(0).
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)0 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Cloning and sequence analysis of human citrate synthase cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
                                                                                                                                                                                                                                                                                 61.9%; Score 2.31; DB 10; Length 339; 84.5%; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.0%; Score 1997; DB 4; Length 466;
                                                                                                                                                                                                                                                                                                                        Indels
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01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                 Pred. No. 0.00e+00;
29; Mismatches 22;
                                                                                                                                                                                                                                               339 AA; 37834 MW; B2DA24A9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51706 MW; C0532604 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 SIGICSQLIWDRALGLPLERPKSVTMELLENHCKKA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  466 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- SIMILARITY: TO OTHER CITRATE SYNTHASES MELL; APOY1042, G2388815. -
PROSITE; PSO0480; CITRATE_SYNTHASE; 1.
LYASE; TRICAPBOXYLIC ACID CYCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                           EMBL; X84227; E276838; -. PFAM; PF00285; citrate_synt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITRATE SYNTHASE (EC 4.1.3.7).
                                                                    VIOLALES; SALICACEAE; POPULUS
                                                                                                                                                                                                                                                                                                 Local Similarity 84.5%; es 284; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPELIMINAPY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                466 AA;
                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OXALOACETATE
                                                                                                                                                                            OXALOACETATE
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                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                  Query Match
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075390;
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KETCHUR K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C.,
FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
KIRKNESS E.F., DOUGHPRIY R.A., MCKENBUS K., ADAMS M.D., LOFTUS B.,
PETERSON S., PETCH C.I., MCNEIL L.K., BADGEP J.H., GLOPEK A., ZHOU L.,
OVERBEEK R., GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T.,
SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII G., GAPLAND S.A.,
MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
                                                                                                                                                                                                                                                                      266
                                                                                                                                                                                                                                                                                                                                           326
                                                                                                                                                                                                                                                                                                                                                            87 PDEGIRFRGFSIPECQKLLPKAKGGEEPLPEGLFWLLVTGCIPTEEQVSWLSKEWAKRAA 146
                                                                                                                                                                 153
                                                                                                                                                                                                  506
                                                                                                                                                                                                                                                                                                       214 AQVPLVAAYVYRRMYKNGNTI-PKDDSLDYGANFAHMLGFSSSDMHELMKLYVTIHSDHE 272
                                                                                                                                                                                                                                                                                                                                                                                                               327 KLRDYIWNTLNSGRVVPGYGHAVLRKTDPRYTCQREFALKHLPNDPMFKLVAQLYKIVPN 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                  333 QLKDYAWKTLKSGKVVPGFGHGVLRKTDPPYTCQPEFALKHLPEDFLFGLVAKLYEVFLQ 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    387 VLLEQGKAKNPWPNVDAHSGVLLQYYGMTEMNYTVLFGVSRALGVLAQLIWSRALGFPL 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93
                                                    27 SASSINLKDILADLIPKEQARIKTFRQQHGKTVVGQITVDMMYGGMRGMKGLVYETSVLD 86
                      Gaps
                                                                                                                                                147 LPSHVVTMLDNFPTNLHPMSQLSAAVTALNSESNFAQAYARGISKTKYWELIYEDSVDLI
                                                                                                                                                                                                                                                                                                                                         GGNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLVWLTQLQKEVGKDVSDE
                                                                                      34 TSSGLDLRSELQELIPEQQDRLKKLKSEHGKVQLGNITVDMVLGGMRGMTGLLWETSLLD
                                                                                                                                                                                                                                154 VPDHVYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLI
                                                                                                                                                                                                                                                                    AKLPCVAAKIYRNLYWEGSGIGAIDSNLDWSHNFTNWLGYTDHQFTELMRLYLTIHSDHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARCHAEOGLOBUS FULGIDUS.
ARCHAEA; EUFYARCHAEOTA: ARCHAEOGLOBALES; ARCHAEOGLOBACEAE;
                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus."; NATURE 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
Best Local Similarity 62.2%; Pred. No. 0.00e+00;
Matches 267; Conservative 76; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 272; DB 1; Pred. No. 7.31e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42270 MW; DB9662BC CRC32;
                76; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-VC-16 / DSM 4304 / ATCC 49558;
MEDLINE; 98049343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00285; citrate_synt; 1. HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05,
08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.9%;
Best Local Similarity 29.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TREMBLREL. 01-JAN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITRATE SYNTHASE (CITZ)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       447 ERPKSMSTE 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           452 ERPKSVTME 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VENTER G.C.;
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Pred. No. 2.12e-26;
59; Mismatches 90; Indels 18; Gaps 15;
76; Conservative 64; Mismatches 95; Indels 23; Gaps 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 AANFLYMLHGEEPTKTAERALDMDLILHAEHEL-NASTFAARIAASTLADIYACVVAATG 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 GANFAHML-GFSSSDMHE-LMKLYVIIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 EEVLYLLWHGALPTGEELDAFSDELAAHRDLDDGVLDVARELAEQDESPMAALRTLVSAM 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 EGLLWLLIGKVPSKEQVDSLSQELRSRATVPDHVYKTIDALPVTAH-PMTQFATGVMAL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 SAYDESA-DFE-DV-TDR--EVNLEKAKRITAKMPSVLA-AYAR-FRRGDDYVEPDESLN 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 QVQSEFQKAYEKGIHKSKLWEPTYEDSMSLIAQVPLVAAYVYRRMYKNGNT-IPKDDSLD 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 HAANFLYMLNGEEPNEVLAETFDMALVLHADH-GLNASTFSAMVTSSTLSDLYSAVTSAI 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 GTLSGSLHGGANANVMRMLKDV-DD-SDMDPTEWVKD-A---LDRGERVAGFVHRVYNVK 271
                                                                                                                                                                              124 EGLLWLLLTGKVPSKEQVDSLSQELRSRATVPDHVYKTIDALPVTAHPMTOFATGVMALO 183
                                                                                                                                                                                                                                                                             97 TATSYLGSLDKKIA-VRTREETFNKAKDLIAKFPTIVAY-YHRI-RTGRNIIPPALEFSH 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 ILMGPLHGGAAQEVM---R-MLREVASP-RRAE--EYVKRKIEAGERIMGFGHRVYRGVM 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 GLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYAWKTLKSGKVVPGFGHGVLRKT- 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)
01-NOV-1998 (TREMELREL. 08, LAST ANDOTATION UPDATE)
01-NOV-1998 (TREMELREC. 08, LAST ANDOTATION UPDATE)
01-JAN-1998 (TREMELREC. 06, LAST ANDOTATION UPDATE)
                                                                                    44 EEVAYLLLYGELPKKYELQDFKIELAERRELPPQI---1-GL-LT-H-LPPYTHPMVVLR 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 YGANFAHML-GFSSSD-MHELMKLYVTIHSDHEGGNVSAHTGHLVASALSDFYLSFAAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-WFD II;
MADDOCKS D.G., CONNARIS H., HOUCH D.W., DANSON M.J.;
MADDOCKS D.G., CONNARIS H., HOUCH D.W., DANSON M.J.;
EMBLYED (CCT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ002075; E1154178; -.
PFAM; PF00285; citrate_synt; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         379 AA
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01-JAN-1998 (TREMBLREL. 05, LAST SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360 DPRYTCOREFALKHLPED 377
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Best Local Similarity 31.3%;
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272 DPR 274
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032705
032705;
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034002
034002;
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Pred. No. 1.14e-25;
88; Mismatches 131; Indels 25; Gaps 22;
                                                                                                                                                                                                                                                                                 GERIKE U., DANSON M.J., RUSSELL N.J., HOUGH D.W.;
"Sequencing and expression of the gene encoding a cold-active citrate
"Supthase from an Antarctic Dacterium, strain DS2-3R.";
EUR. J. BIOCHEM. 248:49-57(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 LLIYGELPSSEQYNNFTKKVAVHSLVNERLHYLFQTFCSSSHPMAIMLAAVGSL---SAF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 EQVAYLLWNSELPNDSELKAFVNFERSHRKLDENVKGAIDLLSTACHPMDVARTAVSVLG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 EGLLWLLLIGKVPSKEQVDSLSQELRSRATVPDHVYKTIDALPVTAHPMTQFAIGVMALQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 --AN-H-A--RA-QDSSP-EANLEKAMSLLATFPSVVAYDQRRR-RGEELIEPRED-LDY 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 SANFLWM-TFGEEAAPEVVEAFNVSMILYAEH-SFNASTFTARVITSTLADLHSAVTGAI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 GANFAHMLGFSSDMHELMKLY-VT-I-HSDHEGGNVSAHTGHLVASALSDPYLSFAAAL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 GALKGPLHGGANEAVMHTFEEIGIRKDESLDEAATRSKAWWVDALAQKKKVMGFGHRVYK 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 NGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYAWR--TLKSGKVVPGFGHGVLR 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275 NGDSRVPTMKS-ALDAMIKHYDRPEMLG-LYNGLEAAMEE-AKQIK-PNLDYPAGPTYNL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 KIDPRYICOREFALKHLPED-PLFOLVAKLYEVFLOFLONLAKLNPWPNVDAHSGVILINY 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.3%; Score 253; DB 2; Length 411; Best Local Similarity 27.4%; Pred. No. 2.11e-24; Matches 88; Conservative 93; Mismatches 110; Indels
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STRAIN-AB BACTERIUM;
STRAIN-AB BACTERIUM;
SAOULT D., RYDKINA E., ROUX V., EREMEEVA M., BALAYEVA N.;
SUBMITIED (UNV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL: U59712: G1390003; -.
PFAM; PF00285; cltrate_synt; 1.
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (FRAGMENT).
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) CITRATE SYNTHASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         417 YGLTEARYYTVLFGVSRALGICSQLIWDRALGLPLERP 454
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U85944; G2431774; -. PFAM; PF00285; citrate_synt; 1. SEQUENCE 379 AA; 41832 MW; 47DB0E16 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.6%;
Best Local Similarity 27.8%;
Matches 94; Conservative
                                                                                      ANTARCTIC BACTERIUM DS2-3R.
BACTERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   MEDLINE; 97454284
                                                                                                                                                                                                                        STRAIN-DS2-3R;
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SEQUENCE
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Q53115
Q53115;
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Query Match 7.3%; Score 251; DB 2; Length 411;
Best Local Similarity 27.2%; Pred. No. 4.83e-24;
Matches 87; Conservative 93; Mismatches 112; Indels 28; Gaps 19;
                                                                               247 AHMLGFSSS-DMH--E-LMK--LY-VTI-HSDHEGGNVSAHTGHLVASALSDPYLSFAAA 298
                                                                                                                                                                                                                  255 IASLWGPAHGGANEAVINMLKEIGSSENIPKYIAKAKDKNDPFRLMGFGHRV--YKNYDL 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 NGLAGPLHGLANQEVLLMIKSV-VEEC-GENISKEQLKDYAWKTLKSGKVVPGFGHGKL 357
                                                          145 ---YP-DLLNFK--EADYELTAIRMIAKIPTIAAMSYK--YSIGOPFIYPDNALDFTENF 196
                                                                                                                                       197 LHMM-FATPCEKYKVNPIIKNALNKIFILHADHEQ-NASTSTVRIAGSSGANPFACVSTG 254
                                                                                                                                                                                                                                                          299 LNGLAGPLHGLANQEVLLWIKSV--VEECGENISKEQLKDYAWKTLKSGKVVPGFGHGVL 355
                                                                                                                                                                                                                                                                                                   313 RAAVLKETCKEVLKELGQLDGNPLLQIAIELEAIALK-DEYFIERKLYPNVDFYSGIIYK 371
                                                                                                                                                                                                                                                                                                                                         357 RKTDPRYTCQREF-ALKHLPEDPLFQLVAKLYEVFLQFLQNLAKLNPWPNVDAHSGVLLN 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 LLIYGELPSGEQYNNFTKQVAHHSLVNERLHYLFQTFGSSSHPMAIMLAAVGSL---SAF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 ---YP-DLLNFK--EADYELTAIRMIAKIPTIAAMSYK--YSIGQPFIYPDNSLDFTENF 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 LHMMFATPCTKYTVNPIIKNALNKIFILHADHEQ-NASTSTVRIAGSSGANPFACISTGI 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 AHML-GFSSSD--MHELMK--LY-VTI-HSDHEGGNVSAHTGHLVASALSDPYLSFAAAL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 ASLWGPAHGGANEAVINMLKEIGSSEYIPKYIAKAKDKNDPFRLMGFGHRV--YKNYDPR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 LLLTGKVPSKEQVDSLSQELRSRATVPDHVYKTIDALPVTAHPMTQFATGVMALQVQSEF 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RACULT D., RYDKINA E., ROUX V., EREMEEVA M., BALAYEVA N.; SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)O +
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RICKETTSIACEAE; RICKETTSIEAE; RICKETTSIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER 411 411
SEQUENCE 411 AA; 46162 MW; 9921533A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   411 AA.
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-!- SIMILAPITY: TO OTHER CITRATE SYNTHASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITPATE SYNTHASE (EC 4 1 3 7) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U59731; G1390011; --
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
PFAM; PF00285; Citrate_Synt; 1
LYASE; TRICARBOXYLIC ACID CYCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                 372 AMGIP-SQMFTVLFAIARTVG 391
                                                                                                                                                                                                                                                                                                                                                                                                                      416 YYGLTEARYYTVLFGVSRALG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Q59777
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Query Match 7.3%; Score 250; DB 2; Length 411;
Best Local Similarity 27.2%; Pred. No. 7.32e-24;
Matches 87; Conservative 93; Mismatches 112; Indels 28; Gaps 19;
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314 AAVLKETCKEVLKELGQLDNNPLLQIAIELEAIALK-DEYFIERKLYPNVDFYSGIIYKA 372
                                      358 KTDPRYTCQREF-ALKHLPEDPLFQLVAKLYEVFLQFLQNLAKLNPWPNVDAHSGVLLNY 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 LLIYGELPSGEQYNNFTKQVAHHSLVNERLHYLFQTFCSSSHPMAIMLAAVGSL---SAF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 LLLTGKVPSKEQVDSLSQELRSRATVPDHVYKTIDALPVTAHPMTQFATGVMALQVQSEF 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 ---YP-DLLNFK--EADYELTAIRMIAKIPTIAAMSYK--YSIGQPFIYPDNSLDFTENF 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 LHMMFATPCTKYKVNPIIKNALNKIFILHADHEQ-NASTSTVRIASSSGANPFACISTGI 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 AAVLKETCKEVLKELGQLDNNPLLQIAIELEAIALK-DEYFIERKLYPNVDFYSGIIYKA 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROUX V., RYDKINA E., EREMEEVA M., RAOULT D.;
SUBMITTED (COT1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF
OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -! - CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)0 +
                                                                                                                                                                                                                                                                                                                                                                  BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RICKETTSIALES;
                                                                                                                                                                                                                                         01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
GLTAATE SYNTHASE (EC 4.1.3.7) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411 411 411 411 411 411 AA; 46266 MW; A54EAICF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    431 AA.
                                                                                                                                                                                                      411 AA.
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-!- SIMILARITY: TO OTHER CITRATE SYNTHASES.
EMBL; U74756; G1658283; --
PROSTIE; PSO0480; CITRATE_SYNTHASE; 1.
PFAM: PFO0285; citrate_synt; 1.
LYASE; TRICARBOXYLIC ACID CYCLE.
                                                                                                                                                                                                                                                                                                                                                                                      RICKETTSIACEAE, RICKETTSIEAE; RICKETTSIA
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01-JAN-1998 (TREMBLREL. 05, CREATED)
                                                                                                                                                                                                      PRT;
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                                                                                                        417 YGLTEARYYTVLFGVSRALG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417 YGLTEARYYTVLFGVSRALG 436
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                                                                               373 MGIP-SQMFTVLFAIARTVG
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                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                 RICKETTSIA MONTANA.
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NON_TER
SEQUENCE
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P77936
P77936;
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033066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 LLIYGELPATDQLAEFTHRIQRHTMLHEDLKRFYDGFPRNAHPMPVLSSVVNALSA-Y-Y 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 QDALD-PMDNGQV-ELS---TIRLLAKLPTIAAYAYKKSVGQPFLYP-DNAFSLVENFLR 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 M-LGFSS-S-DMH-ELMK-LYVT-I-HSDHEGGNVSAHTGHLVASALSDPYLSFAAALNG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           318 RARIVKEQADKILVKLGGDDDLLNIAKGLEEAALT-DDYFIERKLYPNVDFYTGLIYRAL 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 MTFGLPAEPYEPDPEVVRALDMLFILHADHEQ-NCSTSTVRLVGSSRANLFTSISGGINA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262 LWGPLHGGANQAVLEMLEGI-RESGDDVG-GFVQK-V-KNCQAGVKLMGFGHRVYKNYDP 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362 RYTCQREFA---LKHLP-EDPLFQLVAKLYEVFLQFLQNLAKLNPWPNVDAHSGVLLNYY 417
                                                                                                                                                                                                                                                                        EIGLMEIER K., HONORE N., WOODS S.A., CAUDRON B., COLE S.T.; "Use of an ordered cosmid library to deduce the genomic organization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                         BACTERIA: FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE; MYCOBACTERIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302 LAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYAWKTLKSGKVVPGFGHGVLRKTDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91; Mismatches 110; Indels 26;
                                                                                                                                                                                                                                                                                                                                                              -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
                                                                                                                                                                                                                                                                                                     of Mycobacterium leprae.";
MOL. MICROBIOL. 7:197-206(1993).
-:- CATALYTIC ACTIVITY: CITRAIE + COA - ACETYL-COA + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RICKETTSIALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 431;
                                                                                                                                    BADCOCK K., CHURCHER C.M.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                               SEQUENCE FROM N.A.
PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
01-Jan-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (EC 4.1.3.7).
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
GLTRATE SYNTHASE (EC 4.1.3.7) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.3%; Score 252; DB 2;
28.2%; Pred. No. 3.19e-24;
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PFAM; PF00285; Citrate_Synt. 1.
TASE; TRICARBOXYLIC ACID CYCLE.
SEQUENCE 431 AA; 48111 MW; ICFA87BB CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                           OXIDATIVE METABOLISM
-!- SIMILARITY: TO OTHER CITRATE SYNTHASES.
EMBL; 299494; E350411; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 28.2%;
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |: :| :||||:::|
418 GLTEARYYTVLFGVSR 433
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                                                          MYCOBACTERIUM LEPRAE.
                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE; 93188700.
                                                                                                                                                                                                                                                                                                                                                   OXALOACETATE
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Q60047
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1D Q6
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Query Match 7.2%; Score 247; DB 2; Length 411;
Best Local Similarity 26.9%; Pred. No. 2.54e-23;
Matches 86; Conservative 94; Mismatches 112; Indels 28; Gaps 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 LLLTGKVPSKEQVDSLSQELRSRATVPDHVYKTIDALPVTAHPMTQFATGVMALQVQSEF 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 ---YP-DLLNFK--EADYELTAIRMIAKIPTIAAMSYK--YSIGQPFIYPDNALDFTENF 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 QKAYEKGIHKSKLWEPTYE-DSMSLIAQVPLVAAYVYRRMYKNGNT-IPKDDSLDYGANF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 LHMMFATPCTKYTVNPIIKNALNKIFILHADHEQ-NASTSTVRIAGSSGANPFACISTGI 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 ASLWGPAHGGANEAVINMLKEIGSSEYIPKYIAKAKDKNDPFRLMGFGHRV--YKNYDPR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 NGLAGPLHGLANQEVLLWIKSV-VEEC-GENISKEQLKDYAWKTLKSGKVVPGFGHGVLR 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 AAVLKETCKEVLKELGQLDNNPLLQIAIELEAIALK-DEYFIERKLYPNVDFYSGIIYKA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358 KTDPRYTCQREF-ALKHLPEDPLFQLVAKLYEVFLQFLQNLAKLNPWPNVDAHSGVLLNY 416
                                                                                                 STRAIN-NTT-118;
RAOULT D., RYDKINA E., ROUX V., EREMEEVA M., BALAYEVA N.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CITRAIE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF
                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411
46095 MW; 274AAD7C CRC32;
                                                                                                                                                                                                                                                                                                                                           -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- SIMILARITY: TO OTHER CITRATE SYNTHASES.
EMBL: U59726; G1390019; -.
RICKETTSIACEAE; RICKETTSIEAE; RICKETTSIA
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U59726; G1390019; -.
PROSITE; PSOMARO; CITRATE_SYNTHASE; 1.
PFAM; PF00285; Citrate_synt; 1.
LYASE; TRICARBOXVIIC ACID CYCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: Fri Oct 22 17:09:58 1999
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417 YGLTEARYYTVLFGVSRALG 436
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                                                                                                                                                                                                                                                OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411 4
411 AA;
                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        OXALOACETATE
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SEQUENCE
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Matches

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PROSITE; PS00480; CITRATE_SYNTHASE; 1.
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                                    PFAM; PF00285; citrate_synt; 1
HSSP; P23007; 5CSC.
                                                                                                                                                                                                            472 AA; 52941 MW;
                                                                                                                                                                                                                                                  Match 66.5%;
Local Similarity 68.9%;
                                                                                                                                                                                                                                                                                         Conservative
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355
407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 28-464.
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                                                                                            MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 89000665
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                                                                                                                                                                                                                                                                                         328;
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PO0889;
                                                                                                                                                   ACT_SITE
                                                                                                                                                                   ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -:- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-:- SUBUNIT: HOMODIMER.
-:- SUBCELLULAR LOCATION: MITOCHONDRIAL MAIRIX.
-:- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MACNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                 60 SDLGKAQLGNITIDVVIGGMRGMTGLLWETSLLDPDEGIRFRGLSIPECQKLLPAAKPDG 119
                                                                                                                                                                     61 SDM-KGSIGNITVDMVLGGMRGMTGLLWKPHYLDPDEGIRFRGLSIPECQKVLPAAKPGG 119
                                                                                                                                                                                                          120 EPLPEGLLWLLIGKVPSKEQVDGLSKELRDRATVPDYV-YKAIDALPVSAHPMTQFASG :78
                                                                                                                                                                                                                                  179 VMALQVQSEFQEAYEKGIHKSKSWEPTSEDSLNLIARVPVVAAYVYQRIYKDGKIIPKDD 238
                                                                                                                                                                                                                                                                                                                         180 VMALQVQSEFQKAYEKGIHKSKYWEPTYEDSMNLIAQVPLVAAYVYRRMYKNGDIIPKDE 239
                                                                                                                                                                                                                                                                                                                                                                                   239 SLDYGGNFSHMLGFDDPKMLEL-MRLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFLA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                          298 ALNGLAGPLHGLANQEVLLHIKSVVDECGENVTTEQLKDYVWKTLNSGKVVPGFGHGVLR 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                358 KIDPRYTCQREFALKHLPDDPLFQLVSKLYEVVPPILTKLGKVKNPWPNVDAHSGVLLNH 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 KTVPRYTCQREFAMKHLPEDPLFQLVSKLYEVFLLFLQNLAKLK-PWPNVDAHSGVLLNY 418
                                                        1 MASLRSATALSRLRSRAGQQSNLSNSVRWLQMQSSADLDLHSQL-KEMIPEQQERLKKVK 59
                                                                              56; Mismatches 41; Indels 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNGER E.A., HAND J.M., CASHWORE A.R., VASCONCELOS A.C.;
"Isolation of a cDNA encoding mitochondrial citrate synthase from
Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  418 FGLAEARYYTVLFGVSRSLGICSQLIWDRALGLPLERPKSVTLDWIEKNCKKA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLANT MÖL. BIÖL. 13:411-418(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1991 (REL. 17, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
CITRATE SINTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY
    78.4%; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             472 AA.
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                      371; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 91370823.
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CISY\_ARATH P20115;

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EMBL; X17528; E1188578; -. .PIR; JA0149; YKMUM.

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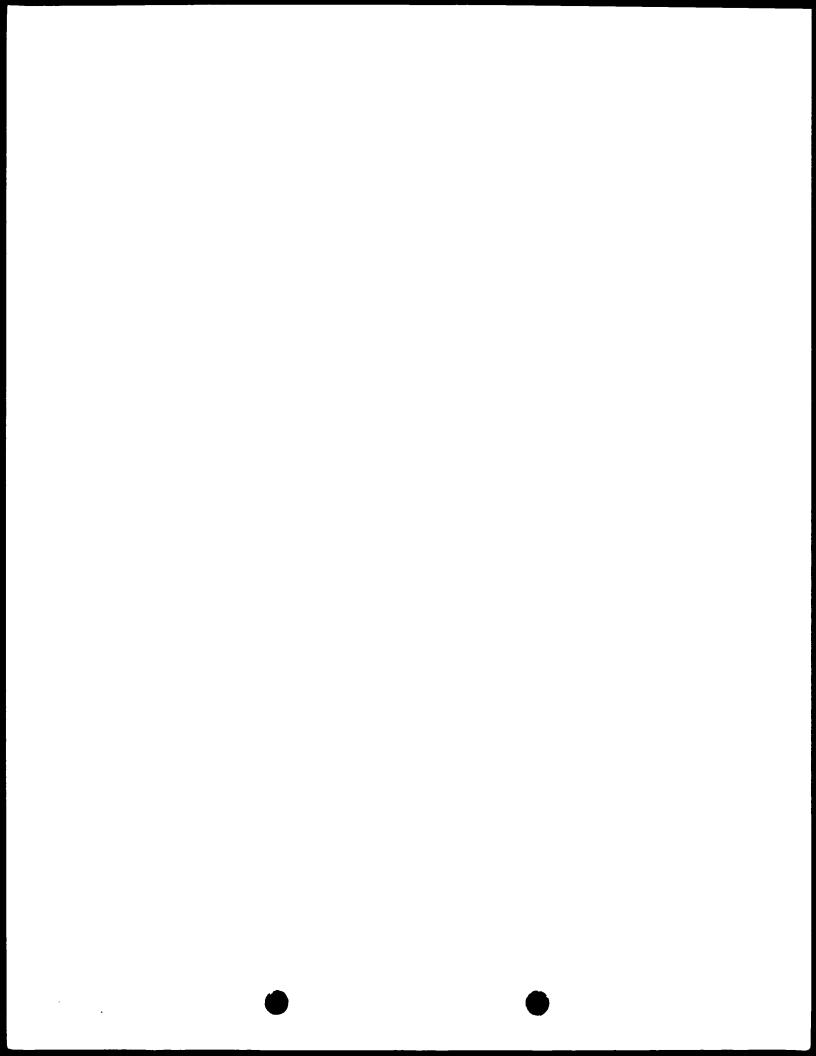
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Gaps 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 KSEHGKVQLGNITVDMVIGGMRGMTGLLWETSLLDPEEVFALGDCRLPECQKALLPTAQS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 GGLNHYRRSFVASLNWKGTL-AKSKLKH-CRKTWNRAAVSDYV-YNAIDALPSTAHPWTQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 GG-EPLPEGLL-WILLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 PSDKSLDYGANFSHMLGFDDERLKEL-MRLTSPSTVMHEGGNVSAHTGHLVGSALSDPYL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFAAALNGLAGPLHGLANQEVLLWIKSVVEECGEDISKEQLKEYVWKTLNSGKVIPGYGH 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    356 GVLRNTDPRYVCQREFALKHHPDDPLFQ-CCKLMKL-ASCLTELESEEPWPNVDAHSGVL 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MVFFRSVSAFTRLRSRVQGQQSSLSNSVRWIQMQSSTDLDLKSQL-QELIPEHKDRLKKL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 82231993.
BLOXEAM D.P., PARMELEE D.C., KUMAR S., WALSH K.A., TITANI K.; "Complete amino acid sequence of porcine heart citrate synthase."; BIOCHEMISTRY 21:2028-2036(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVANS C.T., OWENS D.D., SUMEGI B., KISPAL G., SRERE F.A.; *Isolation, nucleotide sequence, and expression of a cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          414 LNHYGLTEARYYTVLFGVSRSLGICSQLIWDRELLLALERPKSVTMDWLEAHCKKA 469
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                                                                                                                                                                                                                                                                                                                                                                                            Score 2305; DB 1; Length 472;
Pred. No. 0.00e+00;
60; Mismatches 76; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (REL. 12, LAST SEQUENCE UPDATE)
01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                      CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
i, 954AFA81 CRC32;
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                                                                                                           MITOCHONDRION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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983 TAGCCGGACCACTICATGGTTTAGCCAATCAGGAAGTTTTGCTATGGATAAAATCTGTTG 1042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               983 GATACACATGCCAAAGAGAATTTGCGTTGAAGCACTTGCCTGATGACCCATTTTTTCAAT 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 863 TIGATGAATGTGGAGAACATCTCGACAGAGCAGTTGAAAGATTATGTTTGGAAGACAC 922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         803 IGGCIGGGCCACICCAIGGAITAGCCAACCAGGAAGICCIGCIGIGGAITAAAICAGIIG 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        443 AAGGTCTTCTCTGGCTTCTTTTAACAGGAAAGGTGCCATCAAAAGAGCAAGTGAATTCAA 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    386 AIGCICTACCTAITACGGCTCAICAATGACTCAGITITGCACTGGTGTIAIGGCCTTAC 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              446 AGACTCGAAGCGAATTTCAGAAGGCATATGAGAAAGGGATCCATAAGTCAAAGTTTTGGG 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             623 AGGTTCAAAGTGAATTTCAAAAGGCATACGAGAAAGGGGATTCACAAATCAAAGTATTGGG 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                506 AGCCAACATAIGAGGACIGCCITAGIIIGAIIGCICAAGIICCIGIIGIIGCAGCIIAIG 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  683 AACCAACATATGAGGATTCCATGAAICTGATTGCTCAAGTTCCACTTGTTGCTGCTTATG 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    566 TITATCGGAGGATGTATAAGAATGGACAAGTAATACCGCTGGATGACTCCCTTGATTATG 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              626 GTGGAAATTTCGCACACATGTTGGGATTTGATAGCCCTCAGATGCTTGAGCTG---ATGC 682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     743 ATTTGGTGGGTAGTCCACTTTCAGATCCTTATTTGTCATTTGCAGCAGCATTAAATGGTT 802
                                                                                                                                                                                                                                                                                                  89 GTTTCCAGCTGGGGAATATCAATGTTGACATGGTATTGGGCGGAATGAGAGGAATGACTG 148
                                                                                                                                                                                                                                                                                                                                                  265 GGTTCAAT-TGGG-AACATCACAGTTGATATGGTTCTTGGTGGAATGAGAGGAATGACAG 322
                                                                                                                                                                                                                                                                                                                                                                                                  149 GITTACTTTGGGAGACTTCCTTACTCGACCCAGAAGAGGGGTATCCGGTTCAGGGGTTTTT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                 323 GATTACTGTGGAAACCTCATTACCTTGACCCTGATGAGGGAATTCGCTTCCGGGGGTTGT 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 CIATACCTGAATGCCAGAAACTTTTACCCGCTGCAAGTGCTGGTGCAGAGCCATTGCCTG 268
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Pred. No. 0.00e+00;
0; Mismatches 261; Indels 12;
TVLFGVSRSLGICSQLIWDPALGLPLEPPKSVTMEWLEKFCKPRA"
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Local Similarity 78.5%;
Les 997; Conservative
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NVSAHTGHLVGSALSDPYLSFAAALNGLAGPLHGLANQEVLLMIKSVVEECGEDISKE
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DCRLPECQKALLPTAQSGGLNHYRRSFVASLNWKGTLAKSKLKHCRKTWNRAAVSDYV
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CLTELESEEPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRELLLA
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
Rosidae; Capparales; Brassicaceae; Arabidopsis.
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Best Local Similarity 75.6%; Pred. No. 0.00e+00;
Matches 1087; Conservative 0; Mismatches 317; Indels 34; Gaps 29;
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Unger, E.A., Hand, J.M., Cashmore, A.R. and Vasconcelos, A.C.
Isolation of a cDNA encoding mitochondrial citrate synthase fro
Arabidopsis thaliam Plant Mol. 13 (4), 411-418 (1989)
                                                                                                        ATMICITRN 1680 bp mRNA PLN 26-NOV-1997
Arabidopsis thaliana mRNA for mitochondrial citrate synthetase.
X17528
                             1163 GATATACATGCCAGAGAGAGTTCGCTATGAAGCATTTGCCTGAAGATCCACTGTTTCAAC 1222
                                                                             1043 TGGTGTCAAAGTTGTATGAAGTGGTGCCTCCTATTCTATTAGAGGTTGGAAAGGTAAAGA 1102
                                                                                                                                                                                1103 ATCCATGGCCTAATGTTGATGCTCATAGTGGAGTTTTGCTGAACCACTATGGTTTGACAG 1162
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                                                                                                                                                                                                                                                                                1163 AAGCAAGATACTATACGGTTTTGTTTGGGGTATCAAGGAGTCTTGGAATATGCTCACAGC 1222
                                                                                                                                                                                                                                                                                                             57 AATGGTGTTTTTCCGCAGCGTATCGGCCTTTACTAGGCTGAGGTCTCGCGTCCAGGGCCA 116
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
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/protein_id-"CAA35570.1"
/db_xref-"PID:el188578"
/db_xref-"PID:92652924"
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citrate synthase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    472 ITAGCAAAGAGCAAGIIGAAGCACI-GIGGAAAGACIIGGA-AC-CGIGCIGC-IGIGIC 527
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                                                              177 CCTGAAGTCGCAGCTG---CAAGAGTTAATTCCGGAACACAAGGACGCGTCTGAAGAACT 233
                                                                                                                                                             189 TCTGCGTTCTGAGCTGGTACAAGAATTGATTCCTGAACAACAGGATCGCCTGAAAAAGAT 248
                                                                                                                                                                                                         234 GAAGTCAGAACATGGGAAGGTCCAACTGGGAAACATCACTGTTGATATGGTTATTGGTGG 293
                                                                                                                                                                                                                                352 ITCGCTTTAGGGGATTGTCGACTTCCTGAGTGCCAGAAAGCCCTATTACCTACTGCCCAG 411
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  72 AAIGGIGIICIACCGIAGCGIIICGIIGCIGICAAAGCIGGGGIGIGAGA--C-GGIGCA 128
                                      117 ACAATCTICACICAGCAATICIGICAGATGGATICAGATGGAGGGGGGCTCTACGGAGCTGGGA 176
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/db_xref="GI:1648926"
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VMALQVQSEFQKAYEKGIHKSKYWEPTYEDSLSLIARVPIVASYIYRRIYKDGKVIPM
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**RAALNGLAGPLHGLANQEVLLMIKSVVDECGENTTPEDLIDVWWTLNSGKVVPGFG
HGVLRKTVPRYTCORFALKHLPDDELFOLVSKLYEVVPPVLTOLGKVKNPMPWDAH
SGVLLNYYGLTERRYYTVLFGVSRSIGICSQLIWDRALGLPLERPKSVTWELLENHCK
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Cit1 gene; citrate synthase.
Cit1 gene; citrate synthase.
Populus balsamifera subsp. trichocarpa X Populus deltoides.
Populus balsamifera subsp. trichocarpa X Populus deltoides
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Rosidae; Violales; Salicaceae; Populus.
1 (bases 1 to 1378)
La Cognata, U., Landschuetze, V., Willmitzer, L. and Mueller-Roeber, B.
2 (bases 1 to 1378)
La Cognata, U. 1378)
                                                                                                                                                                                                             1378 GCICTIGGCATITGCTCTCAGCTAATITGGGACCGACTCTTGGATGCCGCTAGAGG 1437
                                                                                                                                                                                     1297 CTGAACCACTATGGTCTAACCGAAGCAAGGTACTACACCGTGCTCTTTGGTGTTTCAAGG 1356
                                                                                                                                                                                                                                                                               1198 TIGCCIGAAGAICCACIGITICAACIGGITICAAAACICTACGAAGIIIICCICCIGITC 1257
                                                                                                                                       1258 TTACAGAACTTGGCAAAGTTAAAACCTTGGCCAAATGTTGATGCCCACAGTGGTGTGTTG 1317
                                                                                                                                                                                                                                                                                                                                                                      1417 CCAAAGAGTGTTACCATGGACTGGCTTGAAGCCCATTGTAAGAAAGCTTCATCTGCTT 1474
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1183 CATCCTGACGACCACT-TTTCCAGTG-TTGCAAG-CT-TATGAAGTTGGCCTCCTGT-C
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                                                                                           1238 TCACTGAGCTTGAAAGTGA-AGAACCCTGGCCAAATGTTGATGCTCACAGTGGGGTCTTG
                                                                                                                                                                                                                                                                                                                                                                                                1438 CCAAAGAGTGTCACAATGGAGTGGCTTGAGAACCAGTGCAAGAAGGATGAATTGTTT
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Genbiologische Forschung, Berlin GmbH, Ihnestrasse 63,
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